

GenCore version 5.1.8
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 OM protein - protein search, using sw model
 Run on: May 9, 2006, 12:04:09 ; Search time 49.6667 Seconds
 (without alignments)
 97.312 Million cell updates/sec

Title: US-10-796-158-5
 Perfect score: 80
 Sequence: 1 YCYCFWKTCT 11

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_21.*
 1: Geneseqp1980s.*
 2: Geneseqp1990s.*
 3: Geneseqp2000s.*
 4: Geneseqp2001s.*
 5: Geneseqp2002s.*
 6: Geneseqp2003as.*
 7: Geneseqp2003bs.*
 8: Geneseqp2004s.*
 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	11	8	ADS74377 Somatosta
2	69	86.2	11	2	AAW48645 Somatosta
3	69	86.2	11	8	ADM35520 Somatosta
4	69	86.2	11	9	ADM95422 Somatosta
5	64	80.0	9	2	AAW48642 Somatosta
6	64	80.0	10	7	AD114934 Somatosta
7	64	80.0	10	8	ADU05247 Cyclic so
8	64	80.0	11	7	AD114956 Somatosta
9	64	80.0	11	7	AD114951 Somatosta
10	64	80.0	11	7	AD114959 Somatosta
11	64	80.0	11	7	AD114954 Somatosta
12	64	80.0	11	8	ADS74378 Somatosta
13	64	80.0	11	7	ADU05246 Cyclic so
14	64	80.0	12	7	ADU14894 Somatosta
15	64	80.0	13	7	AD114957 Somatosta
16	64	80.0	13	7	AD114957 Somatosta
17	64	80.0	14	7	AD114952 Somatosta
18	64	80.0	15	6	ABR42184 Somatosta
19	64	80.0	15	7	AD114935 Somatosta
20	64	80.0	15	7	AD114898 Somatosta
21	64	80.0	20	6	ABR42192 Peptide a
22	64	80.0	20	6	ABR42198 Somatosta
23	64	80.0	20	7	AD114936 Somatosta
24	64	80.0	20	7	AD114897 Somatosta

25	64	80.0	22	6	ABR42181	AbR42181 Somatosta
26	64	80.0	25	6	ABR42199	AbR42199 Somatosta
27	64	80.0	30	6	ABR42197	AbR42197 Somatosta
28	62.5	78.1	11	8	ADS74379	AdS74379 Somatosta
29	61	76.2	10	8	ADU05266	Cyclic so
30	61	76.2	11	8	ADU05270	Cyclic so
31	61	76.2	11	8	ADU05281	Cyclic so
32	61	76.2	12	3	AAI94484	Human som
33	61	76.2	12	3	AAI94487	Human som
34	59	73.8	10	7	AD114944	Somatosta
35	59	73.8	11	7	AD114943	Somatosta
36	59	73.8	12	3	AAI94481	Human som
37	59	73.8	12	3	AAI94489	Human som
38	59	73.8	12	3	AAI94485	Human som
39	59	73.8	12	3	AAI94490	Human som
40	59	73.8	12	3	AAI94480	Human som
41	59	73.8	12	6	ABR42183	Somatosta
42	59	73.8	14	3	AAI94482	Human som
43	59	73.8	14	3	AAI94483	Human som
44	59	73.8	15	7	AD114945	Somatosta
45	57	71.2	8	6	AAO26828	Somatosta
46	57	71.2	8	6	AAO26832	Somatosta
47	57	71.2	8	6	AAO26830	Somatosta
48	57	71.2	8	6	AAO26825	Somatosta
49	57	71.2	8	6	AAO26827	Somatosta
50	57	71.2	8	6	AAO26826	Somatosta
51	57	71.2	8	6	AAO26829	Somatosta
52	57	71.2	8	6	AAO26831	Somatosta
53	57	71.2	14	8	ADU97615	Novel cyt
54	57	71.2	14	8	ADU97600	Novel cyt
55	57	71.2	14	8	ADU97630	Novel cyt
56	57	71.2	15	8	ADU97599	Novel cyt
57	57	71.2	15	8	ADU97629	Novel cyt
58	57	71.2	15	8	ADU97614	Novel cyt
59	57	71.2	16	8	ADU97616	Novel cyt
60	57	71.2	16	8	ADU97631	Novel cyt
61	57	71.2	16	8	ADU97601	Novel cyt
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66	56	70.0	10	8	ADU05243	Cyclic so
67	56	70.0	10	8	ADU05276	Cyclic so
68	56	70.0	10	8	ADU05235	Cyclic so
69	56	70.0	10	8	ADU05239	Cyclic so
70	56	70.0	10	8	ADU05271	Cyclic so
71	56	70.0	10	8	ADU95289	Novel cyt
72	56	70.0	10	8	ADU96133	Novel cyt
73	56	70.0	10	8	ADU96505	Novel cyt
74	56	70.0	10	8	ADU95827	Novel cyt
75	56	70.0	10	8	ADU95290	Novel cyt
76	56	70.0	10	8	ADU96194	Novel cyt
77	56	70.0	10	8	ADU97505	Novel cyt
78	56	70.0	10	8	ADU97103	Novel cyt
79	56	70.0	10	8	ADU95224	Novel cyt
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81	56	70.0	10	8	ADU95758	Novel cyt
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83	56	70.0	10	8	ADU96537	Novel cyt
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85	56	70.0	10	8	ADU97531	Novel cyt
86	56	70.0	10	8	ADU97068	Novel cyt
87	56	70.0	10	8	ADU97050	Novel cyt
88	56	70.0	10	8	ADU95318	Novel cyt
89	56	70.0	11	7	AD114990	Somatosta
90	56	70.0	11	7	AD114972	Somatosta
91	56	70.0	11	8	ADU05242	Cyclic so
92	56	70.0	11	8	ADU05238	Cyclic so
93	56	70.0	11	8	ADU05252	Cyclic so
94	56	70.0	11	8	ADU05234	Cyclic so
95	56	70.0	11	8	ADU05280	Cyclic so
96	56	70.0	11	8	ADU05275	Cyclic so
97	56	70.0	11	8	ADU95644	Novel cyt

244 56 70.0 14 8 ADU97504 Novel cyt
245 56 70.0 15 7 ADI14994 Somatostata
246 56 70.0 15 7 ADI14976
247 56 70.0 15 8 ADU95845 Novel cyt
248 56 70.0 15 8 ADU96150 Novel cyt
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334 55 68.8 10 3 AAY94488 Human som
335 55 68.8 10 7 ADI14955 Somatostata
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339 55 68.8 11 7 ADI14958 Somatostata
340 55 68.8 12 6 ABR42190 Peptide a
341 55 68.8 12 6 ABR42188 Peptide a
342 55 68.8 12 6 ABR42189 Peptide a
343 55 68.8 12 7 ADE28588 Cytotoxic
344 55 68.8 12 7 ADE28589 Cyclic cy
345 55 68.8 12 7 ADE28611 Cytotoxic
346 55 68.8 12 7 ADE28612 Cyclic cy
347 55 68.8 13 7 ADE28593 Cytotoxic
348 55 68.8 13 7 ADE28594 Cyclic cy
349 55 68.8 14 7 ADE28595 Cytotoxic
350 55 68.8 15 6 ABR42182 Somatostata
351 55 68.8 15 6 ABR42206 Somatostata
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353 55 68.8 15 6 ABR42202 Somatostata
354 55 68.8 15 6 ABR42200 Somatostata
355 55 68.8 15 6 ABR42191 Peptide a
356 55 68.8 15 6 ABR42209 Somatostata
357 55 68.8 15 6 ABR42205 Somatostata
358 55 68.8 15 6 ABR42180 Control p
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360 55 68.8 15 6 ABR42201 Somatostata
361 55 68.8 15 7 ADE28596 Cytotoxic
362 55 68.8 15 7 ADI14896 Somatostata
363 55 68.8 16 6 ABR42208 Somatostata
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367 55 68.8 18 6 ABR42210 Somatostata
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370 55 68.8 19 7 ADE28600 Cytotoxic
371 55 68.8 20 7 ADE28601 Cytotoxic
372 55 68.8 21 6 ABR42187 Peptide a
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380 55 68.8 27 7 ADE28608 Cytotoxic
381 54 67.5 9 1 AAP40513 Sequence
382 53 66.2 8 1 AAP10586 GH, gastr
383 53 66.2 8 1 AAP10593 GH, gastr
384 53 66.2 8 1 AAP20161 Peptide f
385 53 66.2 8 1 AAP40368 Sequence
386 53 66.2 8 1 AAP50504 Mini-soma
387 53 66.2 8 1 AAP82525 Bridged s
388 53 66.2 8 2 AAR05177 Somatostata
389 53 66.2 8 2 AAR05188 Somatostata

390	53	66.2	8	2	AAR14236	Aar14236 Somatosta	463	53	66.2	8	6	ABG99248	Abg99248 Somatosta
391	53	66.2	8	2	AAR14227	Aar14227 Somatosta	464	53	66.2	8	6	AAO26852	Aao26852 Somatosta
392	53	66.2	8	2	AAR10501	Aar10501 Pamote o	465	53	66.2	8	6	AAO26824	Aao26824 Somatosta
393	53	66.2	8	2	AAR11518	Aar11518 Somatosta	466	53	66.2	8	6	AAO26818	Aao26818 Somatosta
394	53	66.2	8	2	AAR26368	Aar26368 Somatosta	467	53	66.2	8	6	AAO26822	Aao26822 Somatosta
395	53	66.2	8	2	AAR28859	Aar28859 Somatosta	468	53	66.2	8	6	AAO26851	Aao26851 Somatosta
396	53	66.2	8	2	AAR23948	Aar23948 LH-RH, so	469	53	66.2	8	6	AAO26819	Aao26819 Somatosta
397	53	66.2	8	2	AAR40820	Aar40820 Octapepti	470	53	66.2	8	6	AAO26820	Aao26820 Somatosta
398	53	66.2	8	2	AAR41504	Aar41504 Somatosta	471	53	66.2	8	6	AAO26821	Aao26821 Somatosta
399	53	66.2	8	2	AAR41500	Aar41500 Somatosta	472	53	66.2	8	6	AAO26823	Aao26823 Somatosta
400	53	66.2	8	2	AAR39595	Aar39595 Somatosta	473	53	66.2	8	6	ABP55049	Abp55049 Octreotid
401	53	66.2	8	2	AAR31507	Aar31507 Somatosta	474	53	66.2	8	6	ABP55050	Abp55050 Octreotid
402	53	66.2	8	2	AAR31512	Aar31512 Somatosta	475	53	66.2	8	6	ADA41667	Ada41667 Cyclic pe
403	53	66.2	8	2	AAR37097	Aar37097 Octreotid	476	53	66.2	8	7	ADB88527	Adb88527 Somatosta
404	53	66.2	8	2	AAR42651	Aar42651 Somatosta	477	53	66.2	8	7	ABR83029	Abr83029 Somatosta
405	53	66.2	8	2	AAR42655	Aar42655 Somatosta	478	53	66.2	8	7	ADF61742	Adf61742 Somatosta
406	53	66.2	8	2	AAR56777	Aar56777 Somatosta	479	53	66.2	8	7	ADL114899	Adl114899 Somatosta
407	53	66.2	8	2	AAR50278	Aar50278 Octreotid	480	53	66.2	8	7	ADL16034	Adl16034 Octreotid
408	53	66.2	8	2	AAR76206	Aar76206 Somatosta	481	53	66.2	8	8	ADH63166	Adh63166 Octreotid
409	53	66.2	8	2	AAR76201	Aar76201 Somatosta	482	53	66.2	8	8	ADJ56707	Adj56707 Cyclic pe
410	53	66.2	8	2	AAR85572	Aar85572 Somatosta	483	53	66.2	8	8	ADM35518	Adm35518 Somatosta
411	53	66.2	8	2	AAR62014	Aar62014 Somatosta	484	53	66.2	8	8	ADR87508	Adr87508 Backbone
412	53	66.2	8	2	AAy17852	AAy17852 Backbone	485	53	66.2	8	8	ADR87485	Adr87485 Somatosta
413	53	66.2	8	2	AAW33184	AAw33184 Mono-DTPA	486	53	66.2	8	8	ADS12361	Ads12361 Octreote
414	53	66.2	8	2	AAW12315	AAw12315 Site-spec	487	53	66.2	8	8	ADU05219	Adu05219 Cyclic so
415	53	66.2	8	2	AAW19221	AAw19221 Octreotid	488	53	66.2	8	8	ADU95227	Adu95227 Novel cyt
416	53	66.2	8	2	AAW29371	AAw29371 Somatosta	489	53	66.2	8	8	ADU07144	Adu07144 Octreotid
417	53	66.2	8	2	AAW51854	AAw51854 Somatosta	490	53	66.2	8	9	ADM95415	Adm95415 Peptide #
418	53	66.2	8	2	AAW51861	AAw51861 Somatosta	491	53	66.2	8	9	ADM95416	Adm95416 Peptide #
419	53	66.2	8	2	AAW51666	AAw51666 Somatosta	492	53	66.2	8	9	ADM95412	Adm95412 Peptide #
420	53	66.2	8	2	AAy22040	AAy22040 Somatosta	493	53	66.2	8	9	ADM95413	Adm95413 Peptide #
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423	53	66.2	8	2	AAW45742	AAw45742 Somatosta	496	53	66.2	8	9	ADM95419	Adm95419 Peptide #
424	53	66.2	8	2	AAW97183	AAw97183 Somatosta	497	53	66.2	8	9	ADM95414	Adm95414 Peptide #
425	53	66.2	8	2	AAW97187	AAw97187 Somatosta	498	53	66.2	8	9	ADM95417	Adm95417 Peptide #
426	53	66.2	8	2	AAy04039	AAy04039 Octreotid	499	53	66.2	8	9	ADM95420	Adm95420 Peptide #
427	53	66.2	8	2	AAy04041	AAy04041 Octapepti	500	53	66.2	8	9	ADY51780	Ady51780 Cyclic pe
428	53	66.2	8	2	AAy29832	AAy29832 Bifunctio	501	53	66.2	8	9	ADZ99635	Adz99635 Somatosta
429	53	66.2	8	2	AAy23161	AAy23161 Somatosta	502	53	66.2	8	9	ADZ99636	Adz99636 Somatosta
430	53	66.2	8	2	ADH35402	Adh35402 Human som	503	53	66.2	9	1	AAP92299	Aap92299 Peptide s
431	53	66.2	8	2	ADH35403	Adh35403 Human som	504	53	66.2	9	2	AAR28860	Aar28860 Somatosta
432	53	66.2	8	2	ADH68004	Adh68004 Somatosta	505	53	66.2	9	2	AAR81662	Aar81662 Somatosta
433	53	66.2	8	2	ADH68003	Adh68003 Somatosta	506	53	66.2	9	3	AAy95247	Aay95247 Sandostat
434	53	66.2	8	2	ADI24864	Adi24864 Octreotid	507	53	66.2	9	3	ABH15191	Abh15191 Sandostat
435	53	66.2	8	2	ADK11155	Adk11155 Somatosta	508	53	66.2	9	7	ADL14930	Adl14930 Somatosta
436	53	66.2	8	2	ADK11156	Adk11156 Somatosta	509	53	66.2	9	7	ADL14962	Adl14962 Somatosta
437	53	66.2	8	3	AAy82555	AAy82555 Somatosta	510	53	66.2	9	7	ADL14937	Adl14937 Somatosta
438	53	66.2	8	3	AAAB06244	AAb06244 Somatosta	511	53	66.2	9	8	ADU05262	Adu05262 Cyclic so
439	53	66.2	8	3	AAy81017	AAy81017 Somatosta	512	53	66.2	9	8	ADU05244	Adu05244 Cyclic so
440	53	66.2	8	3	AAy81016	AAy81016 Somatosta	513	53	66.2	10	2	AAR14235	Aar14235 Somatosta
441	53	66.2	8	3	AAy83802	AAy83802 Somatosta	514	53	66.2	10	7	ADL14931	Adl14931 Somatosta
442	53	66.2	8	3	AAAB24186	AAb24186 Somatosta	515	53	66.2	11	7	ADL14900	Adl14900 Somatosta
443	53	66.2	8	3	AAAB24182	AAb24182 Somatosta	516	53	66.2	12	2	AAW48646	Aaw48646 Somatosta
444	53	66.2	8	3	AAAB19026	AAb19026 Amine aci	517	53	66.2	12	3	AAy98159	Aay98159 Thiol con
445	53	66.2	8	4	ABH77167	Abh77167 Octreotid	518	53	66.2	12	7	ADL14932	Adl14932 Somatosta
446	53	66.2	8	4	AAU05146	AAu05146 Receptor-	519	53	66.2	13	7	ADC68595	Adc68595 Thiol-con
447	53	66.2	8	4	AAW51439	AAw51439 Somatosta	520	52	65.0	8	1	AAP61467	Aap61467 Cyclic oc
448	53	66.2	8	4	AAy97708	AAy97708 Rat Urote	521	52	65.0	8	2	AAR14238	Aar14238 Somatosta
449	53	66.2	8	4	AAAB45664	AAb45664 Somatosta	522	52	65.0	8	2	AAR10503	Aar10503 Pamote o
450	53	66.2	8	4	AAU08826	AAu08826 Somatosta	523	52	65.0	8	2	AAR23950	Aar23950 LH-RH, so
451	53	66.2	8	4	AAU08827	AAu08827 Somatosta	524	52	65.0	8	2	AAR41503	Aar41503 Somatosta
452	53	66.2	8	4	AAU08925	AAu08925 Somatosta	525	52	65.0	8	2	AAR31509	Aar31509 Somatosta
453	53	66.2	8	5	AAE17934	AAe17934 Somatosta	526	52	65.0	8	2	AAR42654	Aar42654 Somatosta
454	53	66.2	8	5	ABB09976	Abb09976 Octreotid	527	52	65.0	8	2	AAR56779	Aar56779 Somatosta
455	53	66.2	8	5	ABB09974	Abb09974 Straight	528	52	65.0	8	2	AAR76203	Aar76203 Somatosta
456	53	66.2	8	5	ABP53367	Abp53367 Somatosta	529	52	65.0	8	2	AAW85571	Aaw85571 Somatosta
457	53	66.2	8	5	AAE15400	AAe15400 Somatosta	530	52	65.0	8	2	AAW51863	Aaw51863 Somatosta
458	53	66.2	8	5	AAE19360	AAe19360 Somatosta	531	52	65.0	8	2	Aay22042	Aay22042 Somatosta
459	53	66.2	8	5	AAE19364	AAe19364 Somatosta	532	52	65.0	8	2	AAy18227	Aay18227 Somatosta
460	53	66.2	8	5	ADH68884	Adh68884 Synthetic	533	52	65.0	8	2	AAW45741	Aaw45741 Somatosta
461	53	66.2	8	5	ADH68893	Adh68893 Synthetic	534	52	65.0	8	2	AAW97186	Aaw97186 Somatosta
462	53	66.2	8	6	ABG99249	Abg99249 Somatosta	535	52	65.0	8	2	ADH35405	Adh35405 Human som

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543 52 65.0 8 4 AAU08829 Aau08829 Somatosta 616
544 52 65.0 8 5 AAE19363 Aae19363 Somatosta 617
545 52 65.0 8 6 ABG99251 Abg99251 Somatosta 618
546 52 65.0 8 6 AAO26854 Aao26854 Somatosta 619
547 52 65.0 8 9 ADZ99638 Adz99638 Somatosta 620
548 52 65.0 4 4 AAB60181 Aab60181 His-Tyr-3 621
549 52 65.0 14 5 ABB04754 Aab04754 Arg-Gly-A 622
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551 51 63.7 11 8 ADU05250 Adu05250 Cyclic so 624
552 51 63.7 12 3 AAY94486 Aay94486 Human som 625
553 51 63.7 12 7 ADE28616 Ade28616 Cytotoxic 626
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556 51 63.7 15 7 ADI14907 Adi14907 Somatosta 629
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558 50 62.5 7 2 AAW97196 Aaw97196 Somatosta 631
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681 50 62.5 9 2 ADH35428 Adh35428 Human som 681

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683	50	62.5	9	2	ADH68017	Adh68017 Somatosta	756	50	62.5	9	6	AAO26865	Somatosta
684	50	62.5	9	2	ADH68023	Adh68023 Somatosta	757	50	62.5	9	6	AAO26869	Somatosta
685	50	62.5	9	2	ADH68024	Adh68024 Somatosta	758	50	62.5	9	6	AAO26861	Somatosta
686	50	62.5	9	2	ADH68019	Adh68019 Somatosta	759	50	62.5	9	6	AAO26859	Somatosta
687	50	62.5	9	2	ADH68029	Adh68029 Somatosta	760	50	62.5	9	6	AAO26872	Somatosta
688	50	62.5	9	2	ADH68011	Adh68011 Somatosta	761	50	62.5	9	6	AAO26873	Somatosta
689	50	62.5	9	2	ADH68025	Adh68025 Somatosta	762	50	62.5	9	6	AAO26867	Somatosta
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691	50	62.5	9	2	ADH68013	Adh68013 Somatosta	764	50	62.5	9	8	ADO80843	Synthetic
692	50	62.5	9	2	ADH68020	Adh68020 Somatosta	765	50	62.5	9	8	ADU05267	Cyclic so
693	50	62.5	9	2	ADH68022	Adh68022 Somatosta	766	50	62.5	9	8	ADU05224	Cyclic so
694	50	62.5	9	2	ADH68021	Adh68021 Somatosta	767	50	62.5	9	8	ADU05213	Cyclic so
695	50	62.5	9	2	ADK11174	Adk11174 Somatosta	768	50	62.5	9	9	ADV68518	Somatosta
696	50	62.5	9	2	ADK11165	Adk11165 Somatosta	769	50	62.5	9	9	ADV96888	Cyclic Cy
697	50	62.5	9	2	ADK11175	Adk11175 Somatosta	770	50	62.5	9	9	ADZ99644	Somatosta
698	50	62.5	9	2	ADK11179	Adk11179 Somatosta	771	50	62.5	9	9	ADZ99659	Somatosta
699	50	62.5	9	2	ADK11172	Adk11172 Somatosta	772	50	62.5	9	9	ADZ99661	Somatosta
700	50	62.5	9	2	ADK11163	Adk11163 Somatosta	773	50	62.5	9	9	ADZ99654	Somatosta
701	50	62.5	9	2	ADK11171	Adk11171 Somatosta	774	50	62.5	9	9	ADZ99652	Somatosta
702	50	62.5	9	2	ADK11173	Adk11173 Somatosta	775	50	62.5	9	9	ADZ99656	Somatosta
703	50	62.5	9	2	ADK11181	Adk11181 Somatosta	776	50	62.5	9	9	ADZ99643	Somatosta
704	50	62.5	9	2	ADK11164	Adk11164 Somatosta	777	50	62.5	9	9	ADZ99657	Somatosta
705	50	62.5	9	2	ADK11169	Adk11169 Somatosta	778	50	62.5	9	9	ADZ99645	Somatosta
706	50	62.5	9	2	ADK11176	Adk11176 Somatosta	779	50	62.5	9	9	ADZ99655	Somatosta
707	50	62.5	9	3	ADK11177	Adk11177 Somatosta	780	50	62.5	9	9	ADZ99649	Somatosta
708	50	62.5	9	3	AAO6935	Aao6935 Somatosta	781	50	62.5	9	9	ADZ99653	Somatosta
709	50	62.5	9	3	AAH81036	Aah81036 Somatosta	782	50	62.5	9	9	ADZ99651	Somatosta
710	50	62.5	9	3	AAH81025	Aah81025 Somatosta	783	50	62.5	9	9	ABA01716	Somatosta
711	50	62.5	9	3	AAH81045	Aah81045 Somatosta	784	50	62.5	9	9	ADZ87448	Somatosta
712	50	62.5	9	3	AAH81032	Aah81032 Somatosta	785	50	62.5	10	2	AAH56798	Somatosta
713	50	62.5	9	3	AAH81040	Aah81040 Somatosta	786	50	62.5	10	2	AAH56800	Somatosta
714	50	62.5	9	3	AAH81042	Aah81042 Somatosta	787	50	62.5	10	2	AAH22052	Somatosta
715	50	62.5	9	3	AAH81024	Aah81024 Somatosta	788	50	62.5	10	2	AAH18236	Somatosta
716	50	62.5	9	3	AAH81035	Aah81035 Somatosta	789	50	62.5	10	2	ADH35429	Human som
717	50	62.5	9	3	AAH81034	Aah81034 Somatosta	790	50	62.5	10	2	ADH35431	Human som
718	50	62.5	9	3	AAH81037	Aah81037 Somatosta	791	50	62.5	10	2	ADH68032	Somatosta
719	50	62.5	9	3	AAH81030	Aah81030 Somatosta	792	50	62.5	10	2	ADH68030	Somatosta
720	50	62.5	9	3	AAH81033	Aah81033 Somatosta	793	50	62.5	10	2	ADK11182	Somatosta
721	50	62.5	9	3	AAH81038	Aah81038 Somatosta	794	50	62.5	10	2	ADK11184	Somatosta
722	50	62.5	9	3	AAH81026	Aah81026 Somatosta	795	50	62.5	10	3	AAH06936	Somatosta
723	50	62.5	9	4	AAH60076	Aah60076 Somatosta	796	50	62.5	10	3	AAH81043	Somatosta
724	50	62.5	9	4	AAU08834	Aau08834 Somatosta	797	50	62.5	10	4	AAU08853	Somatosta
725	50	62.5	9	4	AAU08846	Aau08846 Somatosta	798	50	62.5	10	4	AAU08855	Somatosta
726	50	62.5	9	4	AAU08852	Aau08852 Somatosta	799	50	62.5	10	6	ABG99277	Somatosta
727	50	62.5	9	4	AAU08844	Aau08844 Somatosta	800	50	62.5	10	6	ABG99275	Somatosta
728	50	62.5	9	4	AAU08847	Aau08847 Somatosta	801	50	62.5	10	6	AAO26880	Somatosta
729	50	62.5	9	4	AAU08835	Aau08835 Somatosta	802	50	62.5	10	6	AAO26878	Somatosta
730	50	62.5	9	4	AAU08843	Aau08843 Somatosta	803	50	62.5	10	8	ADU05268	Cyclic so
731	50	62.5	9	4	AAU08845	Aau08845 Somatosta	804	50	62.5	10	9	ADZ99664	Somatosta
732	50	62.5	9	4	AAU08848	Aau08848 Somatosta	805	50	62.5	10	9	ADZ99662	Somatosta
733	50	62.5	9	4	AAU08842	Aau08842 Somatosta	806	50	62.5	12	1	AAO40570	Sequence
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735	50	62.5	9	4	AAU08840	Aau08840 Somatosta	808	50	62.5	13	2	AAW01513	Ocreotid
736	50	62.5	9	6	AAE35393	Aae35393 Somatosta	809	50	62.5	23	4	AAW51433	Peptide K
737	50	62.5	9	6	ABG99268	Abg99268 Somatosta	810	50	62.5	23	4	AAW51433	Peptide K
738	50	62.5	9	6	ABG99256	Abg99256 Somatosta	811	49	61.3	8	1	AAW0587	GH, gastr
739	50	62.5	9	6	ABG99257	Abg99257 Somatosta	812	49	61.3	8	2	AAW48641	Somatosta
740	50	62.5	9	6	ABG99264	Abg99264 Somatosta	813	49	61.3	10	2	AAW48643	Somatosta
741	50	62.5	9	6	ABG99266	Abg99266 Somatosta	814	49	61.3	20	6	ABR42193	Somatosta
742	50	62.5	9	6	ABG99267	Abg99267 Somatosta	815	49	61.3	20	6	ABR42194	Somatosta
743	50	62.5	9	6	ABG99270	Abg99270 Somatosta	816	49	61.3	21	5	ABP68795	Marine sn
744	50	62.5	9	6	ABG99265	Abg99265 Somatosta	817	49	61.3	25	6	ABR42196	Somatosta
745	50	62.5	9	6	ABG99258	Abg99258 Somatosta	818	49	61.3	40	5	ABP68792	Marine sn
746	50	62.5	9	6	ABG99269	Abg99269 Somatosta	819	49	61.3	93	5	ABP68714	Marine sn
747	50	62.5	9	6	ABG99274	Abg99274 Somatosta	820	48	60.0	7	1	AAW0588	GH, gastr
748	50	62.5	9	6	ABG99262	Abg99262 Somatosta	821	48	60.0	7	2	AAW15361	Somatosta
749	50	62.5	9	6	ABG99272	Abg99272 Somatosta	822	48	60.0	7	2	AAW04040	Haptapapt
750	50	62.5	9	6	AAO26877	Aao26877 Somatosta	823	48	60.0	7	7	ADH22048	Somatosta
751	50	62.5	9	6	AAO26868	Aao26868 Somatosta	824	48	60.0	8	1	AAW0585	GH, gastr
752	50	62.5	9	6	AAO26860	Aao26860 Somatosta	825	48	60.0	8	1	AAW0589	GH, gastr
753	50	62.5	9	6	AAO26871	Aao26871 Somatosta	826	48	60.0	8	1	AAW20266	Peptide s
754	50	62.5	9	6	AAO26875	Aao26875 Somatosta	827	48	60.0	8	1	AAW40502	Sequence

828	48	60.0	8	2	AAR14228	Aar14228	Somatosta	901	47	58.8	8	2	ADK11144	Adk11144	Somatosta
829	48	60.0	8	2	AAR10502	Aar10502	Pamoate o	902	47	58.8	8	3	AAB06233	Aab06233	Somatosta
830	48	60.0	8	2	AAR12863	Aar12863	Somatosta	903	47	58.8	8	3	AAy81002	Aay81002	Somatosta
831	48	60.0	8	2	AAR23949	Aar23949	LH-RH, so	904	47	58.8	8	4	AAy81005	Aay81005	Somatosta
832	48	60.0	8	2	AAR40821	Aar40821	Octapepti	905	47	58.8	8	4	AAy74613	Aay74613	Somatosta
833	48	60.0	8	2	AAR31508	Aar31508	Somatosta	906	47	58.8	8	4	AAU08921	Aau08921	Somatosta
834	48	60.0	8	2	AAR42659	Aar42659	Somatosta	907	47	58.8	8	6	ABG99237	Abg99237	Somatosta
835	48	60.0	8	2	AAR76202	Aar76202	Somatosta	908	47	58.8	8	6	AAO26840	Aao26840	Somatosta
836	48	60.0	8	2	AAR85568	Aar85568	Somatosta	909	47	58.8	8	8	ADU05269	Adu05269	Cyclic so
837	48	60.0	8	2	AAW51862	Aaw51862	Somatosta	910	47	58.8	8	9	ADZ99624	Adz99624	Somatosta
838	48	60.0	8	2	AAy22032	Aay22032	Somatosta	911	47	58.8	45	5	ABP68841	Abp68841	Marine sn
839	48	60.0	8	2	AAy18217	Aay18217	Somatosta	912	47	58.8	95	5	ABP68696	Abp68696	Marine sn
840	48	60.0	8	2	ADH35392	Adh35392	Human som	913	47	58.8	123	4	ABB42531	Abb42531	Peptide #
841	48	60.0	8	2	ADH67993	Adh67993	Somatosta	914	47	58.8	123	4	AAm36344	Aam36344	Peptide #
842	48	60.0	8	2	ADK11145	Adk11145	Somatosta	915	47	58.8	123	4	AAm76234	Aam76234	Human bon
843	48	60.0	8	2	ADK11267	Adk11267	Somatosta	916	47	58.8	123	4	AAm63421	Aam63421	Human bra
844	48	60.0	8	3	AAy77334	Aay77334	Synthetic	917	47	58.8	123	4	ABG57951	Abg57951	Human liv
845	48	60.0	8	3	ABR06234	AbR06234	Somatosta	918	47	58.8	123	5	ABG45563	Abg45563	Human pep
846	48	60.0	8	3	AAy81006	Aay81006	Somatosta	919	46	57.5	8	1	AAPI0590	Aapi0590	GH, gastr
847	48	60.0	8	3	AAAB19022	Aab19022	Amino aci	920	46	57.5	8	1	AAPI0592	Aapi0592	GH, gastr
848	48	60.0	8	4	AAU08278	Aau08278	Somastati	921	46	57.5	8	2	AAr47605	Aar47605	Neuromedi
849	48	60.0	8	4	AAAB45662	Aab45662	Somatosta	922	46	57.5	8	2	AAr91614	Aar91614	Chelator-
850	48	60.0	8	4	AAU08816	Aau08816	Somatosta	923	46	57.5	8	2	AAW33183	Aaw33183	Mono-DTPA
851	48	60.0	8	5	ABG73202	Abg73202	Somatosta	924	46	57.5	8	2	AAW66233	Aaw66233	Somatosta
852	48	60.0	8	5	ABG73203	Abg73203	Somatosta	925	46	57.5	8	2	AAW45985	Aaw45985	Peptide #
853	48	60.0	8	5	AAU76358	Aau76358	Synthetic	926	46	57.5	8	7	ADF61738	Adf61738	Somatosta
854	48	60.0	8	5	AAU76360	Aau76360	Synthetic	927	46	57.5	8	7	ADF61741	Adf61741	Somatosta
855	48	60.0	8	5	ADH68882	Adh68882	Synthetic	928	46	57.5	8	8	ADJ87443	Adj87443	Somatosta
856	48	60.0	8	5	ADH68891	Adh68891	Synthetic	929	46	57.5	8	8	ADU96403	Adu96403	Novel cyt
857	48	60.0	8	6	ABG71789	Abg71789	Somatosta	930	46	57.5	8	8	ADU96088	Adu96088	Novel cyt
858	48	60.0	8	6	ABG99238	Abg99238	Somatosta	931	46	57.5	8	8	ADU96085	Adu96085	Novel cyt
859	48	60.0	8	6	AAO26841	Aao26841	Somatosta	932	46	57.5	8	8	ADU97027	Adu97027	Novel cyt
860	48	60.0	8	7	ADI14938	Adi14938	Somatosta	933	46	57.5	8	8	ADU95718	Adu95718	Novel cyt
861	48	60.0	8	8	ADR87510	Adr87510	Backbone	934	46	57.5	8	8	ADU95223	Adu95223	Novel cyt
862	48	60.0	8	8	ADU07145	Adu07145	Basic for	935	46	57.5	8	8	ADU96400	Adu96400	Novel cyt
863	48	60.0	8	8	ADU07146	Adu07146	Peptide u	936	46	57.5	8	8	ADU97024	Adu97024	Novel cyt
864	48	60.0	8	9	ADZ99625	Adz99625	Somatosta	937	46	57.5	8	8	ADU97450	Adu97450	Novel cyt
865	48	60.0	9	2	AAW14230	Aaw14230	Somatosta	938	46	57.5	8	8	ADU95831	Adu95831	Novel cyt
866	48	60.0	9	2	AAW45984	Aaw45984	Peptide #	939	46	57.5	8	8	ADU97447	Adu97447	Novel cyt
867	48	60.0	9	3	AAy76772	Aay76772	Somatosta	940	46	57.5	9	8	ADU97439	Adu97439	Novel cyt
868	48	60.0	9	4	AAU08284	Aau08284	Assembly	941	46	57.5	9	8	ADU96087	Adu96087	Novel cyt
869	48	60.0	9	5	ABG73217	Abg73217	Somatosta	942	46	57.5	9	8	ADU96404	Adu96404	Novel cyt
870	48	60.0	9	5	ABG73216	Abg73216	Somatosta	943	46	57.5	9	8	ADU97451	Adu97451	Novel cyt
871	48	60.0	9	5	ABG73215	Abg73215	Somatosta	944	46	57.5	9	8	ADU96388	Adu96388	Novel cyt
872	48	60.0	9	5	ABG73214	Abg73214	Somatosta	945	46	57.5	9	8	ADU95717	Adu95717	Novel cyt
873	48	60.0	9	5	ABG73218	Abg73218	Somatosta	946	46	57.5	9	8	ADU95830	Adu95830	Novel cyt
874	48	60.0	9	5	ABP53362	Abp53362	Backbone	947	46	57.5	9	8	ADU96073	Adu96073	Novel cyt
875	48	60.0	9	6	ABG71792	Abg71792	Pacilitaxe	948	46	57.5	9	8	ADU96401	Adu96401	Novel cyt
876	48	60.0	9	6	ABG71793	Abg71793	Somatosta	949	46	57.5	9	8	ADU97028	Adu97028	Novel cyt
877	48	60.0	9	7	ADI14939	Adi14939	Somatosta	950	46	57.5	9	8	ADU97448	Adu97448	Novel cyt
878	48	60.0	9	7	ADI14946	Adi14946	Somatosta	951	46	57.5	9	8	ADU95705	Adu95705	Novel cyt
879	48	60.0	10	5	ABG73212	Abg73212	Somatosta	952	46	57.5	9	8	ADU97016	Adu97016	Novel cyt
880	48	60.0	10	5	ABG73208	Abg73208	Somatosta	953	46	57.5	9	8	ADU97025	Adu97025	Novel cyt
881	48	60.0	10	5	ABG73211	Abg73211	Somatosta	954	46	57.5	9	8	ADU96084	Adu96084	Novel cyt
882	48	60.0	10	5	ABG73209	Abg73209	Somatosta	955	46	57.5	10	8	ADU97017	Adu97017	Novel cyt
883	48	60.0	10	5	ADI14940	Adi14940	Somatosta	956	46	57.5	10	8	ADU95706	Adu95706	Novel cyt
884	48	60.0	11	3	AAy77335	Aay77335	Synthetic	957	46	57.5	10	8	ADU96382	Adu96382	Novel cyt
885	48	60.0	11	3	ABG73210	Abg73210	Somatosta	958	46	57.5	10	8	ADU97433	Adu97433	Novel cyt
886	48	60.0	11	7	ADI14941	Adi14941	Somatosta	959	46	57.5	10	8	ADU96394	Adu96394	Novel cyt
887	48	60.0	12	7	ADI14942	Adi14942	Somatosta	960	46	57.5	10	8	ADU96072	Adu96072	Novel cyt
888	48	60.0	240	4	ABG20353	Abg20353	Novel hum	961	46	57.5	10	8	ADU96074	Adu96074	Novel cyt
889	47	58.8	7	2	AAW48640	Aaw48640	Somatosta	962	46	57.5	10	8	ADU97440	Adu97440	Novel cyt
890	47	58.8	7	2	ADU05225	Adu05225	Cyclic so	963	46	57.5	10	8	ADU96389	Adu96389	Novel cyt
891	47	58.8	8	2	AAr12866	Aar12866	Somatosta	964	46	57.5	10	8	ADU97438	Adu97438	Novel cyt
892	47	58.8	8	2	AAr40818	Aar40818	Octapepti	965	46	57.5	10	8	ADU96083	Adu96083	Novel cyt
893	47	58.8	8	2	AAr99319	Aar99319	Cyclic so	966	46	57.5	10	8	ADU96387	Adu96387	Novel cyt
894	47	58.8	8	2	AAW18455	Aaw18455	Somatosta	967	46	57.5	10	8	ADU95712	Adu95712	Novel cyt
895	47	58.8	8	2	AAW66228	Aaw66228	Somatosta	968	46	57.5	10	8	ADU95704	Adu95704	Novel cyt
896	47	58.8	8	2	AAy22031	Aay22031	Somatosta	969	46	57.5	10	8	ADU95716	Adu95716	Novel cyt
897	47	58.8	8	2	AAy18285	Aay18285	Somatosta	970	46	57.5	10	8	ADU96079	Adu96079	Novel cyt
898	47	58.8	8	2	ADH35391	Adh35391	Human som	971	46	57.5	10	8	ADU97015	Adu97015	Novel cyt
899	47	58.8	8	2	ADH67992	Adh67992	Somatosta	972	46	57.5	10	8	ADU97010	Adu97010	Novel cyt
900	47	58.8	8	2	ADK11294	Adk11294	Somatosta	973	46	57.5	11	8	ADU96390	Adu96390	Novel cyt

974 46 57.5 11 8 ADU97441 Novel cyt
 975 46 57.5 11 8 ADU96078 Novel cyt
 976 46 57.5 11 8 ADU95715 Novel cyt
 977 46 57.5 11 8 ADU97018 Novel cyt
 978 46 57.5 11 8 ADU95711 Novel cyt
 979 46 57.5 11 8 ADU96082 Novel cyt
 980 46 57.5 11 8 ADU96395 Novel cyt
 981 46 57.5 11 8 ADU97011 Novel cyt
 982 46 57.5 11 8 ADU96071 Novel cyt
 983 46 57.5 11 8 ADU95703 Novel cyt
 984 46 57.5 11 8 ADU96383 Novel cyt
 985 46 57.5 11 8 ADU97434 Novel cyt
 986 46 57.5 12 8 ADU96384 Novel cyt
 987 46 57.5 12 8 ADU97446 Novel cyt
 988 46 57.5 12 8 ADU96399 Novel cyt
 989 46 57.5 12 8 ADU97627 Novel cyt
 990 46 57.5 12 8 ADU95702 Novel cyt
 991 46 57.5 12 8 ADU96089 Novel cyt
 992 46 57.5 12 8 ADU96391 Novel cyt
 993 46 57.5 12 8 ADU97023 Novel cyt
 994 46 57.5 12 8 ADU97435 Novel cyt
 995 46 57.5 12 8 ADU97597 Novel cyt
 996 46 57.5 12 8 ADU96077 Novel cyt
 997 46 57.5 12 8 ADU96396 Novel cyt
 998 46 57.5 12 8 ADU97442 Novel cyt
 999 46 57.5 12 8 ADU97012 Novel cyt
 1000 46 57.5 12 8 ADU97612 Novel cyt

ALIGNMENTS

RESULT 1
 ID ADS74377 standard; peptide; 11 AA.

XX AC ADS74377;
 XX DT 16-DEC-2004 (first entry)
 XX DE Somatostatin analogue.
 XX KW Somatostatin analogue; cytostatic; gene therapy.
 XX OS Synthetic.

XX Key Location/Qualifiers
 XX FT Misc-difference 1. .4 /note= "D-form residues"
 XX FT Disulfide-bond 5. .10
 XX FT Misc-difference 7 /note= "D-form residue"
 XX FT Modified-site 11 /note= "C-terminal amide or alcohol"

XX WO2004081031-A2.
 XX PD 23-SEP-2004.
 XX PP 10-MAR-2004; 2004WO-US007143.
 XX PR 10-MAR-2003; 2003US-0452928P.
 XX PA (BIOG-) BIOGEN IDEC INC.
 XX PI Braslawsky GR, Chinn P;
 XX DR WPI; 2004-668933/65.

XX A composition comprising a somatostatin analog useful for thiol-specific
 PT drug attachment to somatostatin and other targeting peptides, or for
 PT diagnosing or treating somatostatin receptor-associated disorders, e.g.
 PT cancer.

XX Claim 4; SEQ ID NO 5; 43pp; English.
 XX The present sequence is that of a synthetic somatostatin analogue. The
 CC peptide can be used as component B in a claimed composition comprising a
 CC somatostatin analogue of formula (A-B), where A is Cys, or a peptide
 CC chain comprising one or more Cys residues, which is suitable for binding
 CC to a drug or chelator via a thiol linkage, and B is a naturally occurring
 CC or synthetic somatostatin peptide, or its fragment, that binds to the
 CC somatostatin receptor (SSTR). The drug or chelator is bound to the Cys
 CC residue(s) of component A by a thiol linkage. The drug is a therapeutic
 CC drug such as a radioisotope, a cytotoxin, an immunostimulant, an
 CC antiangiogenic agent, a therapeutic gene, or a chemotherapeutic agent.
 CC The somatostatin analogue preferably binds to SSTR-positive cells,
 CC especially human cancer cells. A claimed method for detecting SSTR-
 CC positive cells comprises administering the somatostatin analogue in which
 CC a detectable label is bound to the Cys residue(s) of component A, and
 CC detecting the label. A claimed method for treating an SSTR-associated
 CC disorder comprises administering a somatostatin analogue in which a
 CC therapeutic agent is bound to the Cys residue(s) of component A. The SSTR
 CC -associated disorder is especially cancer. Thiol-mediated drug attachment
 CC can also be used with other targeting peptides.

Sequence 11 AA;

Query Match 100.0%; Score 80; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YCYCFWKTCCT 11
 Db 1 YCYCFWKTCCT 11

RESULT 2

AAW48645
 ID AAW48645 standard; peptide; 11 AA.

XX AC AAW48645;
 XX DT 04-AUG-1998 (first entry)

XX DE Somatostatin peptide analog WOC-4.

XX KW Somatostatin; acromegaly; radiolocalisation; blood-brain barrier; cancer;
 XX halogen.
 XX OS Synthetic.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 XX FT Misc-difference 1 /note= "D-form residue"
 XX FT Misc-difference 4 /note= "D-form residue"
 XX FT Disulfide-bond 5. .10
 XX FT Misc-difference 7 /note= "D-form residue"
 XX FT Modified-site 11 /note= "C-terminal amide"

XX WO9639161-A1.

XX PD 12-DEC-1996.

XX PF 03-JUN-1996; 96WO-US008437.

XX PR 05-JUN-1995; 95US-00462223.

XX (TULA) TULANE EDUCATIONAL FUND.
 PA (OHIS) UNIV OHIO STATE RES FOUND.
 PA (LOU) UNIV LOUISIANA STATE MEDICAL CENT FOUND.
 PA (CHIL-) CHILDRENS HOSPITAL INC.

XX PI Coy DH, Woltering EA, Odorisio MS, Odorisio TM, Murphy WA;
 XX XX WPI; 1997-042842/04.
 XX DR
 XX XX Multi-tyrosinated somatostatin analogues - useful for diagnosis and
 XX PT treatment of diseases related to altered somatostatin receptor
 XX FT expression.
 XX PS
 XX PS Claim 7; Page 60; 63pp; English.
 XX CC
 XX CC The invention provides for conventional somatostatin analogues (AAW48638-
 CC W48640 and AAW48664) and multi-tyrosinated analogues (AAW48641-W48645)
 CC CC bind to the present one. The multi-tyrosinated somatostatin analogues
 CC CC bind to somatostatin receptors with practically the same affinity as
 CC CC native somatostatin. The somatostatin analogues are claimed to be useful
 CC CC for treating disease associated with increased production of factors
 CC CC which can be regulated by somatostatin, e.g. acromegaly. Also when
 CC CC radioactively labelled, the analogues are claimed to be useful for
 CC CC diagnosing cancer in vitro or in situ where aberrant expression of
 CC CC somatostatin receptors is involved. When halogenated, these analogues are
 CC CC found to bind somatostatin receptors with such high affinity that binding
 CC CC is nearly irreversible under physiological conditions. Therefore, by
 CC CC using radioactive halogenated analogues, the invention claims for
 CC CC improved sensitivity of radiolocalisation of the receptors. Multi-
 CC CC tyrosinated analogues have increased half-lives in vivo relative to
 CC CC conventional somatostatin analogues, are resistant to enzymatic
 CC CC degradation and have increased blood-brain barrier penetration
 XX CC
 XX SQ Sequence 11 AA;
 Query Match 86.2%; Score 69; DB 2; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.029;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 YCYVCFWKTCCT 11
 Db 1 YYYVCFWKTCCT 11
 RESULT 3
 ADM35520
 ID ADM35520 standard; peptide; 11 AA.
 XX AC
 XX AC ADM35520;
 XX DT
 XX DT 03-JUN-2004 (first entry)
 XX DE
 XX DE Somatostatin analogue, Woc-4D.
 XX KW
 XX KW retinopathy of prematurity; neonatal; somatostatin; Woc-4D; octreotide;
 XX KW lanreotide; vapreotide; Woc-2A; Woc-2B; Woc-3A; Woc-4; Woc-4D;
 XX KW Woc-5; Woc-8; octreotide acetate; cyclic.
 XX OS
 XX OS Synthetic.
 XX SY
 XX SY Key Location/Qualifiers
 XX FT Misc-difference 1. 4
 XX FT Misc-difference /note= "D form residues"
 XX FT Disulfide-bond 5. .10
 XX FT /note= Forms a cyclic region of the peptide
 XX FT Misc-difference 7
 XX FT /note= "D form residue"
 XX FT Modified-site 11
 XX FT /note= "C-terminal amide"
 XX FT
 XX FT US2003207811-A1.
 XX FN
 XX XX 06-NOV-2003.
 XX PD
 XX PF 03-MAY-2002; 2002US-00138554.
 XX XX
 XX PR 03-MAY-2002; 2002US-00138554.

XX PA (SCHR/) SCHRIER B K.
 XX PA (HIGG/) HIGGINS R D.
 XX PI
 XX PI Schrier BK, Higgins RD;
 XX XX WPI; 2004-069300/07.
 XX DR
 XX PT Treatment or prevention of retinopathy of prematurity in neonatal mammal,
 XX FT comprises administering somatostatin analog having composition that
 XX FT provides therapeutic benefit to mammal.
 XX PS
 XX PS Example; Page 5; 12pp; English.
 XX CC
 XX CC The invention relates to a method of treating retinopathy of prematurity
 CC CC in a neonatal mammal. The condition is treated or prevented by
 CC CC administering to the mammal a somatostatin analogue. Also described is a
 CC CC pharmaceutical composition Woc-4D and carrier for treating or preventing
 CC CC retinopathy of prematurity in neonatal mammal. The somatostatin analogue
 CC CC is octreotide, Woc4D, somatostatin analogue having serum half-life of
 CC CC octreotide, or somatostatin analogue having serum half-life more than that
 CC CC of octreotide, or somatostatin analogue having serum half-life of Woc-4D.
 CC CC It is selected from octreotide, lanreotide, vapreotide, Woc-2A, Woc-2B,
 CC CC Woc-3A, Woc-3B, Woc-4, Woc-4D, Woc-5, or Woc-8. The invention provides a
 CC CC therapeutic benefit without affecting growth of the neonates. The present
 CC CC sequence represents somatostatin analogue, Woc-4D.
 XX CC
 XX SQ Sequence 11 AA;
 Query Match 86.2%; Score 69; DB 8; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.029;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 YCYVCFWKTCCT 11
 Db 1 YYYVCFWKTCCT 11
 RESULT 4
 ADM95422
 ID ADM95422 standard; peptide; 11 AA.
 XX AC
 XX AC ADM95422;
 XX DT
 XX DT 07-APR-2005 (first entry)
 XX DE
 XX DE Amino acid sequence of WOC4D.
 XX KW
 XX KW cytostatic; dispersed phase formulation; microspheres;
 XX KW sustained drug release; controlled drug release;
 XX KW testosterone dependent disorder; prostate disease; prostate cancer;
 XX KW octreotide drug; WOC4D.
 XX OS
 XX OS Synthetic.
 XX SY
 XX SY Key Location/Qualifiers
 XX FT Misc-difference 1 /note= "D-form residue with H attached"
 XX FT Misc-difference 2 /note= "D-form residue"
 XX FT Misc-difference 3 /note= "D-form residue"
 XX FT Misc-difference 4 /note= "D-form residue"
 XX FT Misc-difference 5 /note= "D-form residue"
 XX FT Disulfide-bond 5. .10
 XX FT Misc-difference 7
 XX FT /note= "D-form residue"
 XX FT Modified-site 11
 XX FT /note= "NH2 attached"
 XX FT
 XX FT WO2005007122-A2.
 XX FN
 XX XX 27-JAN-2005.

XX 19-JUL-2004; 2004WO-US023324.
 XX
 XX 18-JUL-2003; 2003US-0488573P.
 XX
 XX (OAKW-) OAKWOOD LAB LLC.
 XX
 XX Thanoo BC, Murtagh J, Johns G;
 XX WPI; 2005-122673/13.
 XX
 XX Dispersed phase formulation useful for providing sustained release of
 XX drug suppressing gonadotropin releasing hormone comprises nucleophilic
 XX substance catalyzing ester bond cleavage and causing molecular weight
 XX reduction of polymer.
 XX
 XX Example; Page 63; 114pp; English.
 XX
 XX The specification describes a dispersed phase formulation which comprises
 XX a biocompatible and biodegradable polymer, at least one nucleophilic
 XX substance capable of catalyzing ester bond cleavage and causing molecular
 XX weight reduction of the polymer, and acid additive in an amount such that
 XX the polymer is less susceptible to molecular reduction as compared to the
 XX formulation without the acid additive. The formulation of the invention
 XX is useful for preparing microspheres providing a sustained or controlled
 XX release of drug. This is useful for suppressing gonadotropin releasing
 XX hormone in the treatment of testosterone dependent disorder, benign
 XX prostate hypertrophy or prostate cancer. The present sequence represents
 XX WOC4D (a somatostatin analog), a peptide which was contained in
 XX microspheres of the invention.
 XX
 XX Sequence 11 AA;
 XX
 XX Query Match 86.2%; Score 69; DB 9; Length 11;
 XX Best Local Similarity 90.9%; Pred. No. 0.029;
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX Qy 1 YYCYCFWKTCCT 11
 XX Db 1 YYYCYCFWKTCCT 11
 XX
 XX RESULT 5
 XX AAW48642
 XX ID AAW48642 standard; peptide; 9 AA.
 XX AC AAW48642;
 XX XX
 XX DT 04-AUG-1998 (first entry)
 XX DE Somatostatin peptide analog WOC-2B.
 XX
 XX Somatostatin; acromegaly; radiolocalisation; blood-brain barrier; cancer;
 XX halogen.
 XX
 XX Synthetic.
 XX OS Homo sapiens.
 XX XX
 XX Key Location/Qualifiers
 XX Misc-difference 2 /note= "D-form residue"
 XX Disulfide-bond 3. .8
 XX Misc-difference 5
 XX Modified-site 9 /note= "D-form residue"
 XX /note= "C-terminal amide"
 XX
 XX WO9639161-A1.
 XX
 XX 12-DEC-1996.
 XX
 XX 03-JUN-1996; 96WO-US008437.
 XX

PR 05-JUN-1995; 95US-00462223.
 XX
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX (OHIS) UNIV OHIO STATE RES FOUND.
 XX (LOU) UNIV LOUISIANA STATE MEDICAL CENT FOUND.
 XX (CHIL-) CHILDRENS HOSPITAL INC.
 XX
 XX Coy DH, Woltering EA, Odorisio MS, Odorisio TM, Murphy WA;
 XX WPI; 1997-042842/04.
 XX
 XX Multi-tyrosinated somatostatin analogues - useful for diagnosis and
 XX treatment of diseases related to altered somatostatin receptor
 XX expression.
 XX
 XX Claim 7; Page 60; 63pp; English.
 XX
 XX The invention provides for conventional somatostatin analogues (AAW48638-
 XX W48640 and AAW48664) and multi-tyrosinated analogues (AAW48641-W48645)
 XX bind to somatostatin receptors with practically the same affinity as
 XX native somatostatin. The somatostatin analogues are claimed to be useful
 XX for treating disease associated with increased production of factors
 XX which can be regulated by somatostatin, e.g. acromegaly. Also when
 XX radioactively labelled, the analogues are claimed to be useful for
 XX diagnosing cancer in vitro or in situ where aberrant expression of
 XX somatostatin receptors is involved. When halogenated, these analogues are
 XX found to bind somatostatin receptors with such high affinity that binding
 XX is nearly irreversible under physiological conditions. Therefore, by
 XX using radioactive halogenated analogues, the invention claims for
 XX improved sensitivity of radiolocalisation of the receptors. Multi-
 XX tyrosinated analogues have increased half-lives in vivo relative to
 XX conventional somatostatin analogues, are resistant to enzymatic
 XX degradation and have increased blood-brain barrier penetration
 XX
 XX Sequence 9 AA;
 XX
 XX Query Match 80.0%; Score 64; DB 2; Length 9;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 3 YYCFWKTCCT 11
 XX Db 1 YYCFWKTCCT 9
 XX
 XX RESULT 6
 XX ADI14934
 XX ID ADI14934 standard; peptide; 10 AA.
 XX AC ADI14934;
 XX XX
 XX DT 22-APR-2004 (first entry)
 XX DE Somatostatin-dopamine chimeric analogue-related peptide 45.
 XX
 XX Somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 XX vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 XX anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 XX tranquiliser; antilipæmic; nephrotropic; antiulcer; antiarthritic;
 XX hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 XX somatostatin receptor agonist; lung cancer; glioma; anorexia;
 XX hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 XX acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 XX pancreatic pseudocyst; ascite; VIPoma; nesidoblastosis; hyperinsulinism;
 XX gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 XX AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 XX irritable bowel syndrome; pancreatitis; small bowel obstruction;
 XX gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 XX gonadotropinoma; hyperparathyroidism; Graves disease;
 XX diabetic neuropathy; Paget's disease; polycystic ovary disease;
 XX thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 XX orthostatic; hypotension; postprandial hypotension; panic attack;
 XX

KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 XX Synthetic.
 OS Unidentified.
 XX

Key	Location/Qualifiers
FT	Modified-site 1
FT	/note= "D-form residue"
FT	4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methylsulfany-1-acetic acid. Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methyl-carbamate acid. Optionally bound to carbonic acid mono-(7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methyl) ester. Optionally bound to 4-((7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methyl) carbonyl) butyric acid. Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carboxylic acid. Optionally bound to 3-((1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidopropyl)-gly-
FT	2. .3
FT	/note= "D-form residue"
FT	4
FT	/note= "Residue forms a bond to residue 9 to form a cyclic peptide"
FT	6
FT	/note= "D-form residue"
FT	9
FT	/note= "Residue forms a bond to residue 4 to form a cyclic peptide"
FT	10
FT	/note= "C-terminal OL"
XX	WO2002100888-A1.
XX	19-DEC-2002.
XX	07-JUN-2002; 2002WO-US017859.
XX	08-JUN-2001; 2001US-0237059P.
XX	(SCRC) SCRAS SOC CONSRILS RECH & APPL SCI.
XX	Culler MD, Dong ZX, Kim SH, Moreau J;
XX	WPI; 2003-239103/23.
XX	New somatostatin-dopamine chimeric analogs useful for the treatment of e.g. lung cancer.
XX	Claim 3; Page 133; 85pp; English.
XX	This invention relates to novel somatostatin-dopamine chimeric analogues or their salts. The invention may be useful for the development of compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory, antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic, antibacterial, immunomodulator, hypertensive, tranquiliser, antilipemic, nephrotropic, antitumor, antithyroid, hypotensive, anorectic or antidiarrhoeic activity through action as a dopamine receptor agonist and somatostatin receptor agonist. The invention may be useful for the treatment of lung cancer, glioma, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and internal

CC pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia, meningioma, cancer cachexia, orthostatic, hypotension, postprandial hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH secreting adenomas, prolactin secreting adenomas, insulinoma, glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity, Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon, nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea syndrome, pancreatitis, gastrointestinal hormone secreting tumour, angiogenesis, arthritis, allograft rejection, graft vessel bleeding, portal hypertension, gastrointestinal bleeding, obesity and opioid overdose. The compounds simultaneously elicit dopamine receptor agonist and somatostatin receptor agonist effects in vivo with enhanced biological activity over the native somatostatin and dopamine analogues alone. The present sequence is that of a peptide which was used to produce the somatostatin-dopamine chimeric analogues of the invention.
 XX

Qy	Sequence 10 AA;	Query Match	80.0%;	Score 64;	DB 7;	Length 10;
Db	3 YYCFWKTCCT 11	Best Local Similarity	100.0%;	Pred. No. 0.12;		
	2 YYCFWKTCCT 10	Matches	9;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 ADU05247
 ID ADU05247 standard; peptide; 10 AA.
 XX
 AC ADU05247;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Cyclic somatostatin-dopamine chimeric peptide analogue #37.
 XX
 KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective tissue disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytostatic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antitumor; analgesic;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipemic; analgesic;
 KW antianal; anorectic; immunomodulator; cardiant; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX Synthetic.
 OS

Key	Location/Qualifiers
FT	Modified-site 1
FT	/note= "An N-terminal dopamine derivative (Dop1 to Dop6 inclusive) is attached to a Lys (second dopamine derivative) modified residue, where this second dopamine derivative must match the type occurring at the N-terminus, e.g. Dop1-Lys (Dop1), Dop2-Lys (Dop2) etc."
FT	Misc-difference 2
FT	/note= "D-form residue"
FT	Misc-difference 3
FT	/note= "D-form residue"
FT	Disulfide-bond 4. .9
FT	/note = This disulphide bond cyclises the peptide
FT	Misc-difference 6
FT	/note= "D-form residue"

FT Modified-site 10 /note= "C-terminal alcohol"
 XX WO2004091490-A2.
 XX 28-OCT-2004.
 XX 08-APR-2004; 2004WO-US010891.
 XX 11-APR-2003; 2003US-0462374P.
 XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX Dong ZX, Dewitt Culler M, Shen Y;
 XX WPI; 2004-784484/77.
 XX New chimeric analog comprising at least one moiety which binds to one or
 XX more somatostatin and dopamine receptor(s) useful to treat e.g.
 XX neuroendocrine tumor, vascular diseases, connective tissue disease,
 XX immune disease and cachexia.
 XX Claim 12; Page 103; 138pp; English.
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 XX that comprise at least one moiety that binds to one or more somatostatin
 XX receptors and at least one moiety that binds to one or more dopamine
 XX receptors, or a salt derived thereof. Specifically, it refers to
 XX analogues that may be used in vitro or in vivo for research, diagnostic
 XX and therapeutic agents to enhance the activity of somatostatin and
 XX dopamine i.e. working as receptor agonists. The present invention
 XX describes analogues with specificity for different types of somatostatin
 XX receptor subtypes that are accordingly associated with the treatment of
 XX particular diseases or conditions. As such, these analogues may be used
 XX to treat neoplasia and acromegaly as well as various neuroendocrine
 XX tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
 XX scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
 XX tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
 XX hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
 XX disorder or an opioid overdose. Accordingly, they exhibit activities that
 XX include cytostatic, osteoplastic, antithyroid, vasotropic, antiangiogenic,
 XX ophthalmological, antidiabetic, dermatological, immunosuppressive,
 XX antiarthritic, antirheumatic, antiinflammatory, antitumor, analgesic,
 XX antidiarrhoeic, nephroprotective, hepatotropic, antilipemic, anorectic,
 XX antianginal, anorectic, immunomodulator, cardiant, tranquilizer and
 XX antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
 XX analogue of the invention.
 XX Sequence 10 AA;
 SQ
 Query Match 80.0%; Score 64; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred.No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 Y Y C F W K T C T 11
 D b | | | | | | | | | |
 2 Y Y C F W K T C T 10
 RESULT 8
 ADI14956
 ID ADI14956 standard; peptide; 11 AA.
 XX AC ADI14956;
 XX 22-APR-2004 (first entry)
 XX Somatostatin-dopamine chimeric analogue-related peptide 66.
 XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 XX vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 XX anti-diabetic; osteoplastic; antibacterial; immunomodulator; hypertensive;
 XX tranquiliser; antilipemic; nephroprotective; antitumor; antidiarrhetic;

KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; neuroblastoma; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 XX Synthetic.
 OS Unidentified.
 XX Key Location/Qualifiers
 XX Modified-site 1 /note= "Amino acid is Doc. Bound to 1-(7-allyl-
 XX 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-
 XX carbonyl)-3-ethylureidomethylsulfonyl acetic acid"
 XX Misc-difference 3. .4
 XX Modified-site 5 /note= "D-form residue"
 XX /note= "Residue forms a bond to residue 10 to form a
 XX cyclic peptide"
 XX Misc-difference 7 /note= "D-form residue"
 XX Modified-site 10 /note= "Residue forms a bond to residue 5 to form a
 XX cyclic peptide"
 XX Modified-site 11 /note= "C-terminal amide"
 XX WO2002100888-A1.
 XX 19-DEC-2002.
 XX 07-JUN-2002; 2002WO-US017859.
 XX 08-JUN-2001; 2001US-0297059P.
 XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 XX WPI; 2003-239103/23.
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 XX e.g. lung cancer.
 XX Claim 3; Page 144; 85pp; English.
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 XX or their salts. The invention may be useful for the development of
 XX compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 XX antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteoplastic,
 XX antibacterial, immunomodulator, hypertensive, tranquiliser, antilipemic,
 XX nephroprotective, antitumor, antidiarrhetic, hypotensive, anorectic or
 XX antiaddictive activity through action as a dopamine receptor agonist and
 XX somatostatin receptor agonist. The invention may be useful for the
 XX treatment of lung cancer, glioma, anorexia, hypothroidism,

CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, retestosis, Crohn's disease, systemic sclerosis, external and internal pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis, hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia, meningioma, cancer cachexia, orthostatic, hypotension, postprandial hypotension, panic attacks, GH secreting adenomas, acromegally, TSH secreting adenomas, prolactin secreting adenomas, insulinoma, glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity, Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon, nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea syndrome, pancreatitis, gastrointestinal hormone secreting tumour, angiogenesis, arthritis, allograft rejection, graft vessel bleeding, portal hypertension, gastrointestinal bleeding, obesity and oploid overdose. The compounds simultaneously elicit dopamine receptor agonist and somatostatin receptor agonist effects in vivo with enhanced biological activity over the native somatostatin and dopamine analogues alone. The present sequence is that of a peptide which was used to produce the somatostatin-dopamine chimeric analogues of the invention.

XX Sequence 11 AA;

Query Match 80.0%; Score 64; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTC 11
 |||||
 Db 3 YYCFWKTC 11

RESULT 9

ID ADI14951 standard; peptide; 11 AA.

AC ADI14951;

XX 22-APR-2004 (first entry)

DE Somatostatin-dopamine chimeric analogue-related peptide 61.

KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipaeic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; retestosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidoblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegally; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; oploid overdose.

XX Synthetic.
 OS Unidentified.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "Amino acid is Doc. Bound to 7-propyl-4,6,6a,7,8,9,10,10a-Octahydroindolo[4,3-fg]quinolin-9-yl-methylsulfanyl-acetic acid"
 FT FT Misc-difference 3. 4 /note= "D-form residue"
 FT FT Modified-site 5 /note= "Residue forms a bond to residue 10 to form a cyclic peptide"
 FT FT Misc-difference 7 /note= "D-form residue"
 FT FT Modified-site 10 /note= "Residue forms a bond to residue 5 to form a cyclic peptide"
 FT FT Modified-site 11 /note= "C-terminal amide"

PN WO2002100888-A1.

XX 19-DEC-2002.

XX 07-JUN-2002; 2002WO-US017859.

XX 08-JUN-2001; 2001US-0297059P.

XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.

XX Culler MD, Dong ZX, Kim SH, Moreau J;

XX WPI; 2003-239103/23.

XX New somatostatin-dopamine chimeric analogs useful for the treatment of e.g. lung cancer.

XX Claim 3; Page 144; 85pp; English.

XX This invention relates to novel somatostatin-dopamine chimeric analogues or their salts. The invention may be useful for the development of compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory, antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic, antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeic, nephrotropic, antitumor, antiarthritic, hypotensive, anorectic or somatostatin receptor agonist action as a dopamine receptor agonist and antiaddictive activity through action as a dopamine receptor agonist and treatment of lung cancer, glioma, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, retestosis, Crohn's disease, systemic sclerosis, external and internal pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis, hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia, meningioma, cancer cachexia, orthostatic, hypotension, postprandial hypotension, panic attacks, GH secreting adenomas, acromegally, TSH secreting adenomas, prolactin secreting adenomas, insulinoma, glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity, Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon, nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea syndrome, pancreatitis, gastrointestinal hormone secreting tumour, angiogenesis, arthritis, allograft rejection, graft vessel bleeding, portal hypertension, gastrointestinal bleeding, obesity and oploid overdose. The compounds simultaneously elicit dopamine receptor agonist and somatostatin receptor agonist effects in vivo with enhanced biological activity over the native somatostatin and dopamine analogues alone. The present sequence is that of a peptide which was used to

CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 11 AA;

Query Match 80.0%; Score 64; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 |||||
 Db 3 YYCFWKTCCT 11

RESULT 10
 ID ADI14959 standard; peptide; 11 AA.
 XX
 AC ADI14959;
 XX
 XX
 DT 22-APR-2004 (first entry)
 XX
 XX Somatostatin-dopamine chimeric analogue-related peptide 69.

somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antileptemic; nephrotropic; antileptemic; antidiarrhoeic;
 KW hypotensive; anorectic; antidiarrhoeic; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascites; VIPoma; nesidoblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; dumping syndrome;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiodogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.

XX Synthetic.
 OS Unidentified.
 XX

Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "4-(2-aminoethyl)-1-carboxymethyl-piperazine.
 FT Bound to 1-(7-allyl-4,6,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
 FT ethylureidomethylsulfanyl acetic acid"
 FT Misc-difference 3, 4
 FT /note= "D-form residue"
 FT Modified-site 5
 FT /note= "Residue forms a bond to residue 10 to form a
 FT cyclic peptide"
 FT Misc-difference 7
 FT /note= "D-form residue"
 FT Modified-site 10
 FT /note= "Residue forms a bond to residue 5 to form a
 FT cyclic peptide"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX

PN W02002100888-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 07-JUN-2002; 2002WO-US017859.
 XX
 PR 08-JUN-2001; 2001US-0297059P.
 XX
 PA (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 XX
 PI Culler MD, Dong ZX, Kim SH, Moreau J;
 XX
 DR WPI; 2003-239103/23.
 XX
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 FT e.g. lung cancer.
 XX
 PS Claim 3; Page 145; 85pp; English.
 XX
 CC This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antileptemic,
 CC nephrotropic, antileptemic, antidiarrhoeic, hypotensive, anorectic or
 CC antiaddictive activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulin insensitivity,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, dawn phenomenon,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dumping syndrome,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 11 AA;

Query Match 80.0%; Score 64; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 |||||
 Db 3 YYCFWKTCCT 11

RESULT 11
 ADI14954
 ID ADI14954 standard; peptide; 11 AA.
 XX
 AC ADI14954;
 XX
 DT 22-APR-2004 (first entry)
 XX
 XX Somatostatin-dopamine chimeric analogue-related peptide 64.

XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotrophic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipemic; nephrotropic; antitumor; antidiarrhetic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia; hypothyroidism;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis; AIDS
 KW pancreatic pseudocyst; ascites; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreatocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 OS Synthetic.
 OS Unidentified.

XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "4-(2-aminoethyl)-1-carboxymethyl-piperazine.
 FT Bound to 7-propyl-4,6,6,7,8,9,10,10a-octahydroindolo[4,3
 FT -fg]quinolin-9-yl-methylsulfanyl-acetic acid"
 FT Misc-difference 3. .4
 FT /note= "D-form residue"
 FT Modified-site 5
 FT /note= "Residue forms a bond to residue 10 to form a
 FT cyclic peptide"
 FT Misc-difference 7
 FT /note= "D-form residue"
 FT Modified-site 10
 FT /note= "Residue forms a bond to residue 5 to form a
 FT cyclic peptide"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 FT WO2002100888-A1.
 FN 19-DEC-2002.
 XX 07-JUN-2002; 2002WO-US017859.
 XX 08-JUN-2001; 2001US-0297059P.
 XX (SCRC) SCRAS SOC CONSRILS RECH & APPL SCI.
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 PI WPI; 2003-239103/23.
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 FT e.g. lung cancer.
 XX Claim 3; Page 144; 85pp; English.
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,

CC antibacterial, immunomodulator, hypertensive, tranquiliser, antilipemic,
 CC nephrotropic, antitumor, antidiarrhetic, anti-HIV; dermatological;
 CC anti-addictive activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Peget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreatocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX Sequence 11 AA;
 SQ Query Match 80.0%; Score 64; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 Db 3 YYCFWKTCCT 11
 |||||
 |||||

RESULT 12
 ADS74378
 ID ADS74378 standard; peptide; 11 AA.
 AC ADS74378;
 XX 16-DEC-2004 (first entry)
 DT Somatostatin analogue.
 XX Somatostatin analogue; cytostatic; gene therapy.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1. .4
 FT /note= "D-form residues"
 FT Disulfide-bond 5. .10
 FT Misc-difference 7
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /note= "C-terminal amide or alcohol"
 XX WO2004081031-A2.
 FN 23-SEP-2004.
 XX 10-MAR-2004; 2004WO-US007143.
 XX 10-MAR-2003; 2003US-0452928P.
 XX (BIOG-) BIOGEN IDEC INC.

XX PI Braslawsky GR, Chinn P;
 XX XX WPI; 2004-668933/65.
 XX XX
 XX XX A composition comprising a somatostatin analog useful for thiol-specific
 XX FT drug attachment to somatostatin and other targeting peptides, or for
 XX FT diagnosing or treating somatostatin receptor-associated disorders, e.g.
 XX FT cancer.
 XX FT
 XX FT Claim 4; SEQ ID NO 6; 43pp; English.
 XX FT
 XX CC The present sequence is that of a synthetic somatostatin analogue. The
 XX CC peptide can be used as component B in a claimed composition comprising a
 XX CC somatostatin analogue of formula (A-B), where A is Cys, or a peptide
 XX CC chain comprising one or more Cys residues, which is suitable for binding
 XX CC to a drug or chelator via a thiol linkage, and B is a naturally occurring
 XX CC or synthetic somatostatin peptide, or its fragment, that binds to the
 XX CC somatostatin receptor (SSTR). The drug or chelator is bound to the Cys
 XX CC residue(s) of component A by a thiol linkage. The drug is a therapeutic
 XX CC drug such as a radioisotope, a cytotoxin, an immunostimulant, an
 XX CC antiangiogenic agent, a therapeutic gene, or a chemotherapeutic agent.
 XX CC The somatostatin analogue preferably binds to SSTR-positive cells,
 XX CC especially human cancer cells. A claimed method for detecting SSTR-
 XX CC positive cells comprises administering the somatostatin analogue in which
 XX CC a detectable label is bound to the Cys residue(s) of component A, and
 XX CC detecting the label. A claimed method for treating an SSTR-associated
 XX CC disorder comprises administering a somatostatin analogue in which a
 XX CC therapeutic agent is bound to the Cys residue(s) of component A. The SSTR
 XX CC -associated disorder is especially cancer. Thiol-mediated drug attachment
 XX CC can also be used with other targeting peptides.
 XX CC
 XX CC Sequence 11 AA;
 XX CC
 XX CC Query Match 80.0%; Score 64; DB 8; Length 11;
 XX CC Best Local Similarity 100.0%; Pred. No. 0.12;
 XX CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX CC
 XX QY 3 YYCFWKTKCT 11
 XX DB |||||
 XX 3 YYCFWKTKCT 11
 XX
 XX RESULT 13
 XX ADU05246
 XX ID ADU05246 standard; peptide; 11 AA.
 XX AC
 XX ADU05246;
 XX
 XX DT 13-JAN-2005 (first entry)
 XX
 XX DE Cyclic somatostatin-dopamine chimeric peptide analogue #36.
 XX KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective tissue disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytotactic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antidiabetic;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipemic; analgesic;
 KW antianginal; anorectic; immunomodulator; cardiac; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX FT Modified-site 1
 XX FT /note= "An N-terminal dopamine derivative (Dop1 to Dop6
 XX FT inclusive) is attached to a Lys(dopamine derivative)
 XX FT modified residue, where this second dopamine derivative
 XX FT must match the type occurring at the N-terminus, e.g.
 XX FT

FT Misc-difference 3 Dop1-Lys(Dop1), Dop2-Lys(Dop2) etc."
 FT /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Disulfide-bond 5.10 /note= "This disulphide bond cyclises the peptide"
 FT Misc-difference 7 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal alcohol"
 XX WO2004091490-A2.
 XX 28-OCT-2004.
 XX 08-APR-2004; 2004WO-US010891.
 XX 11-APR-2003; 2003US-0462374P.
 XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX Dong ZX, Dewitt Culler M, Shen Y;
 XX WPI; 2004-784484/77.
 XX New chimeric analog comprising at least one moiety which binds to one or
 XX more somatostatin and dopamine receptor(s) useful to treat e.g.
 XX neuroendocrine tumor, vascular diseases, connective tissue disease,
 XX immune disease and cachexia.
 XX Claim 12; Page 103; 138pp; English.
 XX
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 XX that comprise at least one moiety that binds to one or more somatostatin
 XX receptors and at least one moiety that binds to one or more dopamine
 XX receptors, or a salt derived thereof. Specifically, it refers to
 XX analogues that may be used in vitro or in vivo for research, diagnostic
 XX and therapeutic agents to enhance the activity of somatostatin and
 XX dopamine i.e. working as receptor agonists. The present invention
 XX describes analogues with specificity for different types of somatostatin
 XX receptor subtypes that are accordingly associated with the treatment of
 XX particular diseases or conditions. As such, these analogues may be used
 XX to treat neoplasia and acromegaly as well as various neuroendocrine
 XX tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
 XX scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
 XX tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
 XX hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
 XX disorder or an opioid overdose. Accordingly, they exhibit activities that
 XX include cytostatic, osteopathic, antithyroid, vasotropic, antiangiogenic,
 XX ophthalmological, antidiabetic, dermatological, immunosuppressive,
 XX antiarthritic, antirheumatic, antiinflammatory, antidiabetic, analgesic,
 XX antidiarrhoeic, nephrotropic, hepatotropic, antilipemic, analgesic,
 XX antianginal, anorectic, immunomodulator, cardiac, tranquilizer and
 XX antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
 XX analogue of the invention.
 XX
 XX Query Match 80.0%; Score 64; DB 8; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 0.12;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 3 YYCFWKTKCT 11
 XX DB |||||
 XX 3 YYCFWKTKCT 11
 XX
 XX RESULT 14
 XX ADI14894
 XX ID ADI14894 standard; peptide; 12 AA.
 XX AC ADI14894;
 XX

[illegible]

orthostatic; hypotension; postprandial hypotension; panic attack;
 GH secreting adenoma; acromegaly; TSH secreting adenoma;
 prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 proliferative retinopathy; dawn phenomenon; nephropathy;
 gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 pancreaticocutaneous fistula; dumping syndrome;
 watery diarrhoea syndrome; pancreatitis;
 gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 gastrointestinal rejection; graft vessel bleeding; portal hypertension;
 gastrointestinal bleeding; obesity; opioid overdose; cyclic; circular.
 Synthetic.
 Unidentified.

Key Location/Qualifiers
 Modified-site 1
 /note= "Amino acid is Doc. Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methylsulfonyl-acetic acid. Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methyl-carbamic acid. Optionally bound to carbonic acid mono-(7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methyl) ester. Optionally bound to 4-(7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methyl) butyric acid. Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carboxylic acid. Optionally bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidoethylsulfonyl acetic acid. Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidopropyl)carbamic acid. Optionally bound to carbonic acid mono-(3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureido)propyl)carbamic acid. Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidopropyl)-Gly-. Optionally bound to 4-(3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureido)propyl)carbamic acid"

Modified-site 2. .3
 /note= "Amino acid is Doc"
 Misc-difference 5. .6
 /note= "D-form residue"
 Modified-site 7
 /note= "Residue forms a bond to residue 12 to form a cyclic peptide"
 Misc-difference 9
 /note= "D-form residue"
 Modified-site 12
 /note= "Residue forms a bond to residue 7 to form a cyclic peptide"
 Modified-site 13
 /note= "C-terminal amide"

WO2002100888-A1.
 19-DEC-2002.
 07-JUN-2002; 2002WO-US017859.
 08-JUN-2001; 2001US-0297059P.
 (SCRC) SCRAS SOC CONSIGLS RECH & APPL SCI.
 Culler MD, Dong ZX, Kim SH, Moreau J;
 WPI; 2003-239103/23.
 New somatostatin-dopamine chimeric analogs useful for the treatment of e.g. lung cancer.

PS Claim 3; Page 103; 85pp; English.
 XX This invention relates to novel somatostatin-dopamine chimeric analogues or their salts. The invention may be useful for the development of compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory, antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic, antibacterial, immunomodulator, hypertensive, tranquiliser, antileptemic, nephrotropic, antitumor, antiarthritic, hypotensive, anorectic or antidiabetic activity through action as a dopamine receptor agonist and somatostatin receptor agonist. The invention may be useful for the treatment of lung cancer, glioma, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and internal pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia, meningioma, cancer cachexia, orthostatic, hypotension, postprandial hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH secreting adenomas, prolactin secreting adenomas, insulinoma, glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity, Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon, nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea syndrome, pancreatitis, gastrointestinal hormone secreting tumour, angiogenesis, arthritis, allograft rejection, graft vessel bleeding, portal hypertension, gastrointestinal bleeding, obesity and opioid overdose. The compounds simultaneously elicit dopamine receptor agonist and somatostatin receptor agonist effects in vivo with enhanced biological activity over the native somatostatin and dopamine analogues alone. The present sequence is that of a peptide which was used to produce the somatostatin-dopamine chimeric analogues of the invention.

SQ Sequence 13 AA;
 Query Match 80.0%; Score 64; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 YYCFWKTCCT 11
 | | | | | | | | | |
 Db 5 YYCFWKTCCT 13
 RESULT 17
 ADI14952
 ID ADI14952 standard; peptide; 14 AA.
 AC ADI14952;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Somatostatin-dopamine chimeric analogue-related peptide 62.
 XX
 KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antileptemic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antidiabetic; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;

KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegally; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 XX Synthetic.
 OS Unidentified.
 XX

Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Amino acid is Doc. Bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methylsulfonyl-acetic acid"
 FT Modified-site 2
 FT /note= "Amino acid is Doc"
 FT Misc-difference 6
 FT /note= "D-form residue"
 FT Modified-site 8
 FT /note= "Residue forms a bond to residue 13 to form a
 FT cyclic peptide"
 FT Misc-difference 10
 FT /note= "D-form residue"
 FT Modified-site 13
 FT /note= "Residue forms a bond to residue 8 to form a
 FT cyclic peptide"
 FT Modified-site 14
 FT /note= "C-terminal amide"
 XX WO2002100888-A1.
 XX
 XX 19-DEC-2002.
 XX
 XX 07-JUN-2002; 2002WO-US017859.
 XX
 XX 08-JUN-2001; 2001US-0297059P.
 XX
 XX (SCRC) SCRAS SOC CONSRILS RECH & APPL SCI.
 XX
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 XX
 XX WPI; 2003-239103/23.
 XX
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 XX e.g. lung cancer.
 XX
 XX Claim 3; Page 144; 85pp; English.
 XX
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 XX or their salts. The invention may be useful for the development of
 XX compounds with a cytostatic, antichryroid, vasotropic, anti-inflammatory,
 XX antidarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 XX antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaemic,
 XX nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or
 XX antiaddictive activity through action as a dopamine receptor agonist and
 XX somatostatin receptor agonist. The invention may be useful for the
 XX treatment of lung cancer, glioma, anorexia, hypothyroidism,
 XX hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 XX restenosis, Crohn's disease, systemic sclerosis, external and internal
 XX pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,
 XX hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 XX related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 XX bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 XX reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 XX hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 XX disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 XX meningioma, cancer cachexia, orthostatic, hypotension, postprandial

CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX

Sequence 14 AA;
 SQ

Query Match 80.0%; Score 64; DB 7; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 Db 6 YYCFWKTCCT 14
 |||||
 |||||

RESULT 18
 ABR42184
 ID ABR42184 standard; peptide; 15 AA.
 XX
 XX ABR42184;
 AC
 XX
 DT 28-JUL-2003 (first entry)
 XX
 DE Somatostatin analogue peptide JF-08-87A.
 XX
 KW Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 KW antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "Optional methotrexate-acetyl moiety or 2-bromo-
 FT acetyl-D-tert-butyl or D-tert butyl modification, D-form
 FT residue"
 FT Misc-difference 2
 FT /note= "D-form residue, optional tert-butyl modification"
 FT Misc-difference 3
 FT /note= "D-form residue, optional tert-butyl modification"
 FT Misc-difference 4
 FT /note= "D-form residue, optional tert-butyl modification"
 FT Misc-difference 5
 FT /note= "D-form residue, optional tert-butyl modification"
 FT Modified-site 6
 FT /note= "Optional epsilon-tert-butyloxycarbonyl
 FT modification"
 FT Misc-difference 7
 FT /note= "D-form residue, optional tert-butyl modification"
 FT Modified-site 8
 FT /note= "Optional tert-butyl modification"
 FT Disulfide-bond 9..14
 FT /note= "Optional Cys circularization"
 FT Modified-site 9
 FT /note= "Optional S-trityl modification"
 FT Misc-difference 11
 FT /note= "D-form residue"
 FT Modified-site 12
 FT /note= "Optional epsilon-tert-butyloxycarbonyl
 FT modification"
 FT Modified-site 13
 FT /note= "Optional tert-butyl modification"
 FT Modified-site 14

FT /note= "optional epsilon-tert-butylloxycarbonyl
 FT modification"
 FT 15
 FT Modified-site
 FT /note= "C-terminal amide, optional tert-butyl
 FT modification"
 FT
 PN WO2003028527-A2.
 XX
 XX 10-APR-2003.
 PD
 XX 20-SEP-2002; 2002WO-US030143.
 XX
 XX 21-SEP-2001; 2001US-0323851P.
 PR
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX
 XX Coy DH, Fuselier JA, Murphy WA, Sun L;
 XX
 XX WPI; 2003-441067/41.
 DR
 XX
 XX Biologically active peptides such as somatostatin or bombesin conjugated
 FT to chemical compounds through linkers, useful for treating tumors of the
 FT lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 FT vessels.
 FT
 XX
 PS Disclosure; Page 16; 86pp; English.
 XX
 XX The present sequence is that of somatostatin analogue peptide JF-08-87A.
 CC It is an example of peptide agents of the invention that comprise a
 CC biologically active peptide, such as somatostatin or bombesin, conjugated
 CC to a chemical compound through a linker that maintains the peptide's
 CC biological activity. The peptide agents may also include a cytostatic or
 CC therapeutic agent, label or chelating group and a peptide that increases
 CC the hydrophilic biotransformation of the agent. They are useful for
 CC treating tumors of the lung, breast, brain, eye, prostate, or colon,
 CC tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
 CC angiogenic blood vessels (claimed). Other diseases that can also be
 CC treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
 CC arthritis, neoplastic cells or aberrantly proliferating cells, and
 CC acromegaly. Peptide JF-08-87A has the ability to inhibit growth hormone
 CC release from primary cultures of rat pituitary cells, having an IC50 of
 CC 0.16 nM (compared with 0.15 nM for somatostatin-14). Note: The present
 CC sequence is identified as SEQ ID 2 in the disclosure (page 16), but it is
 CC not the same as the sequence given as SEQ ID 2 in the sequence listing
 XX
 SQ Sequence 15 AA;
 Query Match 80.0%; Score 64; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 YYCPWKTCCT 11
 Db 7 YYCPWKTCCT 15
 RESULT 19
 AD114935
 ID AD114935 standard; peptide; 15 AA.
 XX
 AC AD114935;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX
 XX Somatostatin-dopamine chimeric analogue-related peptide 46.
 DE
 XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquilliser; antilipaeic; nephrotropic; antiulcer; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;

KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetogenic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreatocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "D-form residue. Optionally bound to 7-propyl-
 FT 4, 6, 6a, 7, 8, 9, 10, 10a-octahydroindolo[4, 3-fg]quinolin-9-yl-
 FT methylsulfonyl-acetic acid. Optionally bound to 7-propyl-
 FT 4, 6, 6a, 7, 8, 9, 10, 10a-octahydroindolo[4, 3-fg]quinolin-9-yl-
 FT methyl-carbamic acid. Optionally bound to carbonic acid
 FT mono-(7-propyl-4, 6, 6a, 7, 8, 9, 10, 10a-octahydroindolo[4, 3-
 FT fg]quinolin-9-yl-methyl) ester. Optionally bound to 4-((7-
 FT propyl-4, 6, 6a, 7, 8, 9, 10, 10a-octahydroindolo[4, 3-
 FT fg]quinolin-9-yl-methyl) carbonyl) butyric acid.
 FT Optionally bound to 7-propyl-4, 6, 6a, 7, 8, 9, 10, 10a-
 FT octahydroindolo[4, 3-fg]quinolin-9-carboxylic acid.
 FT Optionally bound to 3-(1-(7-allyl-4, 6, 6a, 7, 8, 9, 10, 10a-
 FT octahydroindolo[4, 3-fg]quinolin-9-carbonyl)-3-
 FT ethylureidopropyl)-gly."
 FT Misc-difference 2. .5
 FT /note= "D-form residue"
 FT Misc-difference 7. .8
 FT /note= "D-form residue"
 FT Modified-site 9
 FT /note= "Residue forms a bond to residue 14 to form a
 FT cyclic peptide"
 FT Misc-difference 11
 FT /note= "D-form residue"
 FT Modified-site 14
 FT /note= "Residue forms a bond to residue 9 to form a
 FT cyclic peptide"
 FT Modified-site 15
 FT /note= "C-terminal OL"
 FT
 XX WO2002100888-A1.
 PN
 XX 19-DEC-2002.
 PD
 XX 07-JUN-2002; 2002WO-US017859.
 PF
 XX 08-JUN-2001; 2001US-0297059P.
 PR
 XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 PA
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 PI
 XX WPI; 2003-239103/23.
 DR
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 FT e.g. lung cancer.
 XX
 PS Claim 3; Page 133; 85pp; English.

XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeamic,
 CC nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or
 CC antiaddictive activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angioneuroma, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX

Sequence 15 AA;
 SQ

Query Match 80.0%; Score 64; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 Db 7 YYCFWKTCCT 15
 |||||
 |||||

RESULT 20
 AD114898
 ID AD114898 standard; peptide; 15 AA.
 XX
 AC AD114898;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Somatostatin-dopamine chimeric analogue-related peptide 11.
 XX
 KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipaeamic; nephrotropic; antiulcer; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidoblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;

KW GH secreting adenoma; acromegally; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angioneuroma; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose; cyclic; circular.
 XX Synthetic.
 OS Unidentified.
 XX

Key	Location/Qualifiers
Modified-site 1	/note= "D-form residue. Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methylsulfonyl-acetic acid. Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methyl-carbamate. Optionally bound to carbonic acid mono-(7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methyl) ester. Optionally bound to 4-(7-fg]quinolin-9-yl-methyl) carbonyl) butyric acid. Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carboxylic acid. Optionally bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carboxyl)-3-ethylureidoethylsulfonyl acetic acid. Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carboxyl)-3-ethylureidopropyl)carbamate. Optionally bound to carbonic acid mono-(3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carboxyl)-3-ethylureido)propyl)carbamate. Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carboxyl)-3-ethylureido)propyl)butyric acid"
Misc-difference 2..5	/note= "D-form residue"
Misc-difference 7..8	/note= "D-form residue"
Modified-site 9	/note= "Residue forms a bond to residue 14 to form a cyclic peptide"
Misc-difference 11	/note= "D-form residue"
Modified-site 14	/note= "Residue forms a bond to residue 9 to form a cyclic peptide"
Modified-site 15	/note= "C-terminal amide"
WO2002100888-A1.	
19-DEC-2002.	
07-JUN-2002; 2002WO-US017859.	
08-JUN-2001; 2001US-0297059P.	
(SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.	
Culler MD, Dong ZX, Kim SH, Moreau J;	
WPI; 2003-239103/23.	
New somatostatin-dopamine chimeric analogs useful for the treatment of e.g. lung cancer.	
Claim 3; Page 103; 85pp; English.	

XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC anti-diarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antileptemic,
 CC nephrotropic, antitumor, antiarthritic, hypotensive, anorectic or
 CC antiaddictive activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC retinosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, vitreous, vitreous, nesidioblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and optoid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX

SQ Sequence 15 AA;
 Query Match 80.0%; Score 64; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 YYCFWKTCCT 11
 Db 7 YYCFWKTCCT 15
 |||||
 |||||

RESULT 21
 ABR42192
 ID ABR42192 standard; peptide; 20 AA.
 XX AC ABR42192;
 XX DT 28-JUL-2003 (first entry)
 XX DE Peptide analogue conjugate.
 XX KW Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 XX KW antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "DOTA moiety or optional DOTA-O-benzyl or O-benzyl
 FT modification, D-form residue"
 FT Misc-difference 2 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 3 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 4 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"

FT Misc-difference 5 residue"
 FT /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 6 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 7 /note= "optionally modified D-with O-benzyl, D-form
 FT residue"
 FT Misc-difference 8 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 9 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 10 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Modified-site 11 /note= "optionally modified with N-epsilon- (2-
 FT chlorobenzylloxycarbonyl)"
 FT Modified-site 12 /note= "optionally modified with O-2,6- dichlorobenzyl"
 FT Modified-site 13 /note= "optionally modified with O-2,6- dichlorobenzyl"
 FT Disulfide-bond 14.19 /note= "Optional Cys circularization"
 FT Modified-site 14 /note= "optionally modified with S-4-methylbenzyl"
 FT Misc-difference 16 /note= "D-form residue"
 FT Modified-site 17 /note= "optionally modified with N-epsilon-(2-
 FT (chlorobenzylloxycarbonyl)"
 FT Modified-site 19 /note= "optionally modified with S-4-methylbenzyl"
 FT Misc-difference 20 /note= "optionally modified with O-benzyl, C-terminal
 FT amide, Rink-amide resin or MBHA resin"
 XX W02003028527-A2.
 XX 10-APR-2003.
 XX 20-SEP-2002; 2002WO-US030143.
 XX 21-SEP-2001; 2001US-0323851P.
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX Coy DH, Fueseller JA, Murphy WA, Sun L;
 XX WPI; 2003-441067/41.
 XX Biologically active peptides such as somatostatin or bombesin conjugated
 XX to chemical compounds through linkers, useful for treating tumors of the
 XX lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 XX vessels.
 XX Example 15; Page 45; 86pp; English.
 XX The present sequence is that of a peptide analogue conjugate that is an
 XX example of peptide agents of the invention that comprise a biologically
 XX active peptide, such as somatostatin or bombesin, conjugated to a
 XX chemical compound through a linker that maintains the peptide's
 XX biological activity. The peptide agents may also include a cytostatic or
 XX therapeutic agent, label or chelating group and a peptide that increases
 XX the hydrophilic biodistribution of the agent. They are useful for
 XX treating tumors of the lung, breast, brain, eye, prostate, or colon,
 XX tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
 XX angiogenic blood vessels (claimed). Other diseases that can also be
 XX treated are inflammatory bowel disease, autoimmune disorders, rheumatoid

CC arthritis, neoplastic cells or aberrantly proliferating cells, and
 CC acromegaly
 XX
 SQ Sequence 20 AA; Query Match 80.0%; Score 64; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
 Db 12 YYCFWKTKCT 20

RESULT 22
 ABR42198
 ID ABR42198 standard; peptide; 20 AA.
 XX
 AC ABR42198;
 XX
 DT 28-JUL-2003 (first entry)
 XX
 XX Somatostatin analogue peptide.
 XX
 XX Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 XX antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 PH Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Misc-difference 6 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 8 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 10 /note= "D-form residue"
 FT Misc-difference 12 /note= "D-form residue"
 FT Misc-difference 13 /note= "D-form residue"
 FT Disulfide-bond 14..19
 FT Misc-difference 16 /note= "D-form residue"
 FT Modified-site 20
 FT /note= "C-terminal amide"
 XX
 XX WO2003028527-A2.
 XX
 PD 10-APR-2003.
 XX
 XX 20-SEP-2002; 2002WO-US030143.
 XX
 XX 21-SEP-2001; 2001US-0323851P.
 PR
 XX (TULA) TULANE EDUCATIONAL FUND.
 PA
 XX Coy DH, Fuselier JA, Murphy WA, Sun L;
 PT
 XX WPI; 2003-441067/41.
 DR

XX Biologically active peptides such as somatostatin or bombesin conjugated
 PT to chemical compounds through linkers, useful for treating tumors of the
 PT lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 PT vessels.
 XX
 PS Example 26; Page 55; 86pp; English.
 XX
 CC The present sequence is that of a somatostatin analogue peptide. It is an
 CC example of peptide agents of the invention that comprise a biologically
 CC active peptide, such as somatostatin or bombesin, conjugated to a
 CC chemical compound through a linker that maintains the peptide's
 CC biological activity. The peptide agents may also include a cytostatic or
 CC therapeutic agent, label or chelating group and a peptide that increases
 CC the hydrophilic biotransformation of the agent. They are useful for
 CC treating tumors of the lung, breast, brain, eye, prostate, or colon,
 CC tumours of neuroendocrine origin (for e.g. carcinoid syndrome), and
 CC angiogenic blood vessels (claimed). Other diseases that can also be
 CC treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
 CC arthritis, neoplastic cells or aberrantly proliferating cells, and
 CC acromegaly. The present peptide has the ability to inhibit growth hormone
 CC release from primary cultures of rat pituitary cells, having an IC50 of
 CC 0.24 nM (compared with 0.15 nM for somatostatin-14)
 XX
 SQ Sequence 20 AA;
 Query Match 80.0%; Score 64; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
 Db 12 YYCFWKTKCT 20

RESULT 23
 ADI14936
 ID ADI14936 standard; peptide; 20 AA.
 XX
 AC ADI14936;
 XX
 DT 22-APR-2004 (first entry)
 XX
 XX Somatostatin-dopamine chimeric analogue-related peptide 47.
 DE
 XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipemic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothalamic; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastrosophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiodysplasia; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 XX

4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methyl carbonyl) butyric acid. Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carboxylic acid. Optionally bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidomethylsulfanyl acetic acid. Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidopropyl)carbamic acid. Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidopropyl)carbamic acid. Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidopropyl)carbamoylbutyric acid"

Misc-difference 2. 10 /note= "D-form residue"

Misc-difference 12. 13 /note= "D-form residue"

Modified-site 14 /note= "Residue forms a bond to residue 19 to form a cyclic peptide"

Misc-difference 16 /note= "D-form residue"

Modified-site 19 /note= "Residue forms a bond to residue 14 to form a cyclic peptide"

Modified-site 20 /note= "C-terminal amide"

WO2002100888-A1.

19-DEC-2002.

07-JUN-2002; 2002WO-US017859.

08-JUN-2001; 2001US-0297059P.

(SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.

Culler MD, Dong ZX, Kim SH, Moreau J;

WPI, 2003-239103/23.

New somatostatin-dopamine chimeric analogs useful for the treatment of e.g. lung cancer.

Claim 3; Page 103; 85pp; English.

This invention relates to novel somatostatin-dopamine chimeric analogues or their salts. The invention may be useful for the development of compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory, antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic, antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeic, nephrotropic, antiulcer, antirheumatic, hypotensive, anorectic or antiaddictive activity through action as a dopamine receptor agonist and somatostatin receptor agonist. The invention may be useful for the treatment of lung cancer, glioma, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and internal pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis, hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia, meningioma, cancer cachexia, orthostatic, hypotension, postprandial hypotension, panic attacks, GH secreting adenomas, acromegally, TSH secreting adenomas, prolactin secreting adenomas, insulinoma, glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,

CC Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon, CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour, CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding, CC portal hypertension, gastrointestinal bleeding, obesity and opioid overdose. The compounds simultaneously elicit dopamine receptor agonist CC and somatostatin receptor agonist effects in vivo with enhanced CC biological activity over the native somatostatin and dopamine analogues CC alone. The present sequence is that of a peptide which was used to CC produce the somatostatin-dopamine chimeric analogues of the invention.

SQ Sequence 20 AA;

Query Match 80.0%; Score 64; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
|||||||

Db 12 YYCFWKTKCT 20

RESULT 25

ABR42181

ID ABR42181 standard; peptide; 22 AA.

XX ABR42181;

AC ABR42181;

XX 28-JUL-2003 (first entry)

XX Somatostatin analogue peptide JF-08-73.

XX Somatostatin; peptide conjugate; cytostatic; antiangiogenic;

KW antiinflammatory; antiarthritic; antirheumatic; cyclic.

XX Synthetic.

Key	Location/Qualifiers
Modified-site 1	/note= "125I-Succinoyl-Aspartic acid, D-form residue"
Misc-difference 2	/note= "D-form residue"
Misc-difference 3	/note= "D-form residue"
Misc-difference 4	/note= "D-form residue"
Misc-difference 5	/note= "D-form residue"
Misc-difference 6	/note= "D-form residue"
Misc-difference 7	/note= "D-form residue"
Misc-difference 8	/note= "D-form residue"
Misc-difference 9	/note= "D-form residue"
Misc-difference 10	/note= "D-form residue"
Misc-difference 11	/note= "D-form residue"
Misc-difference 12	/note= "D-form residue"
Misc-difference 13	/note= "D-form residue"
Misc-difference 14	/note= "D-form residue"
Misc-difference 15	/note= "D-form residue"
Disulfide-bond 16. 21	
Misc-difference 18	/note= "D-form residue"
Modified-site 22	

FT XX /note= "C-terminal amide"

PN WO2003028527-A2.

PD 10-APR-2003.

XX 20-SEP-2002; 2002WO-US030143.

PF 21-SEP-2001; 2001US-0323851P.

PR (TULA) TULANE EDUCATIONAL FUND.

PA Coy DH, Fuselier JA, Murphy WA, Sun L;

XX WPI; 2003-441067/41.

DR Biologically active peptides such as somatostatin or bombesin conjugated

XX to chemical compounds through linkers, useful for treating tumors of the

FT lung and breast, carcinoid syndrome, and tumors of angiogenic blood

FT vessels.

PS Example 19; Page 47; 86pp; English.

XX The present sequence is that of somatostatin analogue peptide JP-08-73.

CC It is an example of peptide agents of the invention that comprise a

CC biologically active peptide, such as somatostatin or bombesin, conjugated

CC to a chemical compound through a linker that maintains the peptide's

CC biological activity. The peptide agents may also include a cytostatic or

CC therapeutic agent, label or chelating group and a peptide that increases

CC the hydrophilic biodistribution of the agent. They are useful for

CC treating tumors of the lung, breast, brain, eye, prostate, or colon,

CC tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and

CC angiogenic blood vessels (claimed). Other diseases that can also be

CC treated are inflammatory bowel disease, autoimmune disorders, rheumatoid

CC arthritis, neoplastic cells or aberrantly proliferating cells, and

CC acromegaly. Peptide JP-08-73 was used in an examination of the

CC biodistribution of hydrophilic peptide agents. A lack of accumulation of

CC radioactivity was noted in normal tissue including liver, but rapid and

CC high efficiency elimination of the peptide agent in urine and faeces.

CC Note: The present sequence is identified as SEQ ID 11 in the disclosure

CC (page 14), but it is not the same as the sequence given as SEQ ID 11 in

CC the sequence listing

XX SQ Sequence 22 AA;

Query Match 80.0%; Score 64; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.22; Mismatches 0; Gaps 0;

Matches 9; Conservative 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11

Db 14 YYCFWKTCCT 22

RESULT 26

ABR42199

ID ABR42199 standard; peptide; 25 AA.

XX ABR42199;

AC 28-JUL-2003 (first entry)

DT Somatostatin analogue peptide.

XX Somatostatin; peptide conjugate; cytostatic; antiangiogenic;

KW antiinflammatory; antiarthritic; antirheumatic; cyclic.

XX Synthetic.

OS Key Location/Qualifiers

FH Modified-site 1

FT /note= "N-terminal 3-N,N-dimethylaminobenzoic acid

FT moiety, D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 3 /note= "D-form residue"

FT Misc-difference 4 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

FT Misc-difference 6 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 8 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Misc-difference 10 /note= "D-form residue"

FT Misc-difference 11 /note= "D-form residue"

FT Misc-difference 12 /note= "D-form residue"

FT Misc-difference 13 /note= "D-form residue"

FT Misc-difference 14 /note= "D-form residue"

FT Misc-difference 15 /note= "D-form residue"

FT Misc-difference 17 /note= "D-form residue"

FT Misc-difference 18 /note= "D-form residue"

FT Disulfide-bond 19. .24

FT Misc-difference 21 /note= "D-form residue"

FT Modified-site 25 /note= "C-terminal amide"

XX WO2003028527-A2.

XX 10-APR-2003.

XX 20-SEP-2002; 2002WO-US030143.

XX 21-SEP-2001; 2001US-0323851P.

XX (TULA) TULANE EDUCATIONAL FUND.

XX Coy DH, Fuselier JA, Murphy WA, Sun L;

XX WPI; 2003-441067/41.

XX Biologically active peptides such as somatostatin or bombesin conjugated

XX to chemical compounds through linkers, useful for treating tumors of the

XX lung and breast, carcinoid syndrome, and tumors of angiogenic blood

XX vessels.

XX Example 26; Page 55; 86pp; English.

XX The present sequence is that of a somatostatin analogue peptide. It is an

XX example of peptide agents of the invention that comprise a biologically

XX active peptide, such as somatostatin or bombesin, conjugated to a

XX chemical compound through a linker that maintains the peptide's

XX biological activity. The peptide agents may also include a cytostatic or

XX therapeutic agent, label or chelating group and a peptide that increases

XX the hydrophilic biodistribution of the agent. They are useful for

XX treating tumors of the lung, breast, brain, eye, prostate, or colon,

XX tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and

XX angiogenic blood vessels (claimed). Other diseases that can also be

XX treated are inflammatory bowel disease, autoimmune disorders, rheumatoid

XX arthritis, neoplastic cells or aberrantly proliferating cells, and

XX acromegaly. The present peptide has the ability to inhibit growth hormone

XX release from primary cultures of rat pituitary cells, having an IC50 of

```
CC 0.27 nM (compared with 0.15 nM for somatostatin-14)
XX
SQ Sequence 25 AA;

Query Match      80.0%; Score 64; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
   |||||
Db 17 YYCFWKTKCT 25

RESULT 27
ABR42197
ID ABR42197 standard; peptide; 30 AA.
XX AC
XX AC
XX ABR42197;
XX
DT 28-JUL-2003 (first entry)
XX
DE Somatostatin analogue peptide.
XX
XX Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
XX antiinflammatory; antiarthritic; antirheumatic; cyclic.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 3 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT Misc-difference 6 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 8 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 10 /note= "D-form residue"
FT Misc-difference 11 /note= "D-form residue"
FT Misc-difference 12 /note= "D-form residue"
FT Misc-difference 13 /note= "D-form residue"
FT Misc-difference 14 /note= "D-form residue"
FT Misc-difference 15 /note= "D-form residue"
FT Misc-difference 16 /note= "D-form residue"
FT Misc-difference 17 /note= "D-form residue"
FT Misc-difference 18 /note= "D-form residue"
FT Misc-difference 19 /note= "D-form residue"
FT Misc-difference 20 /note= "D-form residue"
FT Misc-difference 21 /note= "D-form residue"
FT Misc-difference 22 /note= "D-form residue"
FT Misc-difference 23 /note= "D-form residue"
FT

Disulfide-bond 24..29
Misc-difference 26 /note= "D-form residue"
Modified-site 30 /note= "C-terminal amide"
XX
XX WO2003028527-A2.
XX
XX 10-APR-2003.
XX
XX 20-SEP-2002; 2002WO-US030143.
XX
XX 21-SEP-2001; 2001US-0323851P.
XX
XX (TULA ) TULANE EDUCATIONAL FUND.
XX
XX Coy DH, Fuselier JA, Murphy WA, Sun L;
XX WPI; 2003-441067/41.
XX
XX Biologically active peptides such as somatostatin or bombesin conjugated
XX to chemical compounds through linkers, useful for treating tumors of the
XX lung and breast, carcinoid syndrome, and tumors of angiogenic blood
XX vessels.
XX
XX Example 26; Page 55; 86pp; English.
XX
XX The present sequence is that of a somatostatin analogue peptide. It is an
XX example of peptide agents of the invention that comprise a biologically
XX active peptide, such as somatostatin or bombesin, conjugated to a
XX chemical compound through a linker that maintains the peptide's
XX biological activity. The peptide agents may also include a cytostatic or
XX therapeutic agent, label or chelating group and a peptide that increases
XX the hydrophilic biodistribution of the agent. They are useful for
XX treating tumors of the lung, breast, brain, eye, prostate, or colon,
XX tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
XX angiogenic blood vessels (claimed). Other diseases that can also be
XX treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
XX arthritis, neoplastic cells or aberrantly proliferating cells, and
XX acromegaly
XX
XX Sequence 30 AA;
SQ
Query Match      80.0%; Score 64; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
   |||||
Db 22 YYCFWKTKCT 30

RESULT 28
ADS74379
ID ADS74379 standard; peptide; 11 AA.
XX
XX ADS74379;
XX
XX 16-DEC-2004 (first entry)
XX
XX Somatostatin analogue.
XX
XX Somatostatin analogue; cytostatic; gene therapy.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 1..4 /note= "D-form residues"
FT Disulfide-bond 5..10
FT Misc-difference 7 /note= "D-form residue"
FT Modified-site 11
```

FT XX /note= "C-terminal amide or alcohol"
 PN WO2004081031-A2.
 XX
 XX
 PD 23-SEP-2004.
 XX
 XX 10-MAR-2004; 2004WO-US007143.
 PF
 XX
 XX 10-MAR-2003; 2003US-0452928P.
 PR
 XX (BIOG-) BIOGEN IDEC INC.
 XX
 XX Braslawsky GR, Chinn P;
 PI
 XX WPI; 2004-689933/65.
 DR
 XX
 XX A composition comprising a somatostatin analog useful for thiol-specific
 FT drug attachment to somatostatin and other targeting peptides, or for
 FT diagnosing or treating somatostatin receptor-associated disorders, e.g.
 FT cancer.
 FT
 XX Claim 4; SEQ ID NO 7; 43pp; English.
 PS
 XX The present sequence is that of a synthetic somatostatin analogue. The
 CC peptide can be used as component B in a claimed composition comprising a
 CC somatostatin analogue of formula (A-B), where A is Cys, or a peptide
 CC chain comprising one or more Cys residues, which is suitable for binding
 CC to a drug or chelator via a thiol linkage, and B is a naturally occurring
 CC or synthetic somatostatin peptide, or its fragment, that binds to the
 CC somatostatin receptor (SSTR). The drug or chelator is bound to the Cys
 CC residue(s) of component A by a thiol linkage. The drug is a therapeutic
 CC drug such as a radioisotope, a cytotoxin, an immunostimulant, an
 CC antiangiogenic agent, a therapeutic gene, or a chemotherapeutic agent.
 CC The somatostatin analogue preferably binds to SSTR-positive cells,
 CC especially human cancer cells. A claimed method for detecting SSTR-
 CC positive cells comprises administering the somatostatin analogue in which
 CC a detectable label is bound to the Cys residue(s) of component A, and
 CC detecting the label. A claimed method for treating an SSTR-associated
 CC disorder comprises administering a somatostatin analogue in which a
 CC therapeutic agent is bound to the Cys residue(s) of component A. The SSTR
 CC -associated disorder is especially cancer. Thiol-mediated drug attachment
 CC can also be used with other targeting peptides.
 XX
 XX Sequence 11 AA;
 SQ

Query Match 78.1%; Score 62.5; DB 8; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.19;
 Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1 YCYCFWKTC 11
 Db 2 YC-YCFWKTC 11
 || |||||
 || |||||

RESULT 29
 ADU05266
 ID ADU05266 standard; peptide; 10 AA.
 XX
 AC ADU05266;
 XX
 XX 13-JAN-2005 (first entry)
 DT
 XX
 XX Cyclic somatostatin-dopamine chimeric peptide analogue #56.
 DE
 XX somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective tissue disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cyrostatic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antitumor;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipaeamic; analgesic;

antangiinal; anorectic; immunomodulator; cardiant; tranquillizer;
 antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 Synthetic.
 Location/Qualifiers
 Key Modified-site 1 /note= "An N-terminal dopamine derivative (Dop1, Dop2 or
 FT Dop5) is attached to a Lys(dopamine derivative) modified
 FT residue, where this second dopamine derivative must match
 FT the type occurring at the N-terminus, e.g. Dop1-
 FT Lys(Dop1), Dop2-Lys(Dop2) etc. Optionally Lys can be a D-
 FT form residue."
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Disulfide-bond 4..9 /note= This disulphide bond cyclises the peptide
 FT Modified-site 5 /label= 3-iodo tyrosine
 FT Misc-difference 6 /note= "D-form residue"
 FT Modified-site 10 /note= "C-terminal amide"
 FT
 FT WO2004091490-A2.
 XX
 XX 28-OCT-2004.
 PD
 XX 08-APR-2004; 2004WO-US010891.
 PF
 XX 11-APR-2003; 2003US-0462374P.
 PR
 XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX
 XX Dong ZX, Dewitt Culler M, Shen Y;
 XX WPI; 2004-784484/77.
 DR
 XX New chimeric analog comprising at least one moiety which binds to one or
 PT more somatostatin and dopamine receptor(s) useful to treat e.g.
 PT neuroendocrine tumor, vascular diseases, connective tissue disease,
 PT immune disease and cachexia.
 PT
 XX Claim 12; Page 115; 138pp; English.
 PS
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC that comprise at least one moiety that binds to one or more somatostatin
 CC receptors and at least one moiety that binds to one or more dopamine
 CC receptors, or a salt derived thereof. Specifically, it refers to
 CC analogues that may be used in vitro or in vivo for research, diagnostic
 CC and therapeutic agents to enhance the activity of somatostatin and
 CC dopamine i.e. working as receptor agonists. The present invention
 CC describes analogues with specificity for different types of somatostatin
 CC receptor subtypes that are accordingly associated with the treatment of
 CC particular diseases or conditions. As such, these analogues may be used
 CC to treat neoplasia and acromegaly as well as various neuroendocrine
 CC tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
 CC scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
 CC tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
 CC hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
 CC disorder or an opioid overdose. Accordingly, they exhibit activities that
 CC include cytostatic, osteopathic, antithyroid, vasotropic, antiangiogenic,
 CC ophthalmological, antidiabetic, dermatological, immunosuppressive,
 CC antiarthritic, antirheumatic, antiinflammatory, antitumor,
 CC antidiarrhoeic, nephrotropic, hepatotropic, antilipaeamic, analgesic,
 CC antiangiinal, anorectic, immunomodulator, cardiant, tranquillizer and
 CC antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
 CC analogue of the invention.
 XX
 XX Sequence 10 AA;

Query Match 76.2%; Score 61; DB 8; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.28;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
 Db 2 YYCYWKTKCT 10

RESULT 30
 ADU05270
 ID ADU05270 standard; peptide; 11 AA.
 XX
 AC ADU05270;
 DT 13-JAN-2005 (first entry)
 XX
 DE Cyclic somatostatin-dopamine chimeric peptide analogue #60.
 KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytosatic; osteopathic; antidiabetic; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antitumor;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipemic; analgesic;
 KW antianginal; anorectic; immunomodulator; cardiant; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX
 OS Synthetic.

Key Location/Qualifiers
 Modified-site 1 /note= "An N-terminal dopamine derivative (Dop1, Dop2 or Dop5) is attached to a Lys(dopamine derivative) modified residue, where this second dopamine derivative must match the type occurring at the N-terminus, e.g. Dop1-Lys (Dop1), Dop2-Lys (Dop2) etc. Optionally Lys can be a D-form residue."
 Misc-difference 3 /note= "D-form residue"
 Misc-difference 4 /note= "D-form residue"
 Disulfide-bond 5..10 /note= "D-form residue"
 Modified-site 6 /label= 3-iodo tyrosine
 Misc-difference 7 /note= "D-form residue"
 Modified-site 11 /note= "C-terminal amide"
 WO2004091490-A2.
 PD 28-OCT-2004.
 XX
 PF 08-APR-2004; 2004WO-US010891.
 XX
 PR 11-APR-2003; 2003US-0462374P.
 XX
 PA (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX
 PI Dong ZX, Dewitt Culler M, Shen Y;
 XX
 DR WPI; 2004-784484/77.
 XX
 FT New chimeric analog comprising at least one moiety which binds to one or more somatostatin and dopamine receptor(s) useful to treat e.g. neuroendocrine tumor, vascular diseases, connective tissue disease, immune disease and cachexia.

PS
 XX
 CC This invention relates to novel somatostatin-dopamine chimeric analogues that comprise at least one moiety that binds to one or more somatostatin receptors and at least one moiety that binds to one or more dopamine analogues, or a salt derived thereof. Specifically, it refers to analogues that may be used in vitro or in vivo for research, diagnostic and therapeutic agents to enhance the activity of somatostatin and dopamine i.e. working as receptor agonists. The present invention describes analogues with specificity for different types of somatostatin receptor subtypes that are accordingly associated with the treatment of particular diseases or conditions. As such, these analogues may be used to treat neoplasia and acromegaly as well as various neuroendocrine tumours, vascular diseases e.g. angiogenesis, connective diseases e.g. scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g. hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic disorder or an opioid overdose. Accordingly, they exhibit activities that include cytostatic, osteopathic, antidiabetic, vasotropic, antiangiogenic, ophthalmological, antidiabetic, dermatological, immunosuppressive, antiarthritic, antirheumatic, antiinflammatory, antitumor, antidiarrhoeic, nephrotropic, hepatotropic, antilipemic, analgesic, antianginal, anorectic, immunomodulator, cardiant, tranquilizer and antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric analogue of the invention.

Sequence 11 AA;
 Query Match 76.2%; Score 61; DB 8; Length 11;
 Best Local Similarity 88.9%; Pred. No. 0.3;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
 Db 3 YYCYWKTKCT 11

RESULT 31
 ADU05281
 ID ADU05281 standard; peptide; 11 AA.
 XX
 AC ADU05281;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Cyclic somatostatin-dopamine chimeric peptide analogue #71.
 KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytosatic; osteopathic; antidiabetic; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antitumor;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipemic; analgesic;
 KW antianginal; anorectic; immunomodulator; cardiant; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX
 OS Synthetic.

Key Location/Qualifiers
 Modified-site 1 /note= "An N-terminal dopamine derivative (Dop2) is attached to a Lys(dopamine derivative) modified residue, where this second dopamine derivative must match the type occurring at the N-terminus, i.e. Dop2-Lys (Dop2). Optionally Lys can be a D-form residue."
 Modified-site 2 /label= OTHER
 Misc-difference 3 /note= "OTHER= Aepa, 4-(2-aminoethyl)-1-carboxy methyl-piperazine"

FT Misc-difference 4 /note= "D-form residue"
FT /note= "D-form residue"
FT Disulfide-bond 5 .10
FT /note= This disulphide bond cyclises the peptide
FT Modified-site 6
FT /note= "3-iodo tyrosine"
FT Misc-difference 7
FT /note= "D-form residue"
FT Modified-site 11
FT /note= "C-terminal amide"
XX WO2004091490-A2.
XX 28-OCT-2004.
XX 08-APR-2004; 2004WO-US010891.
XX 11-APR-2003; 2003US-0462374P.
XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
XX Dong ZX, Dewitt Culler M, Shen Y;
XX WPI; 2004-784484/77.
XX
XX New chimeric analog comprising at least one moiety which binds to one or
XX more somatostatin and dopamine receptor(s) useful to treat e.g.
XX neuroendocrine tumor, vascular diseases, connective tissue disease,
XX immune disease and cachexia.
XX
XX Claim 12; Page 116; 138pp; English.
XX
XX This invention relates to novel somatostatin-dopamine chimeric analogues
XX that comprise at least one moiety that binds to one or more somatostatin
XX receptors and at least one moiety that binds to one or more dopamine
XX receptors, or a salt derived thereof. Specifically, it refers to
XX analogues that may be used in vitro or in vivo for research, diagnostic
XX and therapeutic agents to enhance the activity of somatostatin and
XX dopamine i.e. working as receptor agonists. The present invention
XX describes analogues with specificity for different types of somatostatin
XX receptor subtypes that are accordingly associated with the treatment of
XX particular diseases or conditions. As such, these analogues may be used
XX to treat neoplasia and acromegaly as well as various neuroendocrine
XX tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
XX scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
XX tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
XX hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
XX disorder or an opioid overdose. Accordingly, they exhibit activities that
XX include cytostatic, osteopathic, antithyroid, vasotropic, antiangiogenic,
XX ophthalmological, antidiabetic, dermatological, immunosuppressive,
XX antiarthritic, antirheumatic, antiinflammatory, antitumor,
XX antidiarrhoeic, nephrotropic, hepatotropic, antilipaseic, analgesic,
XX antianginal, anorectic, immunomodulator, cardiant, tranquilizer and
XX antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
XX analogue of the invention.
SQ Sequence 11 AA;

Query Match 76.2%; Score 61; DB 8; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YCYCFWKTCCT 11
D5 3 YCYCFWKTCCT 11

RESULT 32
AAY94484
ID AAY944484 standard; peptide; 12 AA.
XX
AC AAY944484;

XX 20-SEP-2000 (first entry)
XX Human somatostatin analog JP-05-43.
XX
XX Human; somatostatin; SRIF; neuropeptide; antineoplastic; psoriasis;
XX protective retinopathy; diabetes-related blindness.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "1,3 diaminopropionic acid"
XX Modified-site 3 /note= "1,3 diaminopropionic acid"
XX Modified-site 5 /note= "1,3 diaminopropionic acid"
XX Disulfide-bond 6 .11
XX Misc-difference 8 /note= "D-form residue"
XX Modified-site 12 /note= "C-terminal amide"
XX WO2000031122-A1.
XX 02-JUN-2000.
XX 20-OCT-1999; 99WO-US024532.
XX 19-NOV-1998; 98US-00196259.
XX (TULA) UNIV TULANE.
XX Coy DH, Murphy WA, Wolterling EA, Fusellier JA, Drouant G;
XX WPI; 2000-400036/34.
XX
XX Somatatin analogs useful for the treatment of neoplastic cells
XX expressing somatostatin receptors and targeting angiogenic blood vessels.
XX Disclosure; Page 10; 35pp; English.
XX
XX The human somatostatin (SRIF) peptide, is an endogenous neuropeptide that
XX acts as a regulator of growth hormone secretion. Novel analogs of SRIF
XX have been synthesised. The present sequence is one such analog, denoted
XX JP-05-43. These analogs may be used as an antineoplastic therapeutic,
XX specifically targeted to angiogenic blood vessels or cells. Angiogenic
XX blood vessel cells which are involved in human diseases, such as
XX psoriasis, protective retinopathy and diabetes-related blindness, may
XX also be targeted. The SRIF analogs act by inhibition of growth hormone
XX release. Radiolabelled analogs can be used to selectively kill a
XX neoplastic cell expressing a somatostatin receptor. The analogs are also
XX useful for imaging cells expressing a receptor to which the analog
XX specifically binds. This may be used for tumour localization. Analogs
XX with multiple tyrosine residues have the advantage that they are
XX hydrophilic, which allows tumours in the liver to visualised
XX
SQ Sequence 12 AA;

Query Match 76.2%; Score 61; DB 3; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YCYCFWKTCCT 11
D5 2 YCYCFWKTCCT 12

RESULT 33
AAY94487
ID AAY944487 standard; peptide; 12 AA.
XX
AC AAY944487;

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XX DT 20-SEP-2000 (first entry)
XX DE Human somatostatin analog JF-06-45.
XX KW Human; somatostatin; SRIF; neuropeptide; antineoplastic; psoriasis;
XX KW protective retinopathy; diabetes-related blindness.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT Modified-site 3 /note= "1,4 diaminobutanoic acid"
XX FT Modified-site 5 /note= "1,4 diaminobutanoic acid"
XX FT Disulfide-bond 6..11 /note= "1,4 diaminobutanoic acid"
XX FT Misc-difference 8
XX FT Modified-site 12 /note= "D-form residue"
XX FT Modified-site 12 /note= "C-terminal amide"
XX FN WO200031122-A1.
XX PD 02-JUN-2000.
XX PF 20-OCT-1999; 99WO-US024532.
XX PX 19-NOV-1998; 98US-00196259.
XX PX (TULA ) UNIV TULANE.
XX PY Coy DH, Murphy WA, Woltering EA, Fueseller JA, Drouant G;
XX PX WPI, 2000-400036/34.
XX PX Somatostatin analogs useful for the treatment of neoplastic cells
XX PX expressing somatostatin receptors and targeting angiogenic blood vessels.
XX PS Disclosure; Page 11; 35pp; English.
XX CC The human somatostatin (SRIF) peptide, is an endogenous neuropeptide that
XX CC acts as a regulator of growth hormone secretion. Novel analogs of SRIF
XX CC have been synthesised. The present sequence is one such analog, denoted
XX CC JF-06-45. These analogs may be used as an antineoplastic therapeutic,
XX CC specifically targeted to angiogenic blood vessels or cells. Angiogenic
XX CC blood vessel cells which are involved in human diseases, such as
XX CC psoriasis, protective retinopathy and diabetes-related blindness, may
XX CC also be targeted. The SRIF analogs act by inhibition of growth hormone
XX CC release. Radiolabelled analogs can be used to selectively kill a
XX CC neoplastic cell expressing a somatostatin receptor. The analogs are also
XX CC useful for imaging cells expressing a receptor to which the analog
XX CC specifically binds. This may be used for tumour localization. Analogs
XX CC with multiple tyrosine residues have the advantage that they are
XX CC hydrophilic, which allows tumours in the liver to visualised
XX SQ Sequence 12 AA;
XX
XX Query Match 76.2%; Score 61; DB 3; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 0.32;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 YCYCFPKMTCT 11
XX Db 2 YXXCFPKMTCT 12
XX
XX RESULT 34
XX ADI14944
XX ID ADI14944 standard; peptide; 10 AA.
XX

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```

AC ADI14944;
XX 22-APR-2004 (first entry)
XX DE Somatostatin-dopamine chimeric analogue-related peptide 55.
XX KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
XX KW vasotropic; anti-inflammatory; antidiarrheic; anti-HIV; dermatological;
XX KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
XX KW tranquiliser; antiileptic; nephrotropic; antitumor; antiarthritic;
XX KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
XX KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
XX KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
XX KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
XX KW pancreatic pseudocyst; ascite; VIPoma; neuroblastosis; hyperinsulinism;
XX KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
XX KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
XX KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
XX KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
XX KW gonadotropinoma; hyperparathyroidism; Graves disease;
XX KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
XX KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
XX KW orthostatic; hypotension; postprandial hypotension; panic attack;
XX KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
XX KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiopathy;
XX KW proliferative retinopathy; dawn phenomenon; nephropathy;
XX KW gastric acid secretion; peptic ulcer; dumping syndrome;
XX KW pancreaticocutaneous fistula; pancreatitis;
XX KW watery diarrhoea syndrome;
XX KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
XX KW allograft rejection; graft vessel bleeding; portal hypertension;
XX KW gastrointestinal bleeding; obesity; opioid overdose.
XX OS Synthetic.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "D-form residue. Optionally bound to 7-propyl-
XX FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
XX FT methylsulfonyl-acetic acid. Optionally bound to 3-(1-(7-
XX FT allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin
XX FT -9-carbonyl)-3-ethylureidopropyl)-Gly-"
XX FT Misc-difference 2..3 /note= "D-form residue"
XX FT Modified-site 4 /note= "Residue forms a bond to residue 9 to form a
XX FT cyclic peptide"
XX FT Misc-difference 6 /note= "D-form residue"
XX FT Modified-site 9 /note= "Residue forms a bond to residue 4 to form a
XX FT cyclic peptide"
XX FT Modified-site 10 /note= "C-terminal amide"
XX FN WO2002100888-A1.
XX PX 19-DEC-2002.
XX PX 07-JUN-2002; 2002WO-US017859.
XX PX 08-JUN-2001; 2001US-0297059P.
XX PX (SCRC ) SCRAS SOC CONSEILS RECH & APPL SCI.
XX PX Culler MD, Dong ZX, Kim SH, Moreau J;
XX PX WPI, 2003-239103/23.
XX PX New somatostatin-dopamine chimeric analogs useful for the treatment of
XX PX e.g. lung cancer.

```

XX	Claim 3; Page 139; 85pp; English.	KW	thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
PS		KW	orthostatic; hypotension; postprandial hypotension; panic attack;
XX		KW	GH secreting adenoma; acromegaly; TSH secreting adenoma;
CC	This invention relates to novel somatostatin-dopamine chimeric analogues	KW	prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
CC	or their salts. The invention may be useful for the development of	KW	hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
CC	compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,	KW	proliferative retinopathy; dawn phenomenon; nephropathy;
CC	antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,	KW	gastric acid secretion; peptic ulcer; enterocutaneous fistula;
CC	antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaemic,	KW	pancreaticocutaneous fistula; dumping syndrome;
CC	nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or	KW	watery diarrhoea syndrome; pancreatitis;
CC	antiaddictive activity through action as a dopamine receptor agonist and	KW	gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
CC	somatostatin receptor agonist. The invention may be useful for the	KW	allograft rejection; graft vessel bleeding; portal hypertension;
CC	treatment of lung cancer, glioma, anorexia, hypothyroidism,	KW	gastrointestinal bleeding; obesity; opioid overdose.
CC	hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,	XX	
CC	restenosis, Crohn's disease, systemic sclerosis, external and internal	OS	Synthetic.
CC	pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,	OS	Unidentified.
CC	hyperinsulinism, gastrinoma, Zollinger-Elison Syndrome, diarrhoea, AIDS	XX	
CC	related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable	PH	Location/Qualifiers
CC	bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal	FT	Modified-site 1
CC	reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,	FT	/note= "Amino acid is Doc. Optionally bound to 7-propyl-
CC	hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's	FT	4,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
CC	disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,	FT	methylsulfonyl-acetic acid. Optionally bound to 3-(1-(7-
CC	meningioma, cancer cachexia, orthostatic, hypotension, postprandial	FT	allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin
CC	hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH	FT	-9-carbonyl)-3-ethylureidopropyl)-Gly-
CC	secreting adenomas, prolactin secreting adenomas, insulinoma,	FT	Misc-difference 3. .4
CC	glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,	FT	/note= "D-form residue"
CC	Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,	FT	Modified-site 5
CC	nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous	FT	/note= "Residue forms a bond to residue 10 to form a
CC	fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea	FT	cyclic peptide"
CC	syndrome, pancreatitis, gastrointestinal hormone secreting tumour,	FT	Modified-site 7
CC	angiogenesis, arthritis, allograft rejection, graft vessel bleeding,	FT	/note= "D-form residue"
CC	portal hypertension, gastrointestinal bleeding, obesity and opioid	FT	Modified-site 10
CC	overdose. The compounds simultaneously elicit dopamine receptor agonist	FT	/note= "Residue forms a bond to residue 5 to form a
CC	and somatostatin receptor agonist effects in vivo with enhanced	FT	cyclic peptide"
CC	biological activity over the native somatostatin and dopamine analogues	FT	Modified-site 11
CC	alone. The present sequence is that of a peptide which was used to	FT	/note= "C-terminal amide"
CC	produce the somatostatin-dopamine chimeric analogues of the invention.	XX	
XX		PN	WO2002100888-A1.
SQ	Sequence 10 AA;	XX	
	Query Match 73.8%; Score 59; DB 7; Length 10;	XX	
	Best Local Similarity 88.9%; Pred. No. 0.49; Indels 0; Gaps 0;	XX	
	Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	XX	
Oy	3 YYCFWKTCCT 11	XX	
		XX	
Db	2 YYCFWKVCT 10	XX	
		XX	
RESULT 35		XX	
AD114943		XX	
ID	AD114943 standard; peptide; 11 AA.	XX	
XX		XX	
AC	AD114943;	XX	
DT	22-APR-2004 (first entry)	XX	
XX		XX	
DE	Somatostatin-dopamine chimeric analogue-related peptide 54.	XX	
XX		XX	
KW	somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;	XX	
KW	vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;	XX	
KW	anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;	XX	
KW	tranquilliser; antilipaemic; nephrotropic; antiulcer; antiarthritic;	XX	
KW	hypotensive; anorectic; antiaddictive; dopamine receptor agonist;	XX	
KW	somatostatin receptor agonist; lung cancer; glioma; anorexia;	XX	
KW	hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;	XX	
KW	acromegaly; restenosis; Crohn's disease; systemic sclerosis;	XX	
KW	pancreatic pseudocyst; ascite; VIPoma; nesidoblastosis; hyperinsulinism;	XX	
KW	gastrinoma; Zollinger-Elison Syndrome; diarrhoea;	XX	
KW	AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;	XX	
KW	irritable bowel syndrome; pancreatitis; small bowel obstruction;	XX	
KW	gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;	XX	
KW	gonadotropinoma; hyperparathyroidism; Graves disease;	XX	
KW	diabetic neuropathy; Paget's disease; polycystic ovary disease;	XX	

CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angioneuroma, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 11 AA;
 Query Match 73.8%; Score 59; DB 7; Length 11;
 Best Local Similarity 88.9%; Pred. No. 0.53;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 YYCFWKVCT 11
 DB 3 YYCFWKVCT 11
 RESULT 36
 AAY94481
 ID AAY94481 standard; peptide; 12 AA.
 AC AAY94481;
 XX
 DT 20-SEP-2000 (first entry)
 XX
 DE Human somatostatin analog JP-05-81.
 XX
 KW Human; somatostatin; SRIF; neuropeptide; antineoplastic; psoriasis;
 KW protective retinopathy; diabetes-related blindness.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 2 /note= "D-form residue"
 FT Disulfide-bond 6..11
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 12 /note= "C-terminal amide"
 FT
 XX WO200031122-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 20-OCT-1999; 99WO-US024532.
 XX
 PR 19-NOV-1998; 98US-00196259.
 XX
 PA (TULA) UNIV TULANE.
 XX
 PI Coy DH, Murphy WA, Wolterling EA, Fuselier JA, Drouant G;
 XX WPI; 2000-400036/34.
 DR
 PT Somatostatin analogs useful for the treatment of neoplastic cells
 PT expressing somatostatin receptors and targeting angiogenic blood vessels.
 XX
 PS Disclosure; Page 10; 35pp; English.
 XX
 CC The human somatostatin (SRIF) peptide, is an endogenous neuropeptide that
 CC acts as a regulator of growth hormone secretion. Novel analogs of SRIF
 CC have been synthesised. The present sequence is one such analog, denoted

CC JP-05-81. These analogs may be used as an antineoplastic therapeutic,
 CC specifically targeted to angiogenic blood vessels or cells. Angiogenic
 CC blood vessel cells which are involved in human diseases, such as
 CC psoriasis, protective retinopathy and diabetes-related blindness, may
 CC also be targeted. The SRIF analogs act by inhibition of growth hormone
 CC release. Radiolabelled analogs can be used to selectively kill a
 CC neoplastic cell expressing a somatostatin receptor. The analogs are also
 CC useful for imaging cells expressing a receptor to which the analog
 CC specifically binds. This may be used for tumour localization. Analogs
 CC with multiple tyrosine residues have the advantage that they are
 CC hydrophilic, which allows tumours in the liver to visualised
 XX
 SQ Sequence 12 AA;
 Query Match 73.8%; Score 59; DB 3; Length 12;
 Best Local Similarity 81.8%; Pred. No. 0.57;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YCYVCFWKVCT 11
 DB 2 YRYRCFWKTC 12
 RESULT 37
 AAY94489
 ID AAY94489 standard; peptide; 12 AA.
 XX
 AC AAY94489;
 XX
 DT 20-SEP-2000 (first entry)
 XX
 DE Human somatostatin analog JP-06-57.
 XX
 KW Human; somatostatin; SRIF; neuropeptide; antineoplastic; psoriasis;
 KW protective retinopathy; diabetes-related blindness.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Disulfide-bond 6..11
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 12 /note= "C-terminal amide"
 FT
 XX WO200031122-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 20-OCT-1999; 99WO-US024532.
 XX
 PR 19-NOV-1998; 98US-00196259.
 XX
 PA (TULA) UNIV TULANE.
 XX
 PI Coy DH, Murphy WA, Wolterling EA, Fuselier JA, Drouant G;
 XX WPI; 2000-400036/34.
 DR
 PT Somatostatin analogs useful for the treatment of neoplastic cells
 PT expressing somatostatin receptors and targeting angiogenic blood vessels.
 XX
 PS Disclosure; Page 11; 35pp; English.
 XX

CC The human somatostatin (SRIF) peptide, is an endogenous neuropeptide that
 CC acts as a regulator of growth hormone secretion. Novel analogs of SRIF
 CC have been synthesised. The present sequence is one such analog, denoted
 CC JP-06-57. These analogs may be used as an antineoplastic therapeutic,
 CC specifically targeted to angiogenic blood vessels or cells. Angiogenic
 CC blood vessel cells which are involved in human diseases, such as
 CC psoriasis, protective retinopathy and diabetes-related blindness, may
 CC also be targeted. The SRIF analogs act by inhibition of growth hormone
 CC release. Radiolabelled analogs can be used to selectively kill a
 CC neoplastic cell expressing a somatostatin receptor. The analogs are also
 CC useful for imaging cells expressing a receptor to which the analog
 CC specifically binds. This may be used for tumour localization. Analogs
 CC with multiple tyrosine residues have the advantage that they are
 CC hydrophilic, which allows tumours in the liver to visualised
 XX
 SQ Sequence 12 AA;

Query Match 73.8%; Score 59; DB 3; Length 12;
 Best Local Similarity 81.8%; Pred. No. 0.57;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYCFWKTCCT 11
 | | | | |
 Db 2 YKYCFWKTCCT 12

RESULT 38
 AAY94485
 ID AAY94485 standard; peptide; 12 AA.
 AC AAY94485;
 XX
 DT 20-SEP-2000 (first entry)
 XX
 DE Human somatostatin analog JP-05-44.
 XX
 KW Human; somatostatin; SRIF; neuropeptide; antineoplastic; psoriasis;
 KW protective retinopathy; diabetes-related blindness.
 KW
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Disulfide-bond 6. .11
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 12 /note= "C-terminal amide"

WO200031122-A1.

02-JUN-2000.

20-OCT-1999; 99WO-US024532.

19-NOV-1998; 98US-00196259.

(TULA) UNIV TULANE.

Coy DH, Murphy WA, Woltering EA, Fuselier JA, Drouant G;

WPI; 2000-400036/34.

Somatostatin analogs useful for the treatment of neoplastic cells

PT expressing somatostatin receptors and targeting angiogenic blood vessels.
 PS Example 4; Page 25; 35pp; English.
 XX

CC The human somatostatin (SRIF) peptide, is an endogenous neuropeptide that
 CC acts as a regulator of growth hormone secretion. Novel analogs of SRIF
 CC have been synthesised. The present sequence is one such analog, denoted
 CC JP-05-44. These analogs may be used as an antineoplastic therapeutic,
 CC specifically targeted to angiogenic blood vessels or cells. Angiogenic
 CC blood vessel cells which are involved in human diseases, such as
 CC psoriasis, protective retinopathy and diabetes-related blindness, may
 CC also be targeted. The SRIF analogs act by inhibition of growth hormone
 CC release. Radiolabelled analogs can be used to selectively kill a
 CC neoplastic cell expressing a somatostatin receptor. The analogs are also
 CC useful for imaging cells expressing a receptor to which the analog
 CC specifically binds. This may be used for tumour localization. Analogs
 CC with multiple tyrosine residues have the advantage that they are
 CC hydrophilic, which allows tumours in the liver to visualised
 XX
 SQ Sequence 12 AA;

Query Match 73.8%; Score 59; DB 3; Length 12;
 Best Local Similarity 81.8%; Pred. No. 0.57;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYCFWKTCCT 11
 | | | | |
 Db 2 YKYCFWKTCCT 12

RESULT 39
 AAY94490
 ID AAY94490 standard; peptide; 12 AA.
 AC AAY94490;
 XX

DT 20-SEP-2000 (first entry)

DE Human somatostatin analog JIC-2D.

KW Human; somatostatin; SRIF; neuropeptide; antineoplastic; psoriasis;
 KW protective retinopathy; diabetes-related blindness.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Modified-site 2 /note= "diiodotyrosine: D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Modified-site 4 /note= "diiodotyrosine: D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Disulfide-bond 6. .11
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 12 /note= "C-terminal amide"

WO200031122-A1.

02-JUN-2000.

20-OCT-1999; 99WO-US024532.

19-NOV-1998; 98US-00196259.

(TULA) UNIV TULANE.

PI Coy DH, Murphy WA, Wolterling EA, Fuselier JA, Drouant G;
 XX WPI; 2000-400036/34.
 XX Somatostatin analogs useful for the treatment of neoplastic cells
 PT expressing somatostatin receptors and targeting angiogenic blood vessels.
 XX Example 5; Page 26; 35pp; English.
 XX The human somatostatin (SRIF) peptide, is an endogenous neuropeptide that
 CC acts as a regulator of growth hormone secretion. Novel analogs of SRIF
 CC have been synthesised. The present sequence is one such analog, denoted
 CC J1C-2D. These analogs may be used as an antineoplastic therapeutic,
 CC specifically targeted to angiogenic blood vessels or cells. Angiogenic
 CC blood vessel cells which are involved in human diseases, such as
 CC psoriasis, protective retinopathy and diabetes-related blindness, may
 CC also be targeted. The SRIF analogs act by inhibition of growth hormone
 CC release. Radiolabelled analogs can be used to selectively kill a
 CC neoplastic cell expressing a somatostatin receptor. The analogs are also
 CC useful for imaging cells expressing a receptor to which the analog
 CC specifically binds. This may be used for tumour localization. Analogs
 CC with multiple tyrosine residues have the advantage that they are
 CC hydrophilic, which allows tumours in the liver to visualised
 XX Sequence 12 AA;
 SQ Query Match 73.8%; Score 59; DB 3; Length 12;
 Best Local Similarity 81.8%; Pred. No. 0.57;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YCYCFWKTCT 11
 DB 2 YKYCFWKTCT 12
 RESULT 40
 AAY94480
 ID AAY94480 standard; peptide; 12 AA.
 AC AAY94480;
 XX 20-SEP-2000 (first entry)
 DT Human somatostatin analog JP-05-59.
 DE Human; somatostatin; SRIF; neuropeptide; antineoplastic; psoriasis;
 KW protective retinopathy; diabetes-related blindness.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1 /note= "D-form residue"
 FT Disulfide-bond 6.11
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 12 /note= "C-terminal amide"
 FT WO200031122-A1.
 FN 02-JUN-2000.
 PD 20-OCT-1999; 99WO-US024532.
 PF 19-NOV-1998; 98US-00196259.
 XX (TULA) UNIV TULANE.
 PA Coy DH, Murphy WA, Wolterling EA, Fuselier JA, Drouant G;
 XX WPI; 2000-400036/34.
 XX

PT Somatostatin analogs useful for the treatment of neoplastic cells
 XX expressing somatostatin receptors and targeting angiogenic blood vessels.
 XX Example 2; Page 23; 35pp; English.
 XX The human somatostatin (SRIF) peptide, is an endogenous neuropeptide that
 CC acts as a regulator of growth hormone secretion. Novel analogs of SRIF
 CC have been synthesised. The present sequence is one such analog, denoted
 CC JP-05-59. These analogs may be used as an antineoplastic therapeutic,
 CC specifically targeted to angiogenic blood vessels or cells. Angiogenic
 CC blood vessel cells which are involved in human diseases, such as
 CC psoriasis, protective retinopathy and diabetes-related blindness, may
 CC also be targeted. The SRIF analogs act by inhibition of growth hormone
 CC release. Radiolabelled analogs can be used to selectively kill a
 CC neoplastic cell expressing a somatostatin receptor. The analogs are also
 CC useful for imaging cells expressing a receptor to which the analog
 CC specifically binds. This may be used for tumour localization. Analogs
 CC with multiple tyrosine residues have the advantage that they are
 CC hydrophilic, which allows tumours in the liver to visualised
 XX Sequence 12 AA;
 SQ Query Match 73.8%; Score 59; DB 3; Length 12;
 Best Local Similarity 81.8%; Pred. No. 0.57;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YCYCFWKTCT 11
 DB 2 YKYCFWKTCT 12
 RESULT 41
 ABR42183
 ID ABR42183 standard; peptide; 12 AA.
 XX ABR42183;
 AC 28-JUL-2003 (first entry)
 DT Somatostatin analogue peptide JP-07-100.
 DE Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 KW antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Modified-site 1 /note= "optional methotrexate-acetyl moiety, D-form
 FT residue"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Disulfide-bond 6.11
 FT Misc-difference 8 /note= "optional Cys circularisation"
 FT Modified-site 12 /note= "D-form residue"
 FT /note= "C-terminal amide"
 XX WO2003028527-A2.
 FN 10-APR-2003.
 PD 20-SEP-2002; 2002WO-US030143.
 PF 21-SEP-2001; 2001US-0323851P.
 XX (TULA) TULANE EDUCATIONAL FUND.
 PA

PI Coy DH, Fuselier JA, Murphy WA, Sun L;
 DR WPI; 2003-441067/41.
 XX
 XX Biologically active peptides such as somatostatin or bombesin conjugated
 PT to chemical compounds through linkers, useful for treating tumors of the
 PT lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 PT vessels.
 XX
 XX Disclosure; Page 16; 86pp; English.
 PS
 PS The present sequence is that of somatostatin analogue peptide JF-07-100.
 XX It is an example of peptide agents of the invention that comprise a
 CC biologically active peptide, such as somatostatin or bombesin, conjugated
 CC to a chemical compound through a linker that maintains the peptide's
 CC biological activity. The peptide agents may also include a cytostatic or
 CC therapeutic agent, label or chelating group and a peptide that increases
 CC the hydrophilic biodistribution of the agent. They are useful for
 CC treating tumors of the lung, breast, brain, eye, prostate, or colon,
 CC tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
 CC angiogenic blood vessels (claimed). Other diseases that can also be
 CC treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
 CC arthritis, neoplastic cells or aberrantly proliferating cells, and
 CC acromegaly. Peptide JF-07-100 has the ability to inhibit growth hormone
 CC release from primary cultures of rat pituitary cells, having an IC50 of
 CC 0.62 nM (compared with 0.15 nM for somatostatin-14). Note: The present
 CC sequence is identified as SEQ ID 1 in the disclosure (page 16), but it is
 CC not the same as the sequence given as SEQ ID 1 in the sequence listing
 XX
 XX Sequence 12 AA;
 SQ

Query Match 73.8%; Score 59; DB 6; Length 12;
 Best Local Similarity 81.8%; Pred. No. 0.57;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYCFWKTCCT 11
 Db 2 YKYCFWKTCCT 12

RESULT 42
 AAY94482
 ID AAY94482 standard; peptide; 14 AA.
 XX
 AC AAY94482;
 XX
 DT 20-SEP-2000 (first entry)
 XX
 DE Human somatostatin analog JF-05-83.
 XX
 KW Human; somatostatin; SRIF; neuropeptide; antineoplastic; psoriasis;
 KW protective retinopathy; diabetes-related blindness.
 KW
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Disulfide-bond 8. 13
 FT Misc-difference 10 /note= "D-form residue"
 FT Modified-site 14 /note= "C-terminal amide"
 FT
 XX WO200031122-A1.
 XX
 XX 02-JUN-2000.
 XX
 XX 20-OCT-1999; 99WO-US024532.
 XX
 XX 19-NOV-1998; 98US-00196259.
 XX
 XX (TULA) UNIV TULANE.
 PA

XX Coy DH, Murphy WA, Woltering EA, Fuselier JA, Drouant G;
 PI WPI; 2000-400036/34.
 XX
 XX Somatostatin analogs useful for the treatment of neoplastic cells
 PT expressing somatostatin receptors and targeting angiogenic blood vessels.
 PT
 XX Disclosure; Page 10; 35pp; English.
 PS
 PS The human somatostatin (SRIF) peptide, is an endogenous neuropeptide that
 CC acts as a regulator of growth hormone secretion. Novel analogs of SRIF
 CC have been synthesised. The present sequence is one such analog, denoted
 CC JF-05-83. These analogs may be used as an antineoplastic therapeutic,
 CC specifically targeted to angiogenic blood vessels or cells. Angiogenic
 CC blood vessel cells which are involved in human diseases, such as
 CC psoriasis, protective retinopathy and diabetes-related blindness, may
 CC also be targeted. The SRIF analogs act by inhibition of growth hormone
 CC release. Radiolabelled analogs can be used to selectively kill a
 CC neoplastic cell expressing a somatostatin receptor. The analogs are also
 CC useful for imaging cells expressing a receptor to which the analog
 CC specifically binds. This may be used for tumour localization. Analogs
 CC with multiple tyrosine residues have the advantage that they are
 CC hydrophilic, which allows tumours in the liver to visualised
 XX
 XX Sequence 14 AA;
 SQ

Query Match 73.8%; Score 59; DB 3; Length 14;
 Best Local Similarity 81.8%; Pred. No. 0.65;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYCFWKTCCT 11
 Db 4 YKYCFWKTCCT 14

RESULT 43
 AAY94483
 ID AAY94483 standard; peptide; 14 AA.
 XX
 AC AAY94483;
 XX
 DT 20-SEP-2000 (first entry)
 XX
 DE Human somatostatin analog JF-05-85.
 XX
 KW Human; somatostatin; SRIF; neuropeptide; antineoplastic; psoriasis;
 KW protective retinopathy; diabetes-related blindness.
 KW
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Disulfide-bond 8. 13
 FT Misc-difference 10 /note= "D-form residue"
 FT Modified-site 14 /note= "C-terminal amide"
 FT
 XX WO200031122-A1.
 XX
 XX 02-JUN-2000.
 XX
 XX 20-OCT-1999; 99WO-US024532.
 XX
 XX 19-NOV-1998; 98US-00196259.
 XX
 XX (TULA) UNIV TULANE.
 PA

XX Coy DH, Murphy WA, Woltering EA, Fuselier JA, Drouant G;
 XX MPI; 2000-400036/34.
 XX Somatostatin analogs useful for the treatment of neoplastic cells
 XX expressing somatostatin receptors and targeting angiogenic blood vessels.
 XX Disclosure; Page 10; 35pp; English.
 XX The human somatostatin (SRIF) peptide, is an endogenous neuropeptide that
 XX acts as a regulator of growth hormone secretion. Novel analogs of SRIF
 XX have been synthesized. The present sequence is one such analog, denoted
 XX JP-05-85. These analogs may be used as an antineoplastic therapeutic,
 XX specifically targeted to angiogenic blood vessels or cells. Angiogenic
 XX blood vessel cells which are involved in human diseases, such as
 XX psoriasis, protective retinopathy and diabetes-related blindness, may
 XX also be targeted. The SRIF analogs act by inhibition of growth hormone
 XX release. Radiolabelled analogs can be used to selectively kill a
 XX neoplastic cell expressing a somatostatin receptor. The analogs are also
 XX useful for imaging cells expressing a receptor to which the analog
 XX specifically binds. This may be used for tumour localization. Analogs
 XX with multiple tyrosine residues have the advantage that they are
 XX hydrophilic, which allows tumours in the liver to visualised
 XX Sequence 14 AA;
 XX
 XX Query Match 73.8%; Score 59; DB 3; Length 14;
 XX Best Local Similarity 81.8%; Pred. No. 0.65;
 XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 1 YCYCFWKTCCT 11
 XX DB 4 YKYCFWKTCCT 14
 XX
 XX RESULT 44
 XX ADI14945
 XX ID ADI14945 standard; peptide; 15 AA.
 XX AC ADI14945;
 XX DT 22-APR-2004 (first entry)
 XX DE Somatostatin-dopamine chimeric analogue-related peptide 56.
 XX
 XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 XX vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 XX anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 XX tranquiliser; antilipaeamic; nephrotropic; antitumor; antidiabetic;
 XX hypertensive; anorectic; antidiabetic; dopamine receptor agonist;
 XX somatostatin receptor agonist; lung cancer; glioma; anorexia;
 XX hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 XX acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 XX pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 XX gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 XX AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 XX irritable bowel syndrome; pancreatitis; small bowel obstruction;
 XX gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 XX gonadotropinoma; hyperparathyroidism; Graves disease;
 XX diabetic neuropathy; Paget's disease; polycystic ovary disease;
 XX thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 XX GH secreting adenoma; acromegaly; TSH secreting adenoma;
 XX prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 XX hyperlipidaemia; insulin insensitivity; Syndrome X; angiotensin;
 XX proliferative retinopathy; dawn phenomenon; nephropathy;
 XX gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 XX pancreaticocutaneous fistula; dumping syndrome;
 XX watery diarrhoea syndrome; pancreatitis;
 XX gastrointestinal hormone secreting tumour; angioneurotic; arthritis;
 XX allograft rejection; graft vessel bleeding; portal hypertension;
 XX gastrointestinal bleeding; obesity; opioid overdose.

XX Synthetic
 XX Unidentified.
 XX Key Location/Qualifiers
 XX Modified-site 1
 XX /note= ". Optionally bound to 7-propyl-
 XX 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 XX methylsulfonyl-acetic acid. Optionally bound to 3-(1-(7-
 XX allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-
 XX 9-carbonyl)-3-ethylureidopropyl)-Gly-"
 XX Misc-difference 2. .5
 XX /note= "D-form residue"
 XX Misc-difference 7. .8
 XX /note= "D-form residue"
 XX Modified-site 9
 XX /note= "Residue forms a bond to residue 14 to form a
 XX cyclic peptide"
 XX Misc-difference 11
 XX /note= "D-form residue"
 XX Modified-site 14
 XX /note= "Residue forms a bond to residue 9 to form a
 XX cyclic peptide"
 XX Modified-site 15
 XX /note= "C-terminal amide"
 XX
 XX W02002100888-A1.
 XX 19-DEC-2002.
 XX 07-JUN-2002; 2002WO-US017859.
 XX 08-JUN-2001; 2001US-0297059P.
 XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 XX MPI; 2003-239103/23.
 XX
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 XX e.g. lung cancer.
 XX Claim 3; Page 140; 85pp; English.
 XX
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 XX or their salts. The invention may be useful for the development of
 XX compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 XX antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 XX antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeamic,
 XX nephrotropic, anorectic, antidiabetic, hypotensive, anorectic or
 XX antidiabetic activity through action as a dopamine receptor agonist and
 XX somatostatin receptor agonist. The invention may be useful for the
 XX treatment of lung cancer, glioma, anorexia, hypothyroidism,
 XX hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 XX restenosis, Crohn's disease, systemic sclerosis, external and internal
 XX pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis,
 XX hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 XX related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 XX bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 XX reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 XX hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 XX disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 XX meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 XX hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH
 XX secreting adenomas, prolactin secreting adenomas, insulinoma,
 XX glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 XX Syndrome X, angiotensin, proliferative retinopathy, dawn phenomenon,
 XX nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 XX fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 XX syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 XX angioneurotic, arthritis, allograft rejection, graft vessel bleeding,
 XX portal hypertension, gastrointestinal bleeding, obesity and opioid

CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 73.8%; Score 59; DB 7; Length 15;
 Best Local Similarity 88.9%; Pred. No. 0.69;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 YYCFWKTCT 11
 Db 7 YYCFWKTCT 15
 |||||

RESULT 45
 AAO26828
 ID AAO26828 standard; peptide; 8 AA.
 AC AAO26828;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Somatostatin agonist compound #11.
 XX
 KW Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipemic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.
 XX

OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4 /note= "Modified by N-Methyl. D-form residue"
 FT Modified-site 8 /note= "C-terminal amide"
 FT
 FT WO200281499-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 08-APR-2002; 2002WO-US010882.
 XX
 PR 09-APR-2001; 2001US-0282526P.
 XX
 PA (TULA) TULANE EDUCATIONAL FUND.
 XX
 PI Coy DH, Rajeswaran WG;
 XX
 DR WPI; 2003-247842/24.
 XX
 XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
 FT hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
 PT Zollinger-Ellison syndrome, characterized by alkylation of amide
 PT nitrogen.
 XX
 PS Claim 19; Page 31; 43pp; English.
 XX

CC The invention relates to novel somatostatin agonists, typically
 CC characterised by alkylation of the amide nitrogen, or its
 CC pharmaceutically acceptable salt. The novel somatostatin agonists are
 CC useful for binding one or more of human somatostatin subtype receptors -
 CC 1,2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
 CC administering a somatostatin agonist or a pharmaceutically acceptable
 CC salt of it to a recipient in need of it. The somatostatin agonists are
 CC useful for treating a disease or condition in a human or other animal,
 CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
 CC Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
 CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
 CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel

CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
 CC cancer, psoriasis, hypotension, panic attacks, scleroderma, small bowel
 CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
 CC disease, polycystic ovary disease, upper gastrointestinal bleeding, cancer
 CC pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
 CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 CC inhibiting the accelerated growth of a solid tumour and decreasing body
 CC weight, treating insulin resistance, Syndrome X, prolonging the survival
 CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
 CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
 CC of a somatostatin agonist compound of the invention
 XX

SQ Sequence 8 AA;
 Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCT 11
 Db 1 YCFWKTCT 8
 |||||

RESULT 46
 AAO26832
 ID AAO26832 standard; peptide; 8 AA.
 XX
 AC AAO26832;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Somatostatin agonist compound #15.
 XX

XX Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipemic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.
 XX

OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 4 /note= "D-form residue"
 FT Modified-site 8 /note= "Modified by N-Methyl. C-terminal amide"
 FT
 FT WO200281499-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 08-APR-2002; 2002WO-US010882.
 XX
 PR 09-APR-2001; 2001US-0282526P.
 XX

XX (TULA) TULANE EDUCATIONAL FUND.
 XX
 PI Coy DH, Rajeswaran WG;
 XX
 DR WPI; 2003-247842/24.
 XX

XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
 FT hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
 PT Zollinger-Ellison syndrome, characterized by alkylation of amide
 PT nitrogen.
 XX

PS Claim 23; Page 32; 43pp; English.
 XX
 XX The invention relates to novel somatostatin agonists, typically
 CC characterised by alkylation of the amide nitrogen, or its
 CC pharmaceutically acceptable salt. The novel somatostatin agonists are
 CC useful for binding one or more of human somatostatin subtype receptors -
 CC 1,2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
 CC administering a somatostatin agonist or a pharmaceutically acceptable

CC salt of it to a recipient in need of it. The somatostatin agonists are
 CC useful for treating a disease or condition in a human or other animal,
 CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
 CC Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
 CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
 CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
 CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
 CC cancer, psoriasis, hypotension, panic attacks, scleroderma, small bowel
 CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
 CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
 CC pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
 CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 CC inhibiting the accelerated growth of a solid tumour and decreasing body
 CC weight, treating insulin resistance, Syndrome X, prolonging the survival
 CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
 CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
 CC of a somatostatin agonist compound of the invention
 XX

SQ Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
 |||||
 Db 1 YCFWKTKCT 8

RESULT 47
 AAO26830
 ID AAO26830 standard; peptide; 8 AA.

XX AC AAO26830;

XX DT 27-AUG-2003 (first entry)

XX DE Somatostatin agonist compound #13.

XX KW Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 XX KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 XX KW antilipaeamic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 XX KW hyperparathyroidism; cancer.

XX OS Unidentified.

XX FH Key Location/Qualifiers
 FT Misc-difference 4 /note= "D-form residue"
 FT Modified-site 6 /note= "Modified by N-Methyl"
 FT Modified-site 8 /note= "C-terminal amide"

FT FT WO200281499-A2.

XX PN 17-OCT-2002.

XX PD 08-APR-2002; 2002WO-US010882.

XX PF 09-APR-2001; 2001US-0282526P.

XX PR (TULA) TULANE EDUCATIONAL FUND.

XX PA Coy DH, Rajeswaran WG;

XX PI WPI; 2003-247842/24.

XX DR Novel somatostatin agonist, useful for treating Cushing's syndrome,
 XX FT hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
 XX FT Zollinger-Ellison syndrome, characterized by alkylation of amide
 XX FT nitrogen.

PS Claim 21; Page 32; 43pp; English.

XX CC The invention relates to novel somatostatin agonists, typically
 CC characterised by alkylation of the amide nitrogen, or its
 CC pharmaceutically acceptable salt. The novel somatostatin agonists are
 CC useful for binding one or more of human somatostatin subtype receptors -
 CC 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
 CC administering a somatostatin agonist or a pharmaceutically acceptable
 CC salt of it to a recipient in need of it. The somatostatin agonists are
 CC useful for treating a disease or condition in a human or other animal,
 CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
 CC Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
 CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
 CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
 CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
 CC cancer, psoriasis, hypotension, panic attacks, scleroderma, small bowel
 CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
 CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
 CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 CC inhibiting the accelerated growth of a solid tumour and decreasing body
 CC weight, treating insulin resistance, Syndrome X, prolonging the survival
 CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
 CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
 CC of a somatostatin agonist compound of the invention
 XX

SQ Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
 |||||
 Db 1 YCFWKTKCT 8

RESULT 48

AAO26825
 ID AAO26825 standard; peptide; 8 AA.

XX AC AAO26825;

XX DT 27-AUG-2003 (first entry)

XX DE Somatostatin agonist compound #8.

XX KW Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 XX KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 XX KW antilipaeamic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 XX KW hyperparathyroidism; cancer.

XX OS Unidentified.

XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "Modified by N-Methyl"
 FT Misc-difference 4 /note= "D-form residue"
 FT Modified-site 8 /note= "C-terminal amide"

XX PN WO200281499-A2.

XX PD 17-OCT-2002.

XX PF 08-APR-2002; 2002WO-US010882.

XX PR 09-APR-2001; 2001US-0282526P.

XX PA (TULA) TULANE EDUCATIONAL FUND.

XX PI Coy DH, Rajeswaran WG;

```

XX DR WPI; 2003-247842/24.
XX PF
XX PR Novel somatostatin agonist, useful for treating Cushing's syndrome,
XX PT hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
XX PT Zollinger-Ellison syndrome, characterized by alkylation of amide
XX PT nitrogen.
XX PS Claim 16; Page 31; 43pp; English.
XX PS
XX SS The invention relates to novel somatostatin agonists, typically
XX CC characterised by alkylation of the amide nitrogen, or its
XX CC pharmaceutically acceptable salt. The novel somatostatin agonists are
XX CC useful for binding one or more of human somatostatin subtype receptors -
XX CC 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
XX CC administering a somatostatin agonist or a pharmaceutically acceptable
XX CC salt of it to a recipient in need of it. The somatostatin agonists are
XX CC useful for treating a disease or condition in a human or other animal,
XX CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
XX CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
XX CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
XX CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
XX CC cancer, psoriasis, hypotension, panic attacks, scleroderma, small bowel
XX CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
XX CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
XX CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
XX CC pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
XX CC inhibiting the accelerated growth of a solid tumour and decreasing body
XX CC weight, treating insulin resistance, Syndrome X, prolonging the survival
XX CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
XX CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
XX CC of a somatostatin agonist compound of the invention
XX SQ Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
Db 1 YCFWKTKCT 8

RESULT 49
AAO26827
ID AAO26827 standard; peptide; 8 AA.
XX AC
XX AC AAO26827;
XX DT
XX DT 27-AUG-2003 (first entry)
XX DE
XX DE Somatostatin agonist compound #10.
XX KW Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
XX KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
XX KW antilipaemic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
XX KW hyperparathyroidism; cancer.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Modified-site 3 /note= "Modified by N-Methyl"
XX FT Misc-difference 4 /note= "D-form residue"
XX FT Modified-site 8 /note= "C-terminal amide"
XX FT
XX PN WO200281499-A2.
XX XX
XX PD 17-OCT-2002.

XX CC The invention relates to novel somatostatin agonists, typically
XX CC characterised by alkylation of the amide nitrogen, or its
XX CC pharmaceutically acceptable salt. The novel somatostatin agonists are
XX CC useful for binding one or more of human somatostatin subtype receptors -
XX CC 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
XX CC administering a somatostatin agonist or a pharmaceutically acceptable
XX CC salt of it to a recipient in need of it. The somatostatin agonists are
XX CC useful for treating a disease or condition in a human or other animal,
XX CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
XX CC Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
XX CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
XX CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
XX CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
XX CC cancer, psoriasis, hypotension, panic attacks, scleroderma, small bowel
XX CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
XX CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
XX CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
XX CC pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
XX CC inhibiting the accelerated growth of a solid tumour and decreasing body
XX CC weight, treating insulin resistance, Syndrome X, prolonging the survival
XX CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
XX CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
XX CC of a somatostatin agonist compound of the invention
XX SQ Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
Db 1 YCFWKTKCT 8

RESULT 50
AAO26826
ID AAO26826 standard; peptide; 8 AA.
XX AC
XX AC AAO26826;
XX DT
XX DT 27-AUG-2003 (first entry)
XX DE
XX DE Somatostatin agonist compound #9.
XX KW Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
XX KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
XX KW antilipaemic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
XX KW hyperparathyroidism; cancer.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Modified-site 2 /note= "Modified by N-Methyl"
XX FT

```


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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:05:35 ; Search time 19.3333 Seconds
(without alignments)
54.744 Million cell updates/sec

Title: US-10-796-158-5
Perfect score: 80
Sequence: 1 YCYCFWKYCT 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: PIR 80.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	62.5	1910	2 H88124	protein T12C9.3 (1
2	45	56.2	529	2 J80200	orphan UDP-glucuro
3	44	55.0	245	2 I51323	proteolipid protei
4	44	55.0	258	1 C69175	heat shock protein
5	44	55.0	285	2 AG1214	methylases homolog
6	44	55.0	597	2 S65673	GABA transport pro
7	44	55.0	602	2 A44409	gamma-aminobutyric
8	44	55.0	602	2 A45078	gamma-aminobutyric
9	44	55.0	614	2 S68236	betaine/GABA trans
10	44	55.0	614	2 A41757	betaine transport
11	44	55.0	614	2 A43390	gamma-aminobutyric
12	44	55.0	622	2 S63539	GABA/beta-alanine
13	44	55.0	627	2 B44409	gamma-aminobutyric
14	44	55.0	627	2 JH0695	gamma-aminobutyric
15	44	55.0	810	2 T00368	hypothetical prote
16	43	53.8	333	2 A96829	probable RING fing
17	42	52.5	528	2 JN0620	UPB-glucuronosyltr
18	42	52.5	529	2 A35366	glucuronosyltransf
19	42	52.5	670	2 H96707	probable receptor
20	42	52.5	686	2 T08919	hypothetical prote
21	42	52.5	998	2 A36368	transcription fact
22	41.5	51.9	155	1 M6WL43	E6 protein - human
23	41.5	51.9	246	2 T28166	hypothetical prote
24	41	51.2	387	2 D84424	hypothetical prote
25	41	51.2	399	2 T21586	hypothetical prote
26	41	51.2	413	2 T10593	hypothetical prote
27	41	51.2	1513	2 A54895	mucin 2, intestina
28	40	50.0	239	2 T26798	hypothetical prote
29	40	50.0	245	2 T30127	hypothetical prote

30	40	50.0	247	2 T27205	hypothetical prote
31	40	50.0	311	2 T27203	hypothetical prote
32	40	50.0	411	2 G97802	tyrosine-trna liga
33	40	50.0	411	2 C71660	tyrosine-trna liga
34	40	50.0	512	2 T30924	hypothetical prote
35	40	50.0	590	2 A47194	taurine and beta-a
36	40	50.0	620	2 G01426	taurine transporte
37	40	50.0	620	2 S46487	taurine transporte
38	40	50.0	621	2 I57939	Na and Cl dependen
39	40	50.0	655	2 A46270	Na and Cl dependen
40	40	50.0	682	1 JH0560	cyclic nucleotide-
41	39.5	49.4	154	2 S36555	E6 protein - human
42	39.5	49.4	154	2 S36584	E6 protein - human
43	39	48.8	104	2 S19430	probable membrane
44	39	48.8	212	2 C87585	hypothetical prote
45	39	48.8	215	2 A49677	endoplasmic reticu
46	39	48.8	337	2 T20644	hypothetical prote
47	39	48.8	348	2 T28806	olfactory receptor
48	39	48.8	367	1 A46355	site-specific DNA-
49	39	48.8	367	2 T18185	probable site-spec
50	39	48.8	618	2 G70350	conserved hypotet
51	39	48.8	660	2 F70101	primosomal protein
52	39	48.8	844	1 T05179	S-receptor kinase
53	39	48.8	965	2 S62935	hypothetical prote
54	39	48.8	2052	2 T18519	myosin X - bovine
55	39	48.8	2058	2 A59267	myosin X - mouse
56	39	48.8	2062	2 A59297	myosin X - mouse
57	38.5	48.1	258	2 S55036	tyrosine-rich hydr
58	38	47.5	12	1 UOGM2	urotensin II - lon
59	38	47.5	12	2 JS0423	urotensin II-A pep
60	38	47.5	12	2 S42765	urotensin II - tel
61	38	47.5	12	2 JS0424	urotensin II-B pep
62	38	47.5	13	2 FQ0445	urotensin II - lau
63	38	47.5	83	2 S10706	urotensin II precu
64	38	47.5	117	2 B82614	hypothetical prote
65	38	47.5	125	2 I50499	urotensin II-gamma
66	38	47.5	125	2 I50498	urotensin II-alpha
67	38	47.5	210	2 T16744	hypothetical prote
68	38	47.5	279	2 C48826	high chorolytic h
69	38	47.5	285	2 S76841	hypothetical prote
70	38	47.5	291	2 T03900	hypothetical prote
71	38	47.5	300	2 T24547	hypothetical prote
72	38	47.5	393	2 G84017	hypothetical prote
73	38	47.5	997	2 JC6067	CCAAAT-binding fact
74	38	47.5	1089	2 T21582	hypothetical prote
75	38	47.5	1487	2 T02850	hypothetical prote
76	38	47.5	2105	1 A44059	genome polypotein
77	37.5	46.9	60	1 H3N33E	cytoxin 3 - cobr
78	37.5	46.9	123	2 T46739	microfilarial shea
79	37.5	46.9	152	2 S36550	E6 protein - human
80	37.5	46.9	354	2 T46740	microfilarial shea
81	37.5	46.9	1551	1 A43364	M polypotein prec
82	37	46.2	51	2 T07535	hypothetical prote
83	37	46.2	54	2 C90372	hypothetical prote
84	37	46.2	54	2 D97847	hypothetical prote
85	37	46.2	61	2 F90819	hypothetical prote
86	37	46.2	88	2 H91290	hypothetical prote
87	37	46.2	97	2 T37478	proteins 191, daue
88	37	46.2	100	2 A12472	hypothetical prote
89	37	46.2	130	2 G71042	hypothetical prote
90	37	46.2	139	2 E72856	AcOrf-53 protein -
91	37	46.2	144	2 T33419	hypothetical prote
92	37	46.2	163	2 T48289	hypothetical prote
93	37	46.2	181	2 D72468	hypothetical prote
94	37	46.2	216	2 E84450	hypothetical prote
95	37	46.2	253	2 T30928	hypothetical prote
96	37	46.2	261	2 T15153	hypothetical prote
97	37	46.2	277	2 T16020	hypothetical prote
98	37	46.2	279	2 T24606	hypothetical prote
99	37	46.2	300	2 T27158	hypothetical prote
100	37	46.2	300	2 G87999	protein Y5485A.1 l
101	37	46.2	300	2 T30400	hypothetical prote
102	37	46.2	314	1 T50537	succinate dehydrog

103	37	46.2	316	1	G90406	succinate dehydrog	176	36	45.0	698	2	T10541	cyclic nucleotide
104	37	46.2	335	2	H84449	hypothetical prote	177	36	45.0	698	2	T51915	hypothetical prote
105	37	46.2	350	2	H84449	hypothetical prote	178	36	45.0	706	2	F86143	cyclic nucleotide
106	37	46.2	352	1	S27357	complement C5a ana	179	36	45.0	716	2	T51354	hypothetical prote
107	37	46.2	392	2	T46418	hypothetical prote	180	36	45.0	718	2	G84902	hypothetical prote
108	37	46.2	392	2	T52445	hypothetical prote	181	36	45.0	774	2	T22309	hypothetical prote
109	37	46.2	397	2	G84461	hypothetical prote	182	36	45.0	779	2	T25173	hypothetical prote
110	37	46.2	436	2	T38812	hypothetical prote	183	36	45.0	799	2	T25174	hypothetical prote
111	37	46.2	493	2	JC5486	membrane glycoprot	184	36	45.0	809	2	T32945	hypothetical prote
112	37	46.2	617	2	T23082	hypothetical prote	185	36	45.0	834	2	S44866	ROSD3.4 protein -
113	37	46.2	639	2	C95342	nitrous-oxide redu	186	36	45.0	998	2	S31735	NAD ADP-ribosyltra
114	37	46.2	644	2	T33132	hypothetical prote	187	36	45.0	1011	1	JH0581	NAD ADP-ribosyltra
115	37	46.2	650	2	T44660	nitrous-oxide redu	188	36	45.0	1013	1	S04200	NAD ADP-ribosyltra
116	37	46.2	1385	2	S14871	suppressor two of	189	36	45.0	1014	1	A29725	zinc finger protei
117	37	46.2	1748	1	JQ1555	genome polyprotein	190	36	45.0	1888	2	T14273	protein-cytosine-p
118	37	46.2	2155	2	T30197	alpha tectorin - m	191	36	45.0	2302	2	T14328	early glycoprotein
119	36.5	45.6	105	2	G75047	2-ketovaleate oxi	192	35.5	44.4	148	1	VGB848	2-succinyl-6-hydro
120	36.5	45.6	105	2	H71113	probable ferredoxi	193	35.5	44.4	595	2	S76520	NUMA protein - hum
121	36.5	45.6	105	2	T45084	2-oxoisovalerate-f	194	35	43.8	45	2	S33414	hypothetical prote
122	36.5	45.6	148	2	S36532	E6 protein - human	195	35	43.8	54	2	E64007	hypothetical prote
123	36.5	45.6	271	2	S36532	peroxisomal assemb	196	35	43.8	76	2	T28486	hypothetical prote
124	36.5	45.6	376	2	A00731	conserved hypothet	197	35	43.8	76	2	F72156	C7L protein - vari
125	36	45.0	60	1	H3NJ1B	cytotoxin 1 - coBr	198	35	43.8	83	2	B72392	Beejin protein - s
126	36	45.0	60	1	H3NJ1B	cytotoxin 1 - Moza	199	35	43.8	99	2	B25439	trans-activating t
127	36	45.0	60	1	H3NJ2C	cytotoxin 2 - Cape	200	35	43.8	100	1	TNLJ51	hypothetical prote
128	36	45.0	60	1	H3NJ2B	cytotoxin 2 - coBr	201	35	43.8	108	2	S69873	nuclear receptor p
129	36	45.0	60	1	H3NJ2M	cytotoxin 2 - Moza	202	35	43.8	113	2	S43435	F11 protein - vacc
130	36	45.0	60	1	H3NJ3C	cytotoxin 3 - Cape	203	35	43.8	124	1	QQVZEL	hypothetical prote
131	36	45.0	60	1	H3NJ3M	cytotoxin 3 - Moza	204	35	43.8	128	2	S69856	succinate dehydrog
132	36	45.0	60	1	H3NJ4E	cytotoxin 4 - coBr	205	35	43.8	132	2	S62755	J5L 15.2K protein
133	36	45.0	60	1	H3NJ5E	cytotoxin 5 - coBr	206	35	43.8	133	2	H42513	hypothetical prote
134	36	45.0	60	1	H3NJ5Y	cytotoxin 5 - Egyp	207	35	43.8	133	2	T28520	hypothetical prote
135	36	45.0	60	1	H3NJ6B	cytotoxin 6 - coBr	208	35	43.8	133	2	H72160	M5L protein - vari
136	36	45.0	60	1	H3NJ6M	cytotoxin 6, minor	209	35	43.8	133	2	S33096	J5L protein - vari
137	36	45.0	60	1	H3NJ7E	cytotoxin 7 - coBr	210	35	43.8	134	2	T30680	hypothetical prote
138	36	45.0	60	1	H3NJ7M	cytotoxin 7, minor	211	35	43.8	139	2	T41797	ACMNPV orf53 - Bom
139	36	45.0	60	1	H3NJ8E	cytotoxin 8 - coBr	212	35	43.8	154	2	T46006	hypothetical prote
140	36	45.0	60	1	H3NJ8E	cytotoxin 3, minor	213	35	43.8	158	2	E90198	hypothetical prote
141	36	45.0	81	2	A45320	transglutaminase s	214	35	43.8	160	2	A72541	small T antigen -
142	36	45.0	138	2	T34049	hypothetical prote	215	35	43.8	172	1	TVPEAJ	probable alanine a
143	36	45.0	144	2	B84450	hypothetical prote	216	35	43.8	183	2	A84728	U155 protein - hum
144	36	45.0	153	2	H86034	hypothetical prote	217	35	43.8	186	1	B48560	U155 protein - hum
145	36	45.0	153	2	G91187	hypothetical prote	218	35	43.8	186	1	WMEXB	U155 protein - hum
146	36	45.0	153	2	S47817	hypothetical 18.1K	219	35	43.8	186	1	WMEXB	U155 protein - hum
147	36	45.0	154	2	C81579	conserved hypothet	220	35	43.8	186	1	T29602	hypothetical prote
148	36	45.0	171	2	D72090	hypothetical prote	221	35	43.8	221	2	D86472	ubiquitin-cytochro
149	36	45.0	171	2	F86532	hypothetical prote	222	35	43.8	250	2	C60944	conserved hypothet
150	36	45.0	237	2	JN0302	hypothetical 237 p	223	35	43.8	250	2	D69182	hypothetical prote
151	36	45.0	246	2	T51418	hypothetical prote	224	35	43.8	255	2	F64503	hypothetical prote
152	36	45.0	262	2	T01562	hypothetical prote	225	35	43.8	258	2	S33535	myosin heavy chain
153	36	45.0	281	2	C82547	hypothetical prote	226	35	43.8	258	2	T30368	probable immediate
154	36	45.0	300	2	A60956	dynein beta heavy	227	35	43.8	266	2	H83260	hypothetical prote
155	36	45.0	304	2	C71637	rod shape-determin	228	35	43.8	276	1	MPBOPL	myelin proteolipid
156	36	45.0	335	2	A13453	transcription regu	229	35	43.8	277	1	MPBOPL	myelin proteolipid
157	36	45.0	337	2	E96543	probable RAV-like	230	35	43.8	277	1	MPRTPL	myelin proteolipid
158	36	45.0	342	2	C47084	spore photoproduct	231	35	43.8	277	1	S34792	myelin proteolipid
159	36	45.0	343	2	H84000	spore photoproduct	232	35	43.8	277	1	S17600	myelin proteolipid
160	36	45.0	344	2	JC6100	CACC-box binding	233	35	43.8	277	2	A43548	myelin proteolipid
161	36	45.0	353	2	JC4875	zinc-finger protei	234	35	43.8	277	2	I51270	myelin proteolipid
162	36	45.0	358	2	T31490	hypothetical prote	235	35	43.8	278	2	JG0164	cytochrome-c oxida
163	36	45.0	378	2	G97147	probable 3-oxoacyl	236	35	43.8	279	2	U0164	LIM protein, FH4
164	36	45.0	411	2	T00567	hypothetical prote	237	35	43.8	304	2	M45989	peroxisome assembl
165	36	45.0	447	2	B82490	probable Na+/H+ an	238	35	43.8	305	2	I52362	peroxisome assembl
166	36	45.0	447	2	I56511	Zic protein - mous	239	35	43.8	305	2	B53782	cytochrome-c oxida
167	36	45.0	485	2	T10792	amidophosphoribos	240	35	43.8	308	2	H97729	hypothetical prote
168	36	45.0	497	2	T27169	hypothetical prote	241	35	43.8	339	2	A97736	cytochrome D ubiqu
169	36	45.0	530	2	G02091	pancreatic zymogen	242	35	43.8	339	2	A71733	hypothetical prote
170	36	45.0	532	2	T06087	amidophosphoribos	243	35	43.8	346	2	T26097	hypothetical prote
171	36	45.0	549	1	D30010	cytochrome-c oxida	244	35	43.8	358	2	F83875	hypothetical prote
172	36	45.0	569	2	T07158	amidophosphoribos	245	35	43.8	361	2	D86327	protein F1804.17
173	36	45.0	605	2	T19818	hypothetical prote	246	35	43.8	369	2	T24022	hypothetical prote
174	36	45.0	652	1	S39409	nitrous-oxide redu	247	35	43.8	399	2	T47873	phosphatidate cyti
175	36	45.0	680	2	T42923	infected cell prot	248	35	43.8	428	2	T46046	hypothetical prote

249	35	43.8	430	2	T16715	hypothetical prote	322	34	42.5	157	2	AG2675	hypothetical prote
250	35	43.8	440	2	S48953	hypothetical prote	323	34	42.5	161	1	Z3BPT9	gene 49.1 protein
251	35	43.8	444	2	F71916	probable lipopolys	324	34	42.5	170	2	JC2326	cryptophan-specifi
252	35	43.8	445	2	T01214	hypothetical prote	325	34	42.5	173	2	G69032	conserved hypotet
253	35	43.8	450	2	T39088	probable vacuolar	326	34	42.5	178	2	T20466	hypothetical prote
254	35	43.8	505	2	C84949	NADH2 dehydrogenas	327	34	42.5	183	1	R5BY32	ribosomal protein
255	35	43.8	508	2	T22626	hypothetical prote	328	34	42.5	188	2	B84637	hypothetical prote
256	35	43.8	511	2	S58399	cellulagin I synt	329	34	42.5	199	2	F91162	hypothetical membr
257	35	43.8	526	2	T23779	hypothetical prote	330	34	42.5	200	2	G86008	hypothetical prote
258	35	43.8	528	2	JN0617	glucuronosyltransf	331	34	42.5	208	2	G97767	hypothetical prote
259	35	43.8	534	2	T22154	hypothetical prote	332	34	42.5	234	2	T48454	hypothetical prote
260	35	43.8	537	2	B33485	spore coat protein	333	34	42.5	245	2	C65206	thiF protein - Esc
261	35	43.8	547	2	T34318	hypothetical prote	334	34	42.5	245	2	A86091	thiamin biosynthes
262	35	43.8	553	2	T03858	hypothetical prote	335	34	42.5	245	2	C91243	thiamin biosynthes
263	35	43.8	556	2	T45066	hypothetical prote	336	34	42.5	250	2	T10079	expansin SI precu
264	35	43.8	562	2	S46281	steroid hormone re	337	34	42.5	252	2	AH0932	thiamin biosynthes
265	35	43.8	566	2	A81682	P element - fruit	338	34	42.5	257	2	T32179	hypothetical prote
266	35	43.8	568	2	G71525	conserved hypotet	339	34	42.5	259	2	B70082	hypothetical prote
267	35	43.8	598	2	F71568	probable outer mem	340	34	42.5	280	2	S31492	hypothetical prote
268	35	43.8	598	2	F46027	gamma-aminobutyric	341	34	42.5	280	2	S31491	myelin proteolipid
269	35	43.8	599	1	ACRTGT	gamma-aminobutyric	342	34	42.5	283	2	T18678	myelin proteolipid
270	35	43.8	599	2	S11073	gamma-aminobutyric	343	34	42.5	284	2	G22848	hypothetical prote
271	35	43.8	610	2	G72494	hypothetical prote	344	34	42.5	287	2	A25877	cytochrome-c oxida
272	35	43.8	611	2	S46260	hypothetical prote	345	34	42.5	288	2	T78556	membrane glycoprot
273	35	43.8	616	2	C86239	creatine transport	346	34	42.5	292	2	T32178	hypothetical prote
274	35	43.8	642	2	G72265	hypothetical prote	347	34	42.5	295	2	T15151	hypothetical prote
275	35	43.8	647	1	JP0078	LiM protein kinase	348	34	42.5	302	2	T20808	hypothetical prote
276	35	43.8	656	1	S59631	endo-1,4-beta-xyla	349	34	42.5	317	1	T45163	succinate dehydrog
277	35	43.8	661	1	S59633	endo-1,4-beta-xyla	350	34	42.5	319	2	T27118	hypothetical prote
278	35	43.8	688	2	B86448	hypothetical prote	351	34	42.5	321	2	T15634	hypothetical prote
279	35	43.8	748	2	C64409	hypothetical prote	352	34	42.5	322	2	AF1031	hypothetical prote
280	35	43.8	786	2	A34095	BP74 protein precu	353	34	42.5	322	2	T25648	hypothetical prote
281	35	43.8	790	2	F50178	cadherin-6B - chic	354	34	42.5	332	2	A81667	conserved hypotet
282	35	43.8	798	2	T34248	hypothetical prote	355	34	42.5	332	2	B71508	hypothetical prote
283	35	43.8	817	2	S51445	probable membrane	356	34	42.5	334	2	JC4681	bradykinin B1 rece
284	35	43.8	845	2	D90130	hypothetical prote	357	34	42.5	334	2	G86565	CT484 hypothetical
285	35	43.8	864	2	A49070	ecdysone-inducible	358	34	42.5	334	2	D72057	conserved hypotet
286	35	43.8	903	2	T20804	hypothetical prote	359	34	42.5	355	2	G83020	heptosyltransferas
287	35	43.8	1043	2	S38034	PAS1 protein - yea	360	34	42.5	358	2	T33417	hypothetical prote
288	35	43.8	1112	2	T02848	hep70-related prot	361	34	42.5	374	1	H70440	conserved hypotet
289	35	43.8	1133	1	S41478	DNA repair protein	362	34	42.5	379	1	B28940	cytochrome d ubiq
290	35	43.8	1186	2	H88869	protein unc-31 lim	363	34	42.5	379	2	AI0591	cytochrome d ubiq
291	35	43.8	1209	2	T21455	hypothetical prote	364	34	42.5	379	2	A99725	cytochrome d ubiq
292	35	43.8	1270	2	T28087	hypothetical prote	365	34	42.5	379	2	B85576	cytochrome d ubiq
293	35	43.8	1360	2	T12064	DNA binding protei	366	34	42.5	379	2	F86793	hypothetical prote
294	35	43.8	1374	2	D85390	myosin-like protei	367	34	42.5	380	2	T20269	hypothetical prote
295	35	43.8	1375	2	T05200	myosin heavy chain	368	34	42.5	381	2	T23250	hypothetical prote
296	35	43.8	1381	1	Q08E45	major capsid prote	369	34	42.5	387	2	B96024	probable transposa
297	35	43.8	1817	2	H71611	probable secreted	370	34	42.5	396	2	T19294	hypothetical prote
298	35	43.8	1879	2	T19481	hypothetical prote	371	34	42.5	398	2	T19293	hypothetical prote
299	35	43.8	3020	2	A43932	mucin 2 precursor,	372	34	42.5	409	2	G82522	type I restriction
300	34.5	43.1	64	1	WMIH22	3b protein - avian	373	34	42.5	413	2	T34123	hypothetical prote
301	34.5	43.1	152	1	VGBEV9	early glycoprotein	374	34	42.5	452	2	C85024	probable polygalac
302	34.5	43.1	332	2	E71916	probable lipopolys	375	34	42.5	457	2	T39751	major facilitator
303	34.5	43.1	389	2	AD1918	alcohol dehydrogen	376	34	42.5	470	2	A65168	hypothetical 49.9
304	34.5	43.1	513	2	F96735	hypothetical prote	377	34	42.5	483	2	C82587	cationic amino aci
305	34.5	43.1	710	2	S22673	ferrioxamine recep	378	34	42.5	488	2	T29562	hypothetical prote
306	34.5	43.1	2704	2	S09118	G surface protein	379	34	42.5	491	2	B86155	probable polygalac
307	34.5	43.1	2718	2	A23475	G surface protein	380	34	42.5	498	2	AH3456	glutamate synthase
308	34	42.5	57	2	D49056	T-cell receptor al	381	34	42.5	506	2	A40679	transcription enha
309	34	42.5	65	2	A38394	neurotoxin AaH IT4	382	34	42.5	507	2	S54303	zinc transport pro
310	34	42.5	89	2	B86741	hypothetical prote	383	34	42.5	513	2	T33512	hypothetical prote
311	34	42.5	100	2	A31201	GlI-related finger	384	34	42.5	518	2	D69539	conserved hypotet
312	34	42.5	108	2	S19112	Ig kappa chain V r	385	34	42.5	521	2	A29249	RNA-directed RNA p
313	34	42.5	109	2	B86050	hypothetical prote	386	34	42.5	523	2	B40679	transcription enha
314	34	42.5	115	1	KVMSK2	Ig kappa chain pre	387	34	42.5	547	2	T03901	hypothetical prote
315	34	42.5	117	2	T38295	hypothetical prote	388	34	42.5	558	2	T40651	pre-mrna splicing
316	34	42.5	122	2	T49405	hypothetical prote	389	34	42.5	569	2	S50771	hexose transport p
317	34	42.5	131	2	S26792	Ig heavy chain V r	390	34	42.5	577	2	T43207	nuclear fusion pro
318	34	42.5	141	2	H91203	hypothetical prote	391	34	42.5	578	2	T15958	hypothetical prote
319	34	42.5	144	2	S14156	hypothetical prote	392	34	42.5	579	2	D88551	protein T2305.5 [1
320	34	42.5	148	2	B43663	host-inducible pro	393	34	42.5	582	2	C90165	conserved hypotet
321	34	42.5	152	2	T15937	hypothetical prote	394	34	42.5	584	2	S69555	myo-inositol trans

395	34	42.5	587	2	B71020	hypothetical prote	468	116	1	A28968	somatostatin I pre
396	34	42.5	608	2	T25018	hypothetical prote	469	116	1	RIBOS1	somatostatin precu
397	34	42.5	612	2	B40338	myo-inositol trans	470	116	1	RIBUS1	somatostatin I pre
398	34	42.5	615	2	T43330	catecholamine tran	471	116	1	RIMSS1	somatostatin precu
399	34	42.5	635	2	A46061	Na(+)-dependent cr	472	116	1	RIRTS1	somatostatin precu
400	34	42.5	635	2	JC2386	creatine transport	473	116	1	S20630	somatostatin precu
401	34	42.5	635	2	G02095	creatine transport	474	116	1	AE2400	hypothetical prote
402	34	42.5	635	2	S23431	choline transport	475	116	1	RIAPSI	somatostatin I pre
403	34	42.5	639	1	S45776	uracil transport p	476	121	2	PH1661	Ig heavy chain V r
404	34	42.5	650	2	T00617	endostyle-specific	477	138	2	S78252	ribosomal protein
405	34	42.5	668	2	C86476	protein F1504.45 [478	140	2	T01027	hypothetical prote
406	34	42.5	697	2	T18681	hypothetical prote	479	144	2	A99374	conserved hypotet
407	34	42.5	711	2	B69121	conserved hypotet	480	146	2	T01683	immobilization ant
408	34	42.5	716	2	J01366	polypeptide - hepa	481	154	2	T17816	hypothetical prote
409	34	42.5	726	2	A27602	complement C3 - ra	482	156	2	T20196	hypothetical prote
410	34	42.5	788	2	T25061	hypothetical prote	483	157	2	S58014	probable olfactory
411	34	42.5	840	2	T33217	hypothetical prote	484	159	2	R82692	hypothetical prote
412	34	42.5	873	1	S53828	cytochrome-c oxida	485	172	2	F89103	protein C18B10.3 [
413	34	42.5	899	2	G36812	hypothetical prote	486	185	2	S78508	heterodisulfide re
414	34	42.5	899	2	T42876	hypothetical prote	487	192	2	T15719	hypothetical prote
415	34	42.5	940	2	T01854	hypothetical prote	488	194	2	T41796	AcMNPV orf52 - Bom
416	34	42.5	975	2	A85318	myosin heavy chain	489	208	2	S76531	hypothetical prote
417	34	42.5	1054	2	A83897	hypothetical prote	490	213	2	T18684	hypothetical prote
418	34	42.5	1063	2	T46284	hypothetical prote	491	214	2	A35349	H+-transporting AT
419	34	42.5	1126	2	T05761	myosin heavy chain	492	215	2	B57055	melanocortin-4 rec
420	34	42.5	1211	2	T30841	serine-repeat anti	493	221	2	S76798	hypothetical prote
421	34	42.5	1238	2	T40120	C2H2 type zinc fin	494	228	2	S55888	C2HH finger protei
422	34	42.5	1309	2	T19170	hypothetical prote	495	229	2	A69762	hypothetical prote
423	34	42.5	1434	2	C90109	DNA-directed RNA p	496	234	2	T30734	hypothetical prote
424	34	42.5	1541	2	T02031	AAA protein L4171	497	234	2	S01320	Ig kappa chain pre
425	34	42.5	1921	2	T13827	kinesin-73 - fruit	498	240	2	B90739	probable enzyme [i
426	34	42.5	2195	2	T34264	hypothetical prote	499	243	2	S73698	hypothetical prote
427	34	42.5	2225	2	T26063	hypothetical prote	500	246	2	I51325	proteolipid protei
428	34	42.5	2233	1	T28669	surface protein 51	501	252	2	T33971	hypothetical prote
429	34	42.5	2395	1	S50820	genome polypeptin	502	253	2	T46029	C2HH finger protei
430	34	42.5	2652	1	VPIHB2	RNA-directed RNA p	503	257	2	T47303	hypothetical prote
431	34	42.5	2875	1	RRVUTW	formin binding pro	504	261	2	A84848	probable C2H2-type
432	34	42.5	2925	2	T00133	hypothetical prote	505	261	2	I78559	cyclic nucleotide-
433	33.5	41.9	27	2	S64717	hypothetical prote	506	262	2	I78560	ATP-binding compon
434	33.5	41.9	42	2	T07581	hypothetical prote	507	262	2	H91264	ATP-binding compon
435	33.5	41.9	64	1	WMIBH2	3b protein - avian	508	262	2	E86105	phosphonates trans
436	33.5	41.9	64	1	WMIBH5	E6 protein - human	509	262	2	A65220	probable membrane
437	33.5	41.9	150	1	W6ML13	hypothetical prote	510	265	2	T50569	probable nicotinam
438	33.5	41.9	198	2	B69192	immediate early pr	511	268	2	E71293	LIM protein FHL-1,
439	33.5	41.9	245	2	T10407	lipopolysaccharide	512	280	2	G01884	early E1A 32K prot
440	33.5	41.9	404	2	C64597	hepatocyte growth	513	280	2	G02741	early E1A 32K prot
441	33.5	41.9	728	1	A60185	hepatocyte growth	514	289	1	Q2AD2	homeotic protein m
442	33.5	41.9	728	1	JH0579	hypothetical prote	515	289	1	Q2AD5	hypothetical prote
443	33.5	41.9	1013	2	T46422	somatostatin - spo	516	295	1	S29399	hypothetical prote
444	33	41.2	14	2	A60622	somatostatin - sli	517	297	2	T29573	hypothetical prote
445	33	41.2	14	2	A60840	somatostatin I - c	518	309	2	T03859	protein K0899.1 [i
446	33	41.2	14	2	C60414	somatostatin I - s	519	314	2	H88991	probable mitochond
447	33	41.2	14	2	B60842	NADH2 dehydrogenas	520	314	2	T39510	reverse transcript
448	33	41.2	14	2	S00172	somatostatin-28 -	521	318	2	S58503	hypothetical prote
449	33	41.2	27	2	T13836	somatostatin-relat	522	319	2	T31752	hypothetical prote
450	33	41.2	28	2	A61322	hypothetical prote	523	320	2	G38989	protein C36C5.8 [i
451	33	41.2	34	2	A32721	hypothetical prote	524	325	2	C69118	heterodisulfide re
452	33	41.2	49	2	F90528	hypothetical prote	525	332	2	A57055	melanocortin recep
453	33	41.2	62	2	S62868	toxin III-8 - Tity	526	333	2	T29242	hypothetical prote
454	33	41.2	62	2	S62866	toxin III-8 - Tity	527	334	2	D71044	tRNA-pseudouridine
455	33	41.2	62	2	A61484	toxin VI - Brazili	528	334	2	E75170	probable pseudouri
456	33	41.2	62	2	B39510	toxin III-8 - Braz	529	343	2	T33945	hypothetical prote
457	33	41.2	84	2	S62868	toxin gamma precu	530	344	2	T18019	probable site-spec
458	33	41.2	84	2	S62867	toxin gamma precu	531	346	2	JC5716	G protein-coupled
459	33	41.2	84	2	S21158	neurotoxin TsVII p	532	347	2	T23944	hypothetical prote
460	33	41.2	85	2	T47596	hypothetical prote	533	352	2	F96548	probable DNA-bindi
461	33	41.2	92	1	RIPG8	somatostatin I pre	534	360	2	S48566	hypothetical prote
462	33	41.2	103	2	JC6167	somatostatin-14 [p	535	369	2	T26849	hypothetical prote
463	33	41.2	109	2	S16437	ribulose-bisphosph	536	380	2	T38012	longevity-assuranc
464	33	41.2	114	1	RIID81	somatostatin-14 pr	537	391	2	T32601	hypothetical prote
465	33	41.2	114	2	I50798	preprosomatostatin	538	394	2	D90315	heme biosynthesis
466	33	41.2	115	2	JC6166	somatostatin-14 pr	539	402	2	A70882	probable PPE prote
467	33	41.2	115	2	T31781	hypothetical prote	540	410	2	D84785	hypothetical prote

541	33	41.2	410	2	S78151	secY protein homol	614	33	41.2	923	2	T38398	hypothetical GTPas
542	33	41.2	411	2	A20359	hypothetical prote	615	33	41.2	959	2	A55913	transcytosis-assoc
543	33	41.2	415	2	F91209	low affinity tryp	616	33	41.2	982	2	T15967	hypothetical prote
544	33	41.2	415	2	A96056	low affinity tryp	617	33	41.2	999	2	S15961	hypothetical prote
545	33	41.2	415	2	A39412	tryptophan transp	618	33	41.2	1008	2	T04462	hypothetical prote
546	33	41.2	424	2	J05921	non-selective cati	619	33	41.2	1023	2	T18520	transhydrogenase h
547	33	41.2	425	2	T38548	hypothetical zinc-	620	33	41.2	1042	2	H75112	molybdenum cofacto
548	33	41.2	426	2	T15285	hypothetical prote	621	33	41.2	1043	2	T13733	Frz-F1 protein - f
549	33	41.2	426	2	B84689	probable RING zinc	622	33	41.2	1069	2	D85383	hypothetical prote
550	33	41.2	442	2	S61165	hypothetical prote	623	33	41.2	1119	2	A88481	protein C16A3.6 [i
551	33	41.2	454	1	IQJVB8	replication initia	624	33	41.2	1122	2	T47424	hypothetical prote
552	33	41.2	454	2	D84931	chromosomal repli	625	33	41.2	1189	2	T39711	calE protein - Agr
553	33	41.2	465	2	T27415	hypothetical prote	626	33	41.2	1227	2	AG2504	hypothetical prote
554	33	41.2	478	2	JQ1301	hemorrhagic protei	627	33	41.2	1321	2	T29308	hypothetical prote
555	33	41.2	478	2	T03548	mannotol 2-dehydro	628	33	41.2	1372	2	T29309	hypothetical prote
556	33	41.2	482	2	T31955	hypothetical prote	629	33	41.2	1377	2	A38926	DNA-binding protei
557	33	41.2	482	2	T02355	hypothetical prote	630	33	41.2	1446	2	T04528	myosin heavy chain
558	33	41.2	495	1	Q1AD52	early E1B 55K prot	631	33	41.2	1477	2	T00957	myosin heavy chain
559	33	41.2	496	1	Q1AD55	early E1B 55K prot	632	33	41.2	1490	2	B84726	probable unconvet
560	33	41.2	502	1	I30010	NADH2 dehydrogen	633	33	41.2	1499	2	AC2555	hypothetical prote
561	33	41.2	503	2	S84302	zinc transporter Z	634	33	41.2	1502	2	T14278	hypothetical prote
562	33	41.2	512	2	A86238	protein F14N23.31	635	33	41.2	1502	2	D84587	myosin-like protei
563	33	41.2	513	2	T31596	hypothetical prote	636	33	41.2	1504	2	T49896	glycine/proline-ri
564	33	41.2	515	2	T30651	hypothetical prote	637	33	41.2	1515	2	S51824	myosin heavy chain
565	33	41.2	519	2	T48488	hypothetical prote	638	33	41.2	1611	2	A84743	probable myosin he
566	33	41.2	548	2	T14793	hypothetical prote	639	33	41.2	1666	1	C3GP	complement C3 prec
567	33	41.2	549	2	T49298	hypothetical prote	640	33	41.2	1733	1	B45344	probable nuclear a
568	33	41.2	552	2	T08148	proline-rich myros	641	33	41.2	1736	2	F86178	hypothetical prote
569	33	41.2	554	2	T11267	NADH2 dehydrogen	642	33	41.2	1839	1	RRMP8M	genome polyprotein
570	33	41.2	560	2	S27874	steroid hormone re	643	33	41.2	1864	2	T18485	hypothetical prote
571	33	41.2	562	2	B70081	hypothetical prote	644	33	41.2	1872	2	B44851	probable membrane
572	33	41.2	570	2	S40757	hypothetical prote	645	33	41.2	1898	2	B40505	hypothetical prote
573	33	41.2	588	2	H84902	hypothetical prote	646	33	41.2	1958	2	T43161	sodium channel pro
574	33	41.2	590	1	Q0UTC5	NADH2 dehydrogen	647	33	41.2	2049	2	T08165	RNA1 polyprotein -
575	33	41.2	590	1	S34960	NADH2 dehydrogen	648	33	41.2	2150	2	T08165	hypothetical prote
576	33	41.2	590	2	T06626	hypothetical prote	649	33	41.2	2342	2	T13412	probable transport
577	33	41.2	623	1	VGVNBE	spike glycoprotein	650	32.5	40.6	96	2	S55366	ig kappa chain V r
578	33	41.2	626	1	RGBY21	cell division cont	651	32.5	40.6	101	2	S39490	hypothetical prote
579	33	41.2	633	2	T52506	hypothetical prote	652	32.5	40.6	102	2	T45500	hypothetical prote
580	33	41.2	636	2	A84903	hypothetical prote	653	32.5	40.6	114	2	T02374	finger protein BBF
581	33	41.2	645	2	I50680	alpha subunit of r	654	32.5	40.6	115	2	A96909	ferredoxin [import
582	33	41.2	654	2	AH2445	hypothetical prote	655	32.5	40.6	121	2	T43130	hypothetical prote
583	33	41.2	654	2	AH2445	hypothetical prote	656	32.5	40.6	150	1	W6WLC1	E6 protein - pygmy
584	33	41.2	659	2	D84633	sensory transducti	657	32.5	40.6	150	1	W6WLC1	E6 protein - human
585	33	41.2	663	1	S46492	probable multipan	658	32.5	40.6	150	1	W6WLC4	E6 protein - human
586	33	41.2	663	1	B69475	gelatinase A (EC 3	659	32.5	40.6	150	1	W6WLC6	E6 protein - human
587	33	41.2	663	2	S11521	DNA topoisomerase	660	32.5	40.6	206	2	C96972	hypothetical prote
588	33	41.2	664	2	S11521	cAMP-gated channel	661	32.5	40.6	221	2	T22771	hypothetical prote
589	33	41.2	664	2	AB1430	cyclic nucleotide-	662	32.5	40.6	234	2	T02370	finger protein BBF
590	33	41.2	664	2	AB1430	hypothetical prote	663	32.5	40.6	238	2	T02373	finger protein BBF
591	33	41.2	686	1	A44842	hypothetical prote	664	32.5	40.6	262	2	T02203	finger protein Dof
592	33	41.2	687	2	S53485	cGMP-gated ion cha	665	32.5	40.6	295	2	T00399	probable AP2 domai
593	33	41.2	688	2	B42161	carnitine O-acetyl	666	32.5	40.6	345	2	T16074	hypothetical prote
594	33	41.2	690	1	S07103	cGMP-gated cation	667	32.5	40.6	351	2	T32717	hypothetical prote
595	33	41.2	690	2	A42161	cGMP-gated cation	668	32.5	40.6	377	2	A39885	MHC class I histoc
596	33	41.2	691	2	J06509	rod cyclic nucleot	669	32.5	40.6	379	2	A35878	class I major hist
597	33	41.2	695	2	S74179	cyclic nucleotide-	670	32.5	40.6	379	2	B35878	class I major hist
598	33	41.2	703	2	T15503	hypothetical prote	671	32.5	40.6	406	2	B35878	hypothetical prote
599	33	41.2	703	2	A54766	metastasis-associa	672	32.5	40.6	552	2	T27427	dolichyl-phosphate
600	33	41.2	706	2	A55231	cyclic nucleotide-	673	32.5	40.6	554	2	S71751	hypothetical prote
601	33	41.2	715	2	T22787	hypothetical prote	674	32.5	40.6	581	2	B90539	hypothetical prote
602	33	41.2	716	2	J05763	dishevelled protei	675	32.5	40.6	634	2	H64508	hypothetical prote
603	33	41.2	732	2	S35691	cyclic nucleotide-	676	32.5	40.6	710	2	T52573	cyclic nucleotide
604	33	41.2	735	2	I50630	alpha subunit of c	677	32.5	40.6	1145	1	GNLJEV	HIV-1 retropepin
605	33	41.2	761	2	A96810	probable Mutator-1	678	32.5	40.6	1146	1	GNLJ22	HIV-1 retropepin
606	33	41.2	761	2	T00940	hypothetical prote	679	32.5	40.6	1146	1	GNLJEW	HIV-1 retropepin
607	33	41.2	779	2	AE2402	alpha-glucosidase	680	32.5	40.6	1291	2	T21267	hypothetical prote
608	33	41.2	810	1	A33380	interleukin-4 rece	681	32	40.0	13	2	PT0304	ig heavy chain CRD
609	33	41.2	830	2	S50810	probable membrane	682	32	40.0	27	1	TZA23	toxin III - snake-
610	33	41.2	839	2	P95334	myosin heavy chain	683	32	40.0	38	2	JN0613	defensin 4K - scor
611	33	41.2	859	1	S65938	nitrate reductase	684	32	40.0	73	2	B81061	hypothetical prote
612	33	41.2	880	2	S56828	finger protein YJL	685	32	40.0	76	2	A48784	ig kappa V regions
613	33	41.2	916	1	S32572	hydroxymethylgluta	686	32	40.0	79	2	T11380	NADH2 dehydrogen

687	32	40.0	80	2	A96772	hypothetical prote	760	32	40.0	345	2	A87338	L-lysine 2,3-amino
688	32	40.0	94	2	JH0787	transcription fact	761	32	40.0	345	2	H83020	heptosyltransferas
689	32	40.0	99	2	C95174	transposase, IS630	762	32	40.0	347	1	A44245	alcohol dehydrogen
690	32	40.0	99	2	D98040	degenerate transpo	763	32	40.0	347	1	S51120	alcohol dehydrogen
691	32	40.0	106	2	JQ0234	hypothetical 12.5K	764	32	40.0	350	1	S75404	probable radical-f
692	32	40.0	109	2	PH1671	Ig heavy chain v r	765	32	40.0	352	2	G98104	probable alcohol d
693	32	40.0	110	2	D48562	hypothetical nucle	766	32	40.0	352	2	P95240	alcohol dehydrogen
694	32	40.0	118	2	A53148	adenyl cyclase t	767	32	40.0	352	2	T51797	hypothetical prote
695	32	40.0	118	2	B53148	adenyl cyclase t	768	32	40.0	357	1	Q0BEG4	HMLF3 protein - hu
696	32	40.0	119	2	D64404	hypothetical prote	769	32	40.0	358	2	T22823	hypothetical prote
697	32	40.0	123	2	S70222	hypothetical prote	770	32	40.0	361	2	C86259	protein T12C24.4 (
698	32	40.0	135	2	S44214	genome polyprotein	771	32	40.0	363	2	C83128	2,3-butanediol deh
699	32	40.0	137	2	B34903	Ig heavy chain pre	772	32	40.0	363	2	AB2890	L-lysine 2,3-amino
700	32	40.0	137	2	T15522	hypothetical prote	773	32	40.0	363	2	G97665	L-lysine 2,3-amino
701	32	40.0	139	2	D97726	DNA-binding protei	774	32	40.0	365	2	E97315	membrane protease
702	32	40.0	145	1	TNLJBT	trans-activating t	775	32	40.0	367	2	AD3631	nitrous-oxide redu
703	32	40.0	145	2	S51907	cryptogene protein	776	32	40.0	372	2	T24891	hypothetical prote
704	32	40.0	148	2	T30627	hypothetical prote	777	32	40.0	373	2	E84647	hypothetical prote
705	32	40.0	149	2	B64475	aspartate carbamoy	778	32	40.0	375	1	E64302	probable radical-f
706	32	40.0	152	2	T34649	hypothetical prote	779	32	40.0	376	2	A98030	coproporphyrinogen
707	32	40.0	159	1	S27195	transforming growt	780	32	40.0	376	2	B95164	hypothetical prote
708	32	40.0	159	1	WPKT1	transforming growt	781	32	40.0	378	2	B83878	alcohol dehydrogen
709	32	40.0	159	2	I57497	transforming growt	782	32	40.0	379	2	C86767	oxygen-independent
710	32	40.0	173	2	D71661	hypothetical prote	783	32	40.0	379	2	B38170	cytochrome d compl
711	32	40.0	174	2	B69213	aspartate carbamoy	784	32	40.0	379	2	I50514	retinoid X recepto
712	32	40.0	183	2	T22604	hypothetical prote	785	32	40.0	381	2	F59101	hypothetical prote
713	32	40.0	186	2	S46450	hypothetical prote	786	32	40.0	381	2	A46358	steroid/thyroid ho
714	32	40.0	187	2	AB1647	hypothetical prote	787	32	40.0	382	2	T34127	hypothetical prote
715	32	40.0	189	2	T23747	hypothetical prote	788	32	40.0	385	2	G83817	coproporphyrinogen
716	32	40.0	194	2	T28889	hypothetical prote	789	32	40.0	385	2	AD1259	coproporphyrinogen
717	32	40.0	205	2	H90532	hypothetical prote	790	32	40.0	385	2	AH1621	conserved hypotet
718	32	40.0	208	2	A29851	gag polyprotein -	791	32	40.0	385	2	A82388	NADH2 dehydrogenas
719	32	40.0	213	2	T35433	hypothetical prote	792	32	40.0	386	2	S60646	hypothetical prote
720	32	40.0	214	2	T34069	hypothetical prote	793	32	40.0	388	2	I29694	transcription fact
721	32	40.0	219	2	B72291	hypothetical prote	794	32	40.0	389	2	I49640	EAR2 protein - mou
722	32	40.0	225	2	A69305	conserved hypotet	795	32	40.0	390	2	S44285	polysialacturonase
723	32	40.0	238	2	B81341	hypothetical prote	796	32	40.0	395	2	T09654	transcription fact
724	32	40.0	241	2	T34379	hypothetical prote	797	32	40.0	397	2	S20617	hypothetical prote
725	32	40.0	243	1	D70456	gufa protein homol	798	32	40.0	398	2	S77230	steroid receptor p
726	32	40.0	245	2	I68673	Gene X123 protein	799	32	40.0	403	2	S35334	steroid receptor p
727	32	40.0	248	2	A10576	thiol,disulfide in	800	32	40.0	403	2	S02709	ear-2 protein - hu
728	32	40.0	256	2	T22715	hypothetical prote	801	32	40.0	410	2	S26669	retinoic acid rece
729	32	40.0	261	2	D86149	TiN6.19 protein -	802	32	40.0	410	2	I50689	orphan receptor CO
730	32	40.0	262	2	A12545	hypothetical prote	803	32	40.0	411	2	S35333	steroid receptor p
731	32	40.0	268	2	C90709	thiol disulfide in	804	32	40.0	414	2	I48975	apolipoprotein A-I
732	32	40.0	268	2	B64794	hypothetical prote	805	32	40.0	414	2	A37133	apolipoprotein A-I
733	32	40.0	268	2	G85559	thiol,disulfide in	806	32	40.0	416	2	A69023	conserved hypotet
734	32	40.0	272	2	T15889	hypothetical prote	807	32	40.0	419	1	A45397	DNA ligase (ATP) (
735	32	40.0	274	2	C69444	conserved hypotet	808	32	40.0	419	2	S23018	DNA ligase (ATP) (
736	32	40.0	274	2	T11947	ribosomal protein	809	32	40.0	419	2	A57000	orphan receptor CO
737	32	40.0	280	2	A35872	steroid hormone re	810	32	40.0	422	2	I50516	retinoid X recepto
738	32	40.0	286	2	T22627	hypothetical prote	811	32	40.0	422	2	I48305	gene COUP-TFI prot
739	32	40.0	288	2	B43253	zinc finger protei	812	32	40.0	423	1	WZVZ17	I7 protein - vacci
740	32	40.0	292	2	T16085	hypothetical prote	813	32	40.0	423	2	T37344	topoisomerase II -
741	32	40.0	294	1	MUSM1	lysozyme (EC 3.2.1	814	32	40.0	423	2	C42511	K7L protein - vacc
742	32	40.0	299	2	A00058	transcription acti	815	32	40.0	423	2	E36843	hypothetical prote
743	32	40.0	303	2	T19310	hypothetical prote	816	32	40.0	423	2	T28499	hypothetical prote
744	32	40.0	305	2	I47040	sterol O-acyltrans	817	32	40.0	423	2	C72158	L7L protein - vari
745	32	40.0	310	2	A70449	hypothetical prote	818	32	40.0	423	2	S02710	transcription fact
746	32	40.0	311	2	B84428	hypothetical prote	819	32	40.0	425	2	D75164	hypothetical prote
747	32	40.0	317	2	S57546	hypothetical prote	820	32	40.0	428	2	T48008	hypothetical prote
748	32	40.0	324	2	A39523	transforming prote	821	32	40.0	428	2	G71177	hypothetical prote
749	32	40.0	326	2	C87578	ISCC3, transposase	822	32	40.0	429	2	S20050	hypothetical prote
750	32	40.0	326	2	I51694	transforming prote	823	32	40.0	434	2	T19205	hypothetical prote
751	32	40.0	326	2	I54339	proto-oncogene bmi	824	32	40.0	437	2	T16477	hypothetical prote
752	32	40.0	333	2	T23618	hypothetical prote	825	32	40.0	438	2	I50517	retinoid X recepto
753	32	40.0	335	2	T18032	probable site-spec	826	32	40.0	441	2	I50515	retinoid X recepto
754	32	40.0	340	2	S75099	hypothetical prote	827	32	40.0	441	2	H96968	integral membrane
755	32	40.0	342	2	A45678	probable transmem	828	32	40.0	443	2	F95243	sensor histidine k
756	32	40.0	342	2	A37991	DNA-binding protei	829	32	40.0	443	2	C98108	histidine kinase (
757	32	40.0	343	2	H96976	tryptophan-tRNA sy	830	32	40.0	446	1	A46335	gag polyprotein -
758	32	40.0	344	2	JN0717	DNA-binding Mel-18	831	32	40.0	446	2	A34418	H-2 region II bind
759	32	40.0	345	2	C90509	sorbitol dehydroge	832	32	40.0	446	2	T31539	hypothetical prote

833	32	40.0	448	2	D41727	retinoid X recepto	906	32	40.0	615	2	D86473	69.8K hypothetical
834	32	40.0	451	2	A41651	retinoic acid rece	907	32	40.0	617	2	S37744	endo-exonuclease y
835	32	40.0	452	2	F83793	DNA-damage-inducib	908	32	40.0	617	2	T00601	hypothetical prote
836	32	40.0	453	2	S47633	RXR protein - Afri	909	32	40.0	619	1	T43348	nuclear steroid ho
837	32	40.0	453	2	A43765	stsl+ protein - fi	910	32	40.0	619	2	C86467	hypothetical prote
838	32	40.0	462	2	A83454	oxygen-independent	911	32	40.0	621	2	B89451	probable zinc meta
839	32	40.0	462	1	S09592	retinoid X recepto	912	32	40.0	625	2	S48941	regulatory protein
840	32	40.0	462	2	S44490	RXR type hormone r	913	32	40.0	627	2	B84482	probable gag-prote
841	32	40.0	463	2	S26670	retinoic acid rece	914	32	40.0	634	1	S24384	nitrous-oxide redu
842	32	40.0	463	2	B41727	retinoid-X recepto	915	32	40.0	636	2	C83322	nitrous-oxide redu
843	32	40.0	467	2	A43781	retinoid-X-recepto	916	32	40.0	638	1	A31845	nitrous-oxide redu
844	32	40.0	467	2	S26668	retinoic acid rece	917	32	40.0	643	2	T04418	probable acyl-CoA
845	32	40.0	467	2	A47278	retinoid X recepto	918	32	40.0	646	2	C86441	probable ABC trans
846	32	40.0	470	2	D41977	retinoid receptor	919	32	40.0	647	1	I48737	LIM protein kinase
847	32	40.0	473	2	D81782	oxygen-independent	920	32	40.0	647	1	I58353	LIM protein kinase
848	32	40.0	473	2	H81204	oxygen-independent	921	32	40.0	651	2	F64417	probable ATP-depen
849	32	40.0	473	2	T04218	hypothetical prote	922	32	40.0	653	2	G96675	hypothetical prote
850	32	40.0	475	2	T33943	hypothetical prote	923	32	40.0	665	2	S52072	DmNGC protein - f
851	32	40.0	477	2	A82866	exoQ-like protein	924	32	40.0	669	2	S65551	factor H - bovine
852	32	40.0	480	2	B82362	oxygen-independent	925	32	40.0	669	2	T01816	translation elonga
853	32	40.0	480	2	H97642	exoQ-like protein	926	32	40.0	669	2	A49585	Na+ channel protei
854	32	40.0	480	2	T18675	hypothetical prote	927	32	40.0	681	2	T19429	hypothetical prote
855	32	40.0	485	1	VHVUJ7	nucleoprotein - Ha	928	32	40.0	683	1	A41785	system b(0,+)-amin
856	32	40.0	485	2	S44819	P44E2.7 protein -	929	32	40.0	685	2	C56591	E75 B steroid rece
857	32	40.0	487	2	T06040	hypothetical prote	930	32	40.0	704	2	F86146	hypothetical prote
858	32	40.0	488	2	C41977	retinoid receptor	931	32	40.0	710	2	T46589	ropy-2 protein lim
859	32	40.0	493	2	C86565	oligopeptide perme	932	32	40.0	711	2	S43464	ecdysteroid-induce
860	32	40.0	493	2	D72059	peptide ABC transp	933	32	40.0	746	2	T01536	hypothetical prote
861	32	40.0	497	1	WMBELM	membrane protein L	934	32	40.0	746	2	B32693	steroid receptor p
862	32	40.0	498	2	PC6300	synaptotagmin X -	935	32	40.0	752	2	T48574	hypothetical prote
863	32	40.0	508	2	S11533	usp protein - frui	936	32	40.0	762	2	S60415	dolichyl-phosphate
864	32	40.0	508	2	T13737	steroid hormone re	937	32	40.0	767	2	G86476	protein F1504.37 [
865	32	40.0	511	2	S52622	amidophosphoribos	938	32	40.0	775	2	T21436	hypothetical prote
866	32	40.0	512	2	JC4164	catalase (EC 1.11.	939	32	40.0	796	2	E96654	hypothetical prote
867	32	40.0	513	2	T48192	hypothetical prote	940	32	40.0	803	2	S45916	hypothetical prote
868	32	40.0	520	2	I84718	RXR-beta1 isoform	941	32	40.0	816	2	C69493	hypothetical prote
869	32	40.0	521	2	T38466	probable NRAMP-fam	942	32	40.0	839	2	A47007	adenylyl cyclase t
870	32	40.0	523	2	T05692	hypothetical prote	943	32	40.0	852	1	GNLJGA	pol polyprotein -
871	32	40.0	525	1	Q08B6	BFLF1 protein - hu	944	32	40.0	852	1	GNLJGA	pol polyprotein -
872	32	40.0	532	2	T42369	catalase (EC 1.11.	945	32	40.0	852	2	S29358	glycoprotein B - a
873	32	40.0	532	2	T28784	hypothetical prote	946	32	40.0	854	2	T03107	prominin - mouse
874	32	40.0	533	2	S37781	retinoid X recepto	947	32	40.0	858	2	T08881	phosphoribosyl-AMP
875	32	40.0	535	2	T13645	hypothetical prote	948	32	40.0	874	2	T29548	hypothetical prote
876	32	40.0	540	1	I49454	sterol O-acyltrans	949	32	40.0	896	2	C85438	hypothetical prote
877	32	40.0	543	2	S65462	glucose transport	950	32	40.0	912	2	C96696	hypothetical prote
878	32	40.0	543	2	A32693	steroid receptor p	951	32	40.0	915	2	T26895	protein F1N21_6 [i
879	32	40.0	548	2	T11065	cytochrome-c oxida	952	32	40.0	916	2	B84473	hypothetical prote
880	32	40.0	550	1	A48026	sterol O-acyltrans	953	32	40.0	919	2	T16459	hypothetical prote
881	32	40.0	553	2	I45067	steroid hormone re	954	32	40.0	921	2	H84921	probable transposo
882	32	40.0	557	2	H96720	probable peptide t	955	32	40.0	1008	2	H85055	hypothetical prote
883	32	40.0	557	2	A55933	paxillin - human	956	32	40.0	1016	1	JS0428	NAD ADP-ribosyltra
884	32	40.0	559	2	B55933	paxillin - chicken	957	32	40.0	1025	2	T21319	hypothetical prote
885	32	40.0	560	2	S23313	hypothetical prote	958	32	40.0	1046	1	GNWEC	genome polyprotein
886	32	40.0	560	2	T14616	hypothetical prote	959	32	40.0	1046	2	T32152	hypothetical prote
887	32	40.0	561	2	T05294	amidophosphoribos	960	32	40.0	1064	2	A41542	adenylate cyclase
888	32	40.0	562	2	G88408	protein nhr-6 [imp	961	32	40.0	1090	2	A41541	adenylate cyclase
889	32	40.0	562	2	S56145	B69 protein - hum	962	32	40.0	1097	2	S68685	adenylate cyclase
890	32	40.0	564	2	T41503	alpha-amylase - fi	963	32	40.0	1099	2	A55405	adenylate cyclase
891	32	40.0	565	2	E84541	amidophosphoribos	964	32	40.0	1107	2	T15884	adenylate cyclase
892	32	40.0	567	2	B55901	conserved hypothet	965	32	40.0	1110	2	A43253	large tra-1 protei
893	32	40.0	589	2	A55968	folate binding pro	966	32	40.0	1132	2	S60433	probable membrane
894	32	40.0	590	2	JC2468	folate transporter	967	32	40.0	1134	2	A41350	adenylate cyclase
895	32	40.0	591	2	I38924	reduced folate car	968	32	40.0	1144	1	A39833	adenylate cyclase
896	32	40.0	591	2	I52728	reduced folate car	969	32	40.0	1159	2	S22768	130K protein - mai
897	32	40.0	596	2	A45195	adenylyl cyclase ty	970	32	40.0	1185	2	A46180	adenylyl cyclase t
898	32	40.0	600	2	C86468	probable auxin res	971	32	40.0	1166	2	A49201	adenylate cyclase
899	32	40.0	600	2	T01259	AMP deaminase homo	972	32	40.0	1167	2	T13927	adenylate cyclase
900	32	40.0	606	2	D86443	probable PPR-repea	973	32	40.0	1180	2	A47202	adenylate cyclase
901	32	40.0	607	2	H88065	protein T16A1.1 [i	974	32	40.0	1184	2	A42904	adenylyl cyclase ty
902	32	40.0	609	2	D49839	odd-paired - fruit	975	32	40.0	1201	2	T00444	hypothetical prote
903	32	40.0	611	2	D82881	zinc metalloprotei	976	32	40.0	1223	2	S29717	hypothetical prote
904	32	40.0	612	2	T18848	hypothetical prote	977	32	40.0	1237	2	A34598	ecdysone-induced p
905	32	40.0	613	2	JC5501	endothelin recepto	978	32	40.0				

979 32 40.0 1242 2 T45976 myosin heavy chain
980 32 40.0 1248 2 A53588 adenylate cyclase
981 32 40.0 1251 2 S48687 type VIII adenyllyl
982 32 40.0 1253 2 T21085 hypothetical prote
983 32 40.0 1260 2 T14276 myosin-like protei
984 32 40.0 1264 2 S41603 type V adenyllyl cy
985 32 40.0 1269 2 T00443 hypothetical prote
986 32 40.0 1273 2 T42405 sax-3 protein - Ca
987 32 40.0 1291 1 S05465 retrovirus-related
988 32 40.0 1309 2 T13158 adenylate cyclase
989 32 40.0 1353 2 JC4279 adenylate cyclase
990 32 40.0 1363 1 A55875 xanthine dehydroge
991 32 40.0 1389 2 H84914 probable WD-40 rep
992 32 40.0 1394 2 B34598 ecdysone-induced p
993 32 40.0 1427 2 S74293 SRB8 protein - yea
994 32 40.0 1443 2 S05979 steroid hormone re
995 32 40.0 1484 2 T29275 hypothetical prote
996 32 40.0 1520 2 S46444 myosin MYAI, class
997 32 40.0 1528 2 T14279 myosin-like protei
998 32 40.0 1545 1 S71841 multidrug resistan
999 32 40.0 1556 2 P96587 hypothetical prote
1000 32 40.0 1583 2 T00727 myosin heavy chain

ALIGNMENTS

RESULT 1
H88134
protein T12C9.3 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C/Accession: H88124
R/anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: H88124
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1910 <STO>
A/Cross-references: UNIPARC:UPI000017A592; GB:chr_II; PIDN:AC71141.1; PID:g1086770; GSPD
A/Note: proline-rich
C/Genetics:
C/Map position: 2

Query Match 62.5%; Score 50; DB 2; Length 1910;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YVCFWKTC 11
: |||||
Db 1378 YVCFWKTC 1386
:
RESULT 2
JB0200
orphan UDP-glucuronosyltransferase (EC 2.4.1.1) - human
N/Alternate names: UGT2B11
C/Species: Homo sapiens (nan)
C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
C/Accession: JB0200
R/Beaulieu, M.; Levesque, E.W.; Hum, D.; Belanger, A.
Biochem. Biophys. Res. Commun. 248, 44-50, 1998
A/Title: Isolation and characterization of a human orphan UDP-glucuronosyltransferase, U
A/Reference number: JB0200; MUID:98340847; PMID:9675083
A/Accession: JB0200
A/Molecule type: mRNA
A/Residues: 1-529 <BEA>
A/Cross-references: UNIPARC:UPI0000178B8F; GB:AF016492

C/Comment: This enzyme catalyzes the transfer of glucuronic acid to a wide range of exoge
C/Superfamily: glucuronosyltransferase
C/Keywords: glycoprotein; glycosyltransferase
F/493-509/Domain: membrane-anchoring #status predicted <MAC>
F/315/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 56.2%; Score 45; DB 2; Length 529;
Best Local Similarity 62.5%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YCYCFWPK 8
: |||||
Db 511 FCLFCFWK 518
:
RESULT 3
I51323
proteolipid protein DM alpha - spiny dogfish
C/Species: Squalus acanthias (spiny dogfish)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I51323
R/Kitagawa, K.; Sinoway, M.P.; Yang, C.; Gould, R.M.; Colman, D.R.
Neuron 11, 433-448, 1993
A/Title: A proteolipid protein gene family: expression in sharks and rays and possible e
A/Reference number: I51323; MUID:94000810; PMID:8398138
A/Accession: I51323
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-245 <KIT>
A/Cross-references: UNIPROT:P36963; UNIPARC:UPI00001294CD; EMBL:U02973; NID:g409969; PID:
C/Superfamily: myelin proteolipid protein

Query Match 55.0%; Score 44; DB 2; Length 245;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YCYCFWKC 10
: |||||
Db 140 YIYTWSTC 149
:
RESULT 4
C69175
heat shock protein X - Methanobacterium thermoautotrophicum (strain Delta H)
C/Species: Methanobacterium thermoautotrophicum
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: C69175
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A/Reference number: A69000; MUID:98037514; PMID:9371463
A/Accession: C69175
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-258 <MTH>
A/Cross-references: UNIPROT:O26669; UNIPARC:UPI000012CE01; GB:AE0000839; GB:AE000666; NID
A/Experimental source: strain Delta H
C/Genetics:
C/Superfamily: heat-shock protein htpX

Query Match 55.0%; Score 44; DB 1; Length 258;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CYCFWKT 9
: |||||
Db 169 CYIFWST 176
:
RESULT 5

AG1214
 methylases homolog lmo119 [imported] - Listeria monocytogenes (strain EGD-e)
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
 C;Accession: AG1214
 R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, P.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Meok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AG1214
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-285 <GLA>
 A;Cross-references: UNIPROT:Q8Y800; UNIPARC:UPI0000055118; GB:NC_003210; PIDN:CAC99197.1
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: lmo119
 C;Superfamily: modification methylase (adenine-specific), M.EcoRV type

Query Match 55.0%; Score 44; DB 2; Length 285;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YCYCFWK 9
 DB 61 YSICYFWKS 69

RESULT 6
 S65673
 GABA transport protein - tobacco hornworm
 C;Species: Manduca sexta (tobacco hornworm)
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S65673
 R;Mbundu, D.; Ross, L.S.; Gill, S.S.
 Arch. Biochem. Biophys. 318, 489-497, 1995
 A;Title: Cloning, functional expression, and pharmacology of a GABA transporter from Manduca sexta.
 A;Reference number: S65673; MUID:95251402; PMID:7733681
 A;Accession: S65673
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-597 <MBU>
 A;Cross-references: UNIPROT:Q25512; UNIPARC:UPI000007A7CB; EMBL:L40373; NID:G695377; PIDN:UPI000007A7CB
 C;Superfamily: gamma-aminobutyric acid transporter

Query Match 55.0%; Score 44; DB 2; Length 597;
 Best Local Similarity 71.4%; Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYCYCFWK 8
 DB 238 CYFCIWK 244

RESULT 7
 A44409
 gamma-aminobutyric acid transport protein 3 - mouse
 N;Alternate names: GABA transporter 3
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C;Accession: A44409
 R;Liu, Q.R.; Lopez-Corcuera, B.; Mandiyan, S.; Nelson, H.; Nelson, N.
 J. Biol. Chem. 268, 2106-2112, 1993
 A;Title: Molecular characterization of four pharmacologically distinct alpha-aminobutyric acid transporters from Mus musculus.
 A;Reference number: A44409; MUID:93131969; PMID:8420981
 A;Accession: A44409
 A;Molecule type: mRNA
 A;Residues: 1-602 <LIU>
 A;Cross-references: UNIPROT:P31649; UNIPARC:UPI00000019C1

A;Experimental source: brain
 A;Note: sequence extracted from NCBI backbone (NCBIP:123177)
 C;Superfamily: gamma-aminobutyric acid transporter
 C;Keywords: brain; glycoprotein; membrane protein; phosphoprotein

Query Match 55.0%; Score 44; DB 2; Length 602;
 Best Local Similarity 71.4%; Pred. No. 78;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYCYCFWK 8
 DB 219 CYFCIWK 225

RESULT 8
 A45078
 gamma-aminobutyric acid transporter protein 2 - rat
 N;Alternate names: GABA transporter 2, GAT-2
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C;Accession: A45078
 R;Borden, L.A.; Smith, K.E.; Hartig, P.R.; Branchek, T.A.; Weinshank, R.L.
 J. Biol. Chem. 267, 21098-21104, 1992
 A;Title: Molecular heterogeneity of the gamma-aminobutyric acid (GABA) transporter system.
 A;Reference number: A45078; MUID:93016029; PMID:1400419
 A;Accession: A45078
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-602 <BOR>
 A;Cross-references: UNIPROT:P31646; UNIPARC:UPI00001354AD; GB:M95762; NID:G202522; PIDN:UPI00001354AD
 A;Experimental source: brain
 A;Note: sequence extracted from NCBI backbone (NCBIP:116199)
 C;Superfamily: gamma-aminobutyric acid transporter
 C;Keywords: brain; glycoprotein; membrane protein; phosphoprotein

Query Match 55.0%; Score 44; DB 2; Length 602;
 Best Local Similarity 71.4%; Pred. No. 78;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYCYCFWK 8
 DB 219 CYFCIWK 225

RESULT 9
 S68236
 betaine/GABA transport protein BGT-1 - human
 C;Species: Homo sapiens (man)
 C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S68236; I56522
 R;Rasola, A.; Galletta, L.J.V.; Barone, V.; Romeo, G.; Bagnasco, S.
 FEBS Lett. 373, 229-233, 1995
 A;Title: Molecular cloning and functional characterization of a GABA/betaine transporter from human brain.
 A;Reference number: S68236; MUID:96033979; PMID:7589472
 A;Accession: S68236
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-614 <RAS>
 A;Cross-references: UNIPROT:P48065; UNIPARC:UPI0000161F4B; EMBL:U27699; NID:G881474; PIDN:UPI0000161F4B
 R;Borden, L.A.; Smith, K.E.; Gustafson, E.L.; Branchek, T.A.; Weinshank, R.L.
 J. Neurochem. 64, 977-984, 1995
 A;Title: Cloning and expression of a betaine/GABA transporter from human brain.
 A;Reference number: I56522; MUID:95165166; PMID:7861179
 A;Accession: I56522
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-9,'Y',11-570,'QL',573-614 <RES>
 A;Cross-references: UNIPARC:UPI00001354A9; GB:L42300; NID:G808695; PIDN:AAA66574.1; PID:G808695
 C;Genetics:
 A;Gene: BGT-1
 A;Map position: 12p13
 C;Superfamily: gamma-aminobutyric acid transporter
 C;Keywords: glycoprotein; phosphoprotein; transmembrane protein

F/45-65/Domain: transmembrane #status predicted <TM1>
 F/72-92/Domain: transmembrane #status predicted <TM2>
 F/116-137/Domain: transmembrane #status predicted <TM3>
 F/213-232/Domain: transmembrane #status predicted <TM4>
 F/238-260/Domain: transmembrane #status predicted <TM5>
 F/287-307/Domain: transmembrane #status predicted <TM6>
 F/321-340/Domain: transmembrane #status predicted <TM7>
 F/373-393/Domain: transmembrane #status predicted <TM8>
 F/423-440/Domain: transmembrane #status predicted <TM9>
 F/456-476/Domain: transmembrane #status predicted <TM10>
 F/496-517/Domain: transmembrane #status predicted <TM11>
 F/538-559/Domain: transmembrane #status predicted <TM12>
 F/40,235/Binding site: phosphate (Thr) (covalent) #status predicted
 F/171,183/Binding site: carboxylate (Asn) (covalent) #status predicted
 F/418/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 55.0%; Score 44; DB 2; Length 614;
 Best Local Similarity 71.4%; Pred. No. 79;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFCWK 8
 ||: ||
 Db 224 CYFCIWK 230

RESULT 10
 A41757
 betaine transport protein, renal - dog
 C/Species: Canis lupus familiaris (dog)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C/Accession: A41757
 R/Yamauchi, A.; Uchida, S.; Kwon, H.M.; Preston, A.S.; Robey, R.B.; Garcia-Perez, A.; B
 J. Biol. Chem. 267, 649-652, 1992
 A/Title: Cloning of a Na(+)- and Cl(-)-dependent betaine transporter that is regulated b
 A/Reference number: A41757; MUID:92112724; PMID:1370453
 A/Accession: A41757
 A/Molecule type: mRNA
 A/Residues: 1-614 <YAM>
 A/Cross-references: UNIPROT:P27799; UNIPARC:UPI00001354A8; GB:M80403; NID:gl64031; PIDN:
 C/Superfamily: gamma-aminobutyric acid transporter
 C/Keywords: membrane protein

Query Match 55.0%; Score 44; DB 2; Length 614;
 Best Local Similarity 71.4%; Pred. No. 79;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFCWK 8
 ||: ||
 Db 224 CYFCIWK 230

RESULT 11
 A43390
 gamma-aminobutyric acid transporter protein GAT2 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C/Accession: A43390; D46027
 R/Lopez-Corcuera, B.; Liu, Q.R.; Mandiyan, S.; Nelson, H.; Nelson, N.
 J. Biol. Chem. 267, 17491-17493, 1992
 A/Title: Expression of a mouse brain cDNA encoding novel gamma-aminobutyric acid transpo
 A/Reference number: A43390; MUID:92388088; PMID:1517200
 A/Accession: A43390
 A/Molecule type: mRNA
 A/Residues: 1-614 <LOP>
 A/Cross-references: UNIPROT:P31651; UNIPARC:UPI0000029EE8
 A/Experimental source: brain
 A/Note: sequence extracted from NCBI backbone (NCBIN:112639, NCBI:P:112640)
 R/Liu, Q.R.; Mandiyan, S.; Nelson, H.; Nelson, N.
 Proc. Natl. Acad. Sci. U.S.A. 89, 6639-6643, 1992
 A/Title: A family of genes encoding neurotransmitter transporters.
 A/Reference number: A46027; MUID:92335351; PMID:1631167
 A/Accession: D46027
 A/Status: preliminary

A/Molecule type: DNA
 A/Residues: 39-71 <LIU>
 A/Cross-references: UNIPARC:UPI00001779C4
 A/Note: sequence extracted from NCBI backbone (NCBIN:108829, NCBI:P:108830)
 C/Superfamily: gamma-aminobutyric acid transporter
 C/Keywords: transmembrane protein

Query Match 55.0%; Score 44; DB 2; Length 614;
 Best Local Similarity 71.4%; Pred. No. 79;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFCWK 8
 ||: ||
 Db 224 CYFCIWK 230

RESULT 12
 S63539
 GABA/beta-alanine transporter - marbled electric ray
 C/Species: Torpedo marmorata (marbled electric ray)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S63539
 R/Guimbal, C.; Klostermann, A.; Kilimann, M.W.
 Eur. J. Biochem. 234, 794-800, 1995
 A/Title: Phylogenetic conservation of 4-aminobutyric acid (GABA) transporter isoforms: c
 A/Reference number: S63539; MUID:96163462; PMID:8575437
 A/Accession: S63539
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-622 <GUI>
 A/Cross-references: UNIPROT:Q91503; UNIPARC:UPI00000FC9AC; EMBL:X87170; NID:gl171629; PTI
 C/Superfamily: gamma-aminobutyric acid transporter

Query Match 55.0%; Score 44; DB 2; Length 622;
 Best Local Similarity 71.4%; Pred. No. 80;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFCWK 8
 ||: ||
 Db 227 CYFCIWK 233

RESULT 13
 B44409
 gamma-aminobutyric acid transporter 4, GAT4 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C/Accession: B44409
 R/Liu, Q.R.; Lopez-Corcuera, B.; Mandiyan, S.; Nelson, H.; Nelson, N.
 J. Biol. Chem. 268, 2106-2112, 1993
 A/Title: Molecular characterization of four pharmacologically distinct alpha-aminobutyri
 A/Reference number: A44409; MUID:93131969; PMID:84420961
 A/Accession: B44409
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-627 <LIU>
 A/Cross-references: UNIPROT:P31650; UNIPARC:UPI0000029EE7
 A/Experimental source: brain
 A/Note: sequence extracted from NCBI backbone (NCBI:P:123179)
 C/Superfamily: gamma-aminobutyric acid transporter
 C/Keywords: transmembrane protein

Query Match 55.0%; Score 44; DB 2; Length 627;
 Best Local Similarity 71.4%; Pred. No. 80;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFCWK 8
 ||: ||
 Db 234 CYFCIWK 240

RESULT 14
 JH0695

gamma-aminobutyric acid transporter protein 3 - rat
 N;Alternate names: GABA transporter 3; gamma-aminobutyric acid transporter protein B
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C;Accession: JH0695; B45078
 R;Clark, J.A.; Deutch, A.Y.; Gallipoli, P.Z.; Amara, S.G.
 Neuron 9, 337-348, 1992
 A;Title: Functional expression and CNS distribution of a beta-alanine-sensitive neuronal
 A;Reference number: JH0695; MUID:92360310; PMID:1497897
 A;Accession: JH0695
 A;Molecule type: mRNA
 A;Residues: 1-627 <CLA>
 A;Cross-references: UNIPROT:P31647; UNIPARC:UPI00001354A7; GB:S42358; NID:g253466; PIDN:
 R;Borden, L.A.; Smith, K.E.; Hartig, P.R.; Branchek, T.A.; Weinshank, R.L.
 J. Biol. Chem. 267, 21098-21104, 1992
 A;Title: Molecular heterogeneity of the gamma-aminobutyric acid (GABA) transport system.
 A;Reference numbers: A45078; MUID:93016029; PMID:1400419
 A;Accession: B45078
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-627 <BOR>
 A;Cross-references: UNIPARC:UPI00001354A7; GB:M95763; NID:g202534; PIDN:AAA0607.1; PID:
 A;Experimental source: brain
 A;Note: sequence extracted from NCBI backbone (NCBIP:116200)
 C;Superfamily: gamma-aminobutyric acid transporter
 C;Keywords: brain; glycoprotein; phosphoprotein; transmembrane protein
 F;54-74/Domain: transmembrane #status predicted <TM1>
 F;81-101/Domain: transmembrane #status predicted <TM2>
 F;116-146/Domain: transmembrane #status predicted <TM3>
 F;223-239/Domain: transmembrane #status predicted <TM4>
 F;248-270/Domain: transmembrane #status predicted <TM5>
 F;297-317/Domain: transmembrane #status predicted <TM6>
 F;330-351/Domain: transmembrane #status predicted <TM7>
 F;383-403/Domain: transmembrane #status predicted <TM8>
 F;433-451/Domain: transmembrane #status predicted <TM9>
 F;468-488/Domain: transmembrane #status predicted <TM10>
 F;509-528/Domain: transmembrane #status predicted <TM11>
 F;548-566/Domain: transmembrane #status predicted <TM12>
 F;182,185,193/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;505,598/Binding site: phosphate (Ser) (covalent) #status predicted
 F;603/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 55.0%; Score 44; DB 2; Length 627;
 Best Local Similarity 71.4%; Pred. No. 80;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYTCFWK 8
 ||: |||
 Db 234 CYTCWK 240

RESULT 15
 T00368
 hypothetical protein KIAA0663 - human
 C;Species: Homo sapiens (man)
 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C;Accession: T00368
 R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
 DNA Res. 5, 169-176, 1998
 A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete
 F;24-528/Product: UDP-glucuronosyltransferase 2B-10 #status predicted <MET>
 A;Reference number: 214142; MUID:98403880; PMID:9734811
 A;Accession: T00368
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-810 <ISH>
 A;Cross-references: UNIPROT:O75152; UNIPARC:UPI000006F3FD; EMBL:AB014563; NID:g3327139;
 A;Experimental source: brain
 C;Genetics:
 A;Note: KIAA0663

Query Match 55.0%; Score 44; DB 2; Length 810;
 Best Local Similarity 60.0%; Pred. No. 95;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CYTCFWKTC 11
 ||: |||
 Db 8 CYFFVSTCT 17

RESULT 16
 A96829
 probable RING finger protein, 84236-82024 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: A96829
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: A96829
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-333 <STO>
 A;Cross-references: UNIPROT:Q9CA86; UNIPARC:UPI00000A2C28; GB:AB005173; NID:g6453877; PID:
 C;Genetics:
 A;Gene: F19K16.23
 A;Map position: 1

Query Match 53.8%; Score 43; DB 2; Length 333;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YCYCFWKTC 10
 |||||
 Db 297 YCYCIRTRC 306

RESULT 17
 JN0620
 UDP-glucuronosyltransferase (EC 2.4.1.-) 2B-10 precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C;Accession: JN0620
 R;Jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.
 Biochem. Biophys. Res. Commun. 194, 496-503, 1993
 A;Title: cDNA cloning and expression of two new members of the human liver UDP-glucuronosyltransferase
 A;Reference number: JN0619; MUID:93326164; PMID:8333863
 A;Accession: JN0620
 A;Molecule type: mRNA
 A;Residues: 1-528 <JIN>
 A;Cross-references: UNIPROT:P36537; UNIPARC:UPI0000137A96; GB:X63359; NID:g516149; PIDN:
 A;Experimental source: liver
 C;Superfamily: glucuronosyltransferase
 C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-528/Product: UDP-glucuronosyltransferase 2B-10 #status predicted <MET>
 F;491-508/Domain: transmembrane #status predicted <TM>
 F;66,314,481/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 52.5%; Score 42; DB 2; Length 528;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYTCFWK 8
 ||: |||
 Db 511 CLFCFWK 517

RESULT 18

A35366
 glucuronosyltransferase (EC 2.4.1.17) UDPGTh-2 precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 09-Jul-2004
 C/Accession: A35366
 R/Ritter, J.K.; Sheen, Y.Y.; Owens, I.S.
 J. Biol. Chem. 265, 7900-7906, 1990
 A/Title: Cloning and expression of human liver UDP-glucuronosyltransferase in COS-1 cell
 A/Reference number: A35366; MUID:90243659; PMID:2159463
 A/Accession: A35366
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-529 <RT>
 A/Cross-references: UNIPROT:P16662; UNIPARC:UPI0000137A93; GB:J05428; NID:g340079; PIDN:
 C/Genetics:
 A/Gene: GDB:UGT2B7; UGT2B9
 A/Cross-references: GDB:S892203; OMIM:600218
 A/Map position: 4q13-4q13
 C/Superfamily: glucuronosyltransferase
 C/Keywords: Glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 52.5%; Score 42; DB 2; Length 529;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8

|:|:|:|

Db 512 CLCFWK 518

RESULT 19

H96707
 probable receptor kinase T2B12.5 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
 C/Accession: H96707
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C/A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: H96707
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-670 <STO>
 A/Cross-references: UNIPROT:Q9M9C5; UNIPARC:UPI0000048421; GB:AE005173; NID:g6714351; PI
 C/Genetics:
 A/Gene: T2B12.5
 A/Map position: 1
 C/Superfamily: Receptor-like protein kinase

Query Match 52.5%; Score 42; DB 2; Length 670;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YCFWK 8

|:|:|:|

Db 296 YCFWR 301

RESULT 20

T08919
 hypothetical protein T32A16.170 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C/Accession: T08919

R/Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May
 submitted to the Protein Sequence Database, May 1999
 A/Reference number: Z16518
 A/Accession: T08919
 A/Molecule type: DNA
 A/Residues: 1-686 <BEV>
 A/Cross-references: UNIPROT:Q9T0B3; UNIPARC:UPI00000489D5; EMBL:AL078468; GSPDB:GN000062;
 A/Experimental source: cultivar Columbia; BAC clone T32A16
 C/Genetics:
 A/Gene: ATSP:T32A16.170
 A/Map position: 4
 A/Introns: 192/3; 242/3; 390/3

Query Match 52.5%; Score 42; DB 2; Length 686;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYCFW 7

|:|:|:|

Db 473 YCHYAFW 479

RESULT 21

A36368
 transcription factor CBF, CCAAT-binding - human
 C/Species: Homo sapiens (man)
 C/Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
 C/Accession: A36368
 R/Lum, L.S.Y.; Sultzman, L.A.; Kaufman, R.J.; Linzer, D.I.H.; Wu, B.J.
 Mol. Cell. Biol. 10, 6709-6717, 1990
 A/Title: A cloned human CCAAT-box-binding factor stimulates transcription from the human
 A/Reference number: A36368; MUID:91061780; PMID:2247079
 A/Accession: A36368
 A/Molecule type: mRNA
 A/Residues: 1-998 <LUM>
 A/Cross-references: UNIPROT:Q03701; UNIPARC:UPI0000127180; GB:M37197; NID:g179968; PIDN:
 C/Genetics:
 A/Gene: GDB:CBP4; CBP
 A/Cross-references: GDB:128839; OMIM:116897
 A/Map position: 19q13.1-19q13.1

Query Match 52.5%; Score 42; DB 2; Length 998;

Best Local Similarity 62.5%; Pred. No. 2e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YCFWTC 10

|:|:|:|

Db 465 YCFPRTC 472

RESULT 22

W6WL43
 E6 protein - human papillomavirus type 43
 C/Species: human papillomavirus type 43
 A/Note: host Homo sapiens (man)
 C/Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
 C/Accession: A34144
 R/Loeferincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
 J. Virol. 63, 2829-2834, 1989
 A/Title: Cloning and partial DNA sequencing of two new human papillomavirus types associ
 A/Reference number: A34144; MUID:89259065; PMID:2542593
 A/Accession: A34144
 A/Molecule type: DNA
 A/Residues: 1-155 <LOE>
 A/Cross-references: UNIPROT:P19709; UNIPARC:UPI00001383D6; GB:M27022; NID:g341596; PIDN:
 C/Superfamily: papillomavirus E6 protein
 C/Keywords: DNA binding; early protein; transforming protein; zinc finger
 F:31-67/Region: zinc finger CCCC motif
 F:104-140/Region: zinc finger CCCC motif

Query Match 51.9%; Score 41.5; DB 1; Length 155;

Best Local Similarity 60.0%; Pred. No. 66;

Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 YCYCFWKTC 10
||:|||||
Db 136 YCLHC-WKSC 144

RESULT 23

T28166

hypothetical protein ORF5 - Melanoplus sanguinipes entomopoxvirus (isolate Tuscon)

C;Species: Melanoplus sanguinipes entomopoxvirus

C;Variety: isolate Tuscon

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C;Accession: T28166

R;Alonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.P.; Rock, D.L.

J. Virol. 73, 533-552, 1999

A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A;Reference number: Z20484; MUID:99102612; PMID:9847359

A;Accession: T28166

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-246 <AFO>

A;Cross-references: UNIPROT:Q9YW87; UNIPARC:UPI00000F11B2; EMBL:AF063866; NID:G4049647;

A;Experimental source: isolate Tuscon

C;Genetics:

A;Note: MSV005

Query Match 51.9%; Score 41.5; DB 2; Length 246;

Best Local Similarity 60.0%; Pred. No. 91;

Matches 6; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 1 YC---YYCFW 7

||:|||||

Db 220 YCYFYCYW 229

RESULT 24

D84424

hypothetical protein At2g01410 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: D84424

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: D84424

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-387 <STO>

A;Cross-references: UNIPROT:Q9ZQ05; UNIPARC:UPI00000A7899; GB:AE002093; NID:G3785971; PI

C;Genetics:

A;Gene: At2g01410

A;Map position: 2

Query Match 51.2%; Score 41; DB 2; Length 387;

Best Local Similarity 50.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYCFWK 8

||:|||||

Db 365 PAYCFWR 372

RESULT 25

T21586

hypothetical protein F31B9.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T21586

R;Steward, C.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19445

A;Accession: T21586

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-399 <WIL>

A;Cross-references: UNIPROT:O62189; UNIPARC:UPI000007522C; EMBL:Z81520; PTDN:CAB04223.1;

A;Experimental source: clone F31B9

C;Genetics:

A;Gene: CESP:F31B9.1

A;Map position: X

A;Introns: 151/3; 176/3; 218/2; 263/3; 293/1; 322/2

C;Superfamily: neurokinin 1 receptor

Query Match 51.2%; Score 41; DB 2; Length 399;

Best Local Similarity 83.3%; Pred. No. 1.5e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YCYCFWK 8

||:|||||

Db 206 YCFWK 211

RESULT 26

T10593

hypothetical protein F9F13.160 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T10593

R;Bavan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke

submitted to the Protein Sequence Database, June 1999

A;Reference number: Z16991

A;Accession: T10593

A;Molecule type: DNA

A;Residues: 1-413 <BEV>

A;Cross-references: UNIPROT:Q9SUM8; UNIPARC:UPI00000A4686; EMBL:AL080253; GSPDB:GN000062;

A;Experimental source: cultivar Columbia; BAC clone F9F13

C;Genetics:

A;Gene: ATSP:F9F13.160

A;Map position: 4

A;Introns: 324/2; 344/1

Query Match 51.2%; Score 41; DB 2; Length 413;

Best Local Similarity 83.3%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFW 7

||:|||||

Db 403 CYCFW 408

RESULT 27

A54895

mucin 2, intestinal/tracheal - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 31-Dec-2004

C;Accession: A54895

R;Ohmori, H.; Dohrman, A.F.; Gallup, M.; Tsuda, T.; Kai, H.; Gum Jr., J.R.; Kim, Y.S.; B-

J. Biol. Chem. 269, 17833-17840, 1994

A;Title: Molecular cloning of the amino-terminal region of a rat MUC 2 mucin gene homolo

A;Reference number: A54895; MUID:94299489; PMID:8027037

A;Accession: A54895

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1513 <OHM>

A;Cross-references: UNIPROT:Q62635; UNIPARC:UPI000012F8D0; GB:U07615

C;Superfamily: von Willebrand factor type C repeat homology

C;Keywords: intestine

Query Match 51.2%; Score 41; DB 2; Length 1513;

Best Local Similarity 57.1%; Pred. No. 3.6e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10

A:Molecule type: DNA
A:Residues: 1-247 <WIL>
A:Cross-references: UNIPROT:O62493; UNIPARC:UPI0000082F55; EMBL:AL023847; PIDN:CAA19551.1
A:Experimental source: Clone Y57A10C
C:Genetics:
A:Gene: CESP:Y57A10C.9
A:Map position: 2
A:Introns: 38/2; 110/3; 138/3; 200/1

Query Match 50.0%; Score 40; DB 2; Length 247;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYTCFWK 8
Db 31 YIIYCFWR 38

RESULT 31
T27203
hypothetical protein Y57A10C.7 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27203
F:Smyle, R.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z20327
A:Accession: T27203
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-311 <WIL>
A:Cross-references: UNIPROT:O62491; UNIPARC:UPI000007FB73; EMBL:AL023847; PIDN:CAA19549.1
A:Experimental source: clone Y57A10C
C:Genetics:
A:Gene: CESP:Y57A10C.7
A:Map position: 2
A:Introns: 41/2; 117/3; 184/3; 211/3; 272/1; 297/3

Query Match 50.0%; Score 40; DB 2; Length 311;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYTCFWK 8
Db 34 YIIYCFWR 41

RESULT 32
G97802
tyrosine-tRNA ligase (EC 6.1.1.1) - *Rickettsia conorii* (strain Malish 7)
C:Species: *Rickettsia conorii*
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97802
F:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: G97802
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <KUR>
A:Cross-references: UNIPROT:Q92HE8; UNIPARC:UPI0000136769; GB:AE006914; PIDN:AAL03361.1
C:Genetics:
A:Gene: tyrs
C:Superfamily: tyrosine-tRNA ligase
C:Keywords: ligase

Query Match 50.0%; Score 40; DB 2; Length 411;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YCYTCFWKTC 10

Db 250 YDYQYWRNC 259

RESULT 33
C71660
A:Title: tyrosine-tRNA ligase (EC 6.1.1.1) (tyrS) RP556 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: C71660
R:Anderson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sacheritz-Ponten, T.; Alsmark, U.
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: C71660
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-411 <AND>
A:Cross-references: UNIPROT:O92C24; UNIPARC:UPI000013676A; GB:AJ235272; GB:AJ235269; NID:
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: tyrS; RP556
C:Superfamily: tyrosine-tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 50.0%; Score 40; DB 2; Length 411;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YCYCFWKC 10
|:|:|:|:
Db 250 YDYQYWRNC 259

RESULT 34
T30924
A:Title: hypothetical protein D1007.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jan-2000
C:Accession: T30924
R:Davidson, S.; Rohlfing, T.
submitted to the EMBL Data Library, August 1999
A:Description: The sequence of C. elegans cosmid D1007.
A:Reference number: Z20934
A:Accession: T30924
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-512 <DAV>
A:Cross-references: UNIPARC:UPI0000179267; EMBL:AF003151; PIDN:ABBS4224.1
A:Experimental source: strain Bristol N2; clone D1007
C:Genetics:
A:Map position: 1
A:Introns: 82/3; 110/3; 172/2; 207/2; 309/3; 430/3
A:Note: D1007.5
C:Superfamily: Caenorhabditis elegans hypothetical protein D1007.5

Query Match 50.0%; Score 40; DB 2; Length 512;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 11
|:|:|:|:
Db 106 CFWKTC 112

RESULT 35
A47194
A:Title: taurine and beta-alanine transporter, TAUT - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47194
R:Liu, Q.R.; Lopez-Corcuera, B.; Nelson, H.; Mandiyan, S.; Nelson, N.
Proc. Natl. Acad. Sci. U.S.A. 89, 12145-12149, 1992
A:Title: Cloning and expression of a cDNA encoding the transporter of taurine and beta-a

A:Reference number: A47194; MUID:93101684; PMID:1465453
A:Accession: A47194
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-590 <LIU>
A:Cross-references: UNIPROT:O35316; UNIPARC:UPI00001779BF
A:Experimental source: neonatal brain
A:Note: sequence extracted from NCBI backbone (NCBIN:120721, NCBIPI:120725)
C:Superfamily: gamma-aminobutyric acid transporter
C:Keywords: transmembrane protein

Query Match 50.0%; Score 40; DB 2; Length 590;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8
|:|:|:|:
Db 231 CPFCWK 237

RESULT 36
G01426
A:Title: taurine transporter - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G01426
R:Miyamoto, Y.
submitted to the EMBL Data Library, April 1994
A:Reference number: G06991
A:Accession: G01426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-620 <MIY>
A:Cross-references: UNIPROT:P31641; UNIPARC:UPI000013549A; EMBL:U09220; NID:g799338; PID:
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 50.0%; Score 40; DB 2; Length 620;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8
|:|:|:|:
Db 231 CPFCWK 237

RESULT 37
S46487
A:Title: taurine transporter - human
C:Species: Homo sapiens (man)
C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S46487
R:Ramamoorthy, S.; Leibach, F.H.; Mahesh, V.B.; Han, H.; Yang-Feng, T.; Blakely, R.D.; G:
Biochem. J. 300, 893-900, 1994
A:Title: Functional characterization and chromosomal localization of a cloned taurine tr:
A:Reference number: S46487; MUID:94280419; PMID:8010975
A:Accession: S46487
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-620 <RAM>
A:Cross-references: UNIPROT:P31641; UNIPARC:UPI000016A140; GB:U16120; NID:g559852; PIDN:
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 50.0%; Score 40; DB 2; Length 620;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8
|:|:|:|:
Db 231 CPFCWK 237

RESULT 38
I57939

taurine transporter - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: J57939
 R/Smith, K.E.; Borden, L.A.; Wang, C.
 Mol. Pharmacol. 42, 563-569, 1992
 A/Title: Cloning and expression of a high-affinity taurine transporter from rat brain.
 A/Reference number: J57939; MUID:93062816; PMID:1435737
 A/Accession: J57939
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-621 <RES>
 A/Cross-references: UNIPROT:P31643; UNIPARC:UPI000013549C; GB:M96601; NID:g207541; PIDN:
 C/Superfamily: gamma-aminobutyric acid transporter

Query Match 50.0%; Score 40; DB 2; Length 621;
 Best Local Similarity 57.1%; Pred. No. 2.7e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCYCFWK 8
 Db 231 CFFCIWK 237
 :|||
 :|||

RESULT 39
 A46270
 Na and Cl dependent taurine transporter - dog
 C/Species: Canis lupus familiaris (dog)
 C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C/Accession: A46270
 R/Uchida, S.; Kwon, H.M.; Yamauchi, A.; Preston, A.S.; Marumo, F.; Handler, J.S.
 Proc. Natl. Acad. Sci. U.S.A. 89, 8230-8234, 1992
 A/Title: Molecular cloning of the cDNA for an MCK cell Na(+) - and Cl(-) - dependent taurine
 A/Reference number: A46270; MUID:92390420; PMID:1518851
 A/Accession: A46270
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-655 <UCH>
 A/Cross-references: UNIPROT:Q00589; UNIPARC:UPI00001779C0
 A/Experimental source: Madin-Darby canine kidney cells
 A/Note: sequence extracted from NCBI backbone (NCBIP:113086)
 C/Superfamily: gamma-aminobutyric acid transporter
 C/Keywords: transmembrane protein

Query Match 50.0%; Score 40; DB 2; Length 655;
 Best Local Similarity 57.1%; Pred. No. 2.8e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCYCFWK 8
 Db 231 CFFCIWK 237
 :|||
 :|||

RESULT 40
 JH0560
 cyclic nucleotide-gated channel - channel catfish
 C/Species: Ictalurus punctatus (channel catfish)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: JH0560
 R/Goulding, E.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Siegelbaum, S.A.; Cheses
 Neuron 8, 45-58, 1992
 A/Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated
 A/Reference number: JH0560; MUID:92110008; PMID:1370374
 A/Accession: JH0560
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-682 <GOU>
 A/Cross-references: UNIPROT:P55934; UNIPARC:UPI0000127C25; GB:M83111
 A/Experimental source: olfactory epithelium
 C/Comment: This cyclic nucleotide-gated channel is activated equally well by both cAMP &
 C/Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
 C/Keywords: cAMP binding; cGMP binding; ion channel; ion transport; olfaction; transmemb
 R/137-157/Domain: transmembrane #status predicted <TS1>

F/173-193/Domain: transmembrane #status predicted <TS2>
 F/217-236/Domain: transmembrane #status predicted <TS3>
 F/241-261/Domain: transmembrane #status predicted <TS4>
 F/277-297/Domain: transmembrane #status predicted <TS5>
 F/319-337/Domain: transmembrane #status predicted <TS6>
 F/350-370/Domain: transmembrane #status predicted <TS6>
 F/447-571/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 50.0%; Score 40; DB 1; Length 682;
 Best Local Similarity 61.5%; Pred. No. 2.9e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

Qy 1 YCYCYCFWKTC 11
 Db 315 FCYCYCFWSTLT 327
 :|||
 :|||

RESULT 41
 S36555
 E6 protein - human papillomavirus type 40
 C/Species: human papillomavirus type 40
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C/Accession: S36555
 R/Deliuss, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A/Description: Primer-directed sequencing of human papillomavirus types.
 A/Reference number: S36469
 A/Accession: S36555
 A/Molecule type: DNA
 A/Residues: 1-154 <DBL>
 A/Cross-references: UNIPROT:P36812; UNIPARC:UPI00001383D3; EMBL:X74478; NID:g397014; PID:
 C/Superfamily: papillomavirus E6 protein
 C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 49.4%; Score 39.5; DB 2; Length 154;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 YCYCYCFWKTC 10
 Db 135 YCLHC-WKCC 143
 :|||
 :|||

RESULT 42
 S36584
 E6 protein - human papillomavirus type 7
 C/Species: human papillomavirus type 7
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C/Accession: S36584
 R/Deliuss, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A/Description: Primer-directed sequencing of human papillomavirus types.
 A/Reference number: S36469
 A/Accession: S36584
 A/Molecule type: DNA
 A/Residues: 1-154
 A/Cross-references: UNIPROT:P36800; UNIPARC:UPI00001383B3; EMBL:X74463; NID:g397060; PID:
 C/Superfamily: papillomavirus E6 protein
 C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 49.4%; Score 39.5; DB 2; Length 154;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 YCYCYCFWKTC 10
 Db 135 YCLHC-WKCC 143
 :|||
 :|||

RESULT 43
 S19430
 probable membrane protein YCR001w - yeast (Saccharomyces cerevisiae)
 N/Alternate names: protein 21

C;Species: Saccharomyces cerevisiae
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: S19430; S20186
 R;van der Aart, Q.J.M.; Steensma, H.Y.
 submitted to the Protein Sequence Database, March 1992
 A;Reference number: S19400
 A;Accession: S19430
 A;Molecule type: DNA
 A;Residues: 1-104 <AAR>
 A;Cross-references: UNIPROT:P25347; UNIPARC:UPI000013A6F4; EMBL:X59720; NID:g1907116; PI
 R;Steensma, H.Y.; van der Aart, Q.J.M.
 Yeast 7, 425-429, 1991
 A;Title: Sequence of the CDC10 region at chromosome III of Saccharomyces cerevisiae.
 A;Reference number: S20186; MUID:91335898; PMID:1872033
 A;Accession: S20186
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-104 <STE>
 A;Cross-references: UNIPARC:UPI000013A6F4; EMBL:S48552; NID:G233477; PIDN:AAD13855.1; PI
 C;Genetics:
 A;Map position: 3R
 A;Cross-references: SGD:S0000594
 C;Superfamily: Saccharomyces cerevisiae probable membrane protein YCR001W
 C;Keywords: transmembrane protein
 F;70-86/Domain: transmembrane #status predicted <TM>

Query Match 48.8%; Score 39; DB 2; Length 104;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YYCFWKTC 10
 :|||
 Db 26 FYCFWKLC 33

RESULT 44
 C87585
 hypothetical protein CC2714 [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: C87585
 R;Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: C87585
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-212 <STO>
 A;Cross-references: UNIPROT:Q9A4W1; UNIPARC:UPI000000C7801; GB:AE005673; NID:g13424303; F
 C;Genetics:
 A;Gene: CC2714

Query Match 48.8%; Score 39; DB 2; Length 212;
 Best Local Similarity 57.1%; Pred. No. 1.8e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTC 11
 :|||
 Db 202 CFWRSCS 208

RESULT 45
 A49677
 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana
 N;Alternate names: 26K endoplasmic reticulum retention receptor
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A49677
 R;Lee, H.I.; Gal, S.; Newman, T.C.; Raikhel, N.V.
 Proc. Natl. Acad. Sci. U.S.A. 90, 11433-11437, 1993

A;Title: The Arabidopsis endoplasmic reticulum retention receptor functions in yeast.
 A;Reference number: A49677; MUID:94068617; PMID:8248265
 A;Contents: ecotype Columbia
 A;Accession: A49677
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-215 <LEE>
 A;Cross-references: UNIPROT:P35402; UNIPARC:UPI000000117D
 C;Function:
 A;Description: achieves retention of proteins specific to the lumen of the endoplasmic r
 usually KDEL in animal cells and HDL in budding yeasts
 C;Superfamily: KDEL receptor
 C;Keywords: Golgi apparatus; protein trafficking; sorting signal recognition; transmembr

Query Match 48.8%; Score 39; DB 2; Length 215;
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YCYCFWKTC 11
 :|||
 Db 199 YYYVSKTNT 209

RESULT 46
 T20644
 hypothetical protein F09C6.7 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T20644
 R;Mortimore, B.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19305
 A;Accession: T20644
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-337 <WIL>
 A;Cross-references: UNIPROT:O45326; UNIPARC:UPI00000079728; EMBL:Z81496; PIDN:CAB04066.1;
 A;Experimental source: clone F09C6
 C;Genetics:
 A;Gene: CESP:F09C6.7
 A;Map position: 5
 A;Introns: 5/3; 78/2; 110/3; 157/3; 250/3; 277/1
 Query Match 48.8%; Score 39; DB 2; Length 337;
 Best Local Similarity 45.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 2; Gaps 1;

Qy 1 YCYCF--WKT 9
 :|||
 Db 101 FCYCYNLWKS 111

RESULT 47
 T28806
 olfactory receptor ODR-10 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T28806
 R;Du, Z.
 submitted to the EMBL Data Library, December 1995
 A;Description: The sequence of C. elegans cosmid C53B7.
 A;Reference number: Z20526
 A;Accession: T28806
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-348 <DUZ>
 A;Cross-references: UNIPROT:Q18807; UNIPARC:UPI000017BD46; EMBL:U42830; PIDN:AAC48279.1;
 A;Experimental source: strain Bristol N2; clone C53B7
 C;Genetics:
 A;Gene: CESP:odr-10
 A;Map position: X
 A;Introns: 65/3; 120/2; 174/2; 196/3; 221/3; 263/3; 323/1

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Query Match      48.8%; Score 39; DB 2; Length 348;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YCYCFWKT 9
   ||| |||
Db 230 YCGYATWKT 238

RESULT 48
A46355
site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) - Chlorella virus
N;Alternate names: cytosine-specific DNA methylase; cytosine-specific DNA methyltransferase;
C;Species: Chlorella virus IL-2A
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 31-Dec-2004
C;Accession: A46355
R;Shields, S.L.; Burbank, D.E.; Grabherr, R.; van Etten, J.L.
Virology 176, 16-24, 1990
A;Title: Cloning and sequencing the cytosine methyltransferase gene M.CviJI from Chlorella
A;Reference number: A46355; MUID:90232725; PMID:2158687
A;Accession: A46355
A;Molecule type: DNA
A;Residues: 1-367 <SHR>
A;Cross-references: UNIPROT:P36216; UNIPARC:UPI000012F77F; GB:M27265; NID:g323314; PIDN:
C;Superfamily: modification methylase (cytosine-specific), M.EcoRII type
C;Keywords: methyltransferase; restriction modification system; S-adenosylmethionine
F73/Active site: Cys #status predicted

Query Match      48.8%; Score 39; DB 1; Length 367;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YYCFWKT 10
   | | | | |
Db 134 YFCKWVTC 141

RESULT 49
T18185
probable site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) - Chlorella
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T18185
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T18185
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-367 <GRA>
A;Cross-references: UNIPROT:O41165; UNIPARC:UPI00000F3484; EMBL:U42580; NID:g4028896; PI
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: A683L
C;Superfamily: modification methylase (cytosine-specific), M.EcoRII type
C;Keywords: methyltransferase; restriction modification system; S-adenosylmethionine

Query Match      48.8%; Score 39; DB 2; Length 367;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YYCFWKT 10
   | | | | |
Db 134 YFCKWVTC 141

RESULT 50
G70350
conserved hypothetical protein aq_563 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70350

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R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: G70350
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-618 <AQF>
A;Cross-references: UNIPROT:O66835; UNIPARC:UPI00000563BD; GB:AE000696; NID:g2983196; PI
A;Experimental source: strain VFS
C;Genetics:
A;Gene: aq_563

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Query Match      48.8%; Score 39; DB 2; Length 618;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YCYYC 5
   |||||
Db 385 YCYYC 389

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Search completed: May 9, 2006, 12:10:28
Job time : 25.3333 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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105	41.5	51.9	214	2	08JTG8_9PAPI	Q81tg8 human papill	178	40	50.0	309	2	062491_CAEBL	062491 caenorhabdi
106	41.5	51.9	246	2	Q9Yw87_MSEPV	Q9Yw87 melanoplus	179	40	50.0	320	2	Q61Q75_BRARE	061q75 brachydanio
107	41	51.2	65	2	Q8R8H5_ATHN	Q8R8H5 tharidopaeis	180	40	50.0	320	2	Q7Zuz8_BRARE	07Zuz8 brachydanio
108	41	51.2	128	2	Q8G273_ATHN	Q8G273 tharidopaeis	181	40	50.0	321	2	Q4T284_TETNG	04T284 tetraodon n
109	41	51.2	165	2	Q4RMU9_TETNG	Q4RMU9 tetraodon n	182	40	50.0	357	2	Q7RNG0_PLAYO	Q7rng0 plasmodium
110	41	51.2	180	2	Q92518_9VIRU	Q92518 beet virus	183	40	50.0	367	2	Q59GD7_HUMAN	Q59gd7 homo sapien
111	41	51.2	214	2	Q61GP0_DROME	Q61gp0 drosophila	184	40	50.0	372	2	Q60WN2_CAEBR	060wn2 caenorhabdi
112	41	51.2	246	2	Q6PBN1_BRARE	Q6pbn1 brachydanio	185	40	50.0	373	2	Q7QVg1_GIALA	07qv1 giardia lam
113	41	51.2	285	2	Q6NNA6_DROME	Q6nna6 drosophila	186	40	50.0	384	2	Q9V612_DROME	Q9v612 drosophila
114	41	51.2	289	2	Q50YX8_ENTHI	Q50yx8 entamoeba h	187	40	50.0	387	2	Q8VD70_MOUSE	Q8vd70 mus musculus
115	41	51.2	293	2	Q953M6_ECHGR	Q953m6 echinococcu	188	40	50.0	402	2	Q86GV0_CAEBL	Q86gv0 caenorhabdi
116	41	51.2	293	2	Q958U5_ECHGR	Q958u5 echinococcu	189	40	50.0	411	1	SYI_RICPN	Q92h8 rickettsia
117	41	51.2	293	2	Q9TE77_ECHMU	Q9te77 echinococcu	190	40	50.0	411	1	SYI_RICPN	Q92c4 rickettsia
118	41	51.2	299	2	Q6PPG7_9BACT	Q6ppg7 uncultured	191	40	50.0	411	2	Q7P8X2_RICSI	07p8x2 rickettsia
119	41	51.2	325	2	Q706P3_PSEPU	Q706p3 pseudomonas	192	40	50.0	411	2	Q4UL45_RICFE	04ul45 rickettsia
120	41	51.2	325	2	Q73B39_BACCI	Q73b39 bacillus ce	193	40	50.0	411	2	Q68WH9_RICTY	Q68wh9 rickettsia
121	41	51.2	331	2	Q74D10_GEOSL	Q74d10 geobacter s	194	40	50.0	413	2	Q99MM1_MOUSE	Q99mm1 mus musculus
122	41	51.2	335	2	Q52VH9_CIOIN	Q52vh9 ciona intes	195	40	50.0	456	2	Q513E7_ENTHI	Q513e7 entamoeba h
123	41	51.2	338	2	Q5AYV7_EMENI	Q5aya7 aspergillus	196	40	50.0	477	2	Q01870_CAEBL	001870 caenorhabdi
124	41	51.2	358	2	Q6IQM4_BRARE	Q6iqm4 brachydanio	197	40	50.0	478	2	Q60PF1_CAEBR	060pf1 caenorhabdi
125	41	51.2	358	2	Q6GR30_XENLA	Q6gr30 xenopus lae	198	40	50.0	529	2	Q4IN09_GIBZE	04in09 gibberella
126	41	51.2	387	2	Q9ZNM5_ARATH	Q9znm5 arabidopsis	199	40	50.0	533	2	Q5BFG7_EMENI	Q5bfg7 aspergillus
127	41	51.2	393	2	Q61412_CAEBR	Q61412 caenorhabdi	200	40	50.0	570	2	Q4HVE7_GIBZE	Q4hve7 gibberella
128	41	51.2	399	2	Q62189_CAEBL	Q62189 caenorhabdi	201	40	50.0	570	2	Q4WT96_ASPFU	Q4wt96 aspergillus
129	41	51.2	405	2	Q5BC16_EMENI	Q5bc16 aspergillus	202	40	50.0	573	2	Q7R131_GIALA	Q7r131 giardia lam
130	41	51.2	409	2	Q59827_ARNAL	Q59e27 arabidopsis	203	40	50.0	584	2	Q4SWT7_TETNG	Q4swt7 tetraodon n
131	41	51.2	423	2	Q58UM8_ARNAL	Q58um8 arabidopsis	204	40	50.0	584	2	Q4RJV9_TETNG	Q4rjv9 tetraodon n
132	41	51.2	423	2	Q75JQ3_DICDI	Q75jq3 dictyostell	205	40	50.0	605	2	Q7Z6C5_HUMAN	Q7z6c5 homo sapien
133	41	51.2	426	2	Q7NMP2_GLOVI	Q7nmp2 gloeobacter	206	40	50.0	620	1	SC6A6_BOVIN	Qm234 bos taurus
134	41	51.2	439	2	Q59RM6_CANAL	Q59rm6 candida alb	207	40	50.0	620	1	SC6A6_CANFA	Q00599 canis famil
135	41	51.2	468	2	Q81619_HAIRO	Q81619 halocynthia	208	40	50.0	620	1	SC6A6_HUMAN	Q31641 homo sapien
136	41	51.2	521	2	Q4HLQ6_CAMLA	Q4hlq6 campylobact	209	40	50.0	621	1	SC6A6_MOUSE	Q35316 mus musculus
137	41	51.2	659	2	Q9H623_HUMAN	Q9h623 homo sapien	210	40	50.0	621	1	SC6A6_RAT	Q31643 rattus norv
138	41	51.2	699	2	Q9LQ28_ARNAL	Q9lq28 arabidopsis	211	40	50.0	625	2	Q8JHX8_SALSA	Q8jhx8 salmo salar
139	41	51.2	729	2	Q8VZK9_ARNAL	Q8vzk9 arabidopsis	212	40	50.0	625	2	Q91BH6_CYPCA	Q91bh6 cyprinus ca
140	41	51.2	748	2	Q636W5_BACCI	Q636w5 bacillus ce	213	40	50.0	627	2	Q5BDM5_EMENI	Q5bdm5 aspergillus
141	41	51.2	780	2	Q81G17_DROME	Q81g17 drosophila	214	40	50.0	629	2	Q9DS16_OREMO	Q9ds16 oreochromis
142	41	51.2	814	2	Q5R9U0_PONPY	Q5r9u0 pongo pygma	215	40	50.0	630	2	Q7S3D2_NEURO	Q7s3d2 neurospora
143	41	51.2	816	2	Q6GNZ1_DROME	Q6gnz1 drosophila	216	40	50.0	631	2	Q5F431_CHICK	Q5f431 gallus gall
144	41	51.2	879	2	Q7S4B4_NEUCR	Q7s4b4 neurospora	217	40	50.0	640	2	Q7XH17_ORYSA	Q7xh17 oryza sativ
145	41	51.2	888	2	Q5JVA7_HUMAN	Q5jva7 homo sapien	218	40	50.0	640	2	Q9AYH6_ORYSA	Q9ayh6 oryza sativ
146	41	51.2	890	2	Q4V6V5_DROME	Q4v6v5 drosophila	219	40	50.0	653	1	CTL3_HUMAN	Q84m1 homo sapien
147	41	51.2	993	2	Q8CDQ6_MOUSE	Q8cdq6 mus musculus	220	40	50.0	682	1	CNG ICTPU	P55934 ictalurus p
148	41	51.2	1094	2	Q8MCL1_DROME	Q8mcl1 drosophila	221	40	50.0	706	2	Q4INB9_GIBZE	Q4ine9 gibberella
149	41	51.2	1271	2	Q86BD8_DROME	Q86bd8 drosophila	222	40	50.0	787	2	Q891A4_CLOTE	Q891a4 clostridium
150	41	51.2	1283	2	Q9V7F0_DROME	Q9v7f0 drosophila	223	40	50.0	814	2	Q5CLA9_CRYHO	Q5cla9 cryptospori
151	41	51.2	1495	2	Q5KIY9_CRYNE	Q5kiy9 cryptococcu	224	40	50.0	1060	2	Q4MZ12_THEPA	Q4mz12 theileria p
152	41	51.2	1513	1	MUC2_RAT	Q5kiy9 rattus norv	225	39.5	49.4	113	2	Q4S4K5_TETNG	Q4s4k5 tetraodon n
153	41	51.2	1525	2	Q55TE9_CRYNE	Q55te9 cryptococcu	226	39.5	49.4	130	2	Q5ZKH2_CHICK	Q5zkh2 gallus gall
154	41	51.2	1749	1	K113A_MOUSE	Q9eqw7 mus musculus	227	39.5	49.4	131	2	Q677W8_9VIRU	Q677w8 lymphococ
155	41	51.2	1749	2	Q8H193_HUMAN	Q8h193 homo sapien	228	39.5	49.4	135	2	Q4L822_STAHL	Q4l822 staphylococ
156	41	51.2	1757	2	Q9H194_HUMAN	Q9h194 homo sapien	229	39.5	49.4	143	2	Q5PZY9_HCMV	Q5pzy9 human cytom
157	41	51.2	1768	2	Q5THQ2_HUMAN	Q5thq2 homo sapien	230	39.5	49.4	154	1	VE6_HPV40	Q36800 human papil
158	41	51.2	1803	2	Q5THQ3_HUMAN	Q5thq3 homo sapien	231	39.5	49.4	243	2	Q4WIM6_ASPFU	Q4wim6 aspergillus
159	41	51.2	1805	1	K113A_HUMAN	Q9h1h9 homo sapien	232	39.5	49.4	244	2	Q91BO9_9NUCL	Q91bo9 spodoptera
160	41	51.2	2527	2	Q9V7P2_DROME	Q9v7f2 drosophila	233	39.5	49.4	863	2	Q76148_9DIPT	Q76148 anopheles s
161	40.5	50.6	89	2	Q89Z82_BACTN	Q89z82 bacteroides	234	39.5	49.4	867	2	Q7QEJ3_ANOGA	Q7qej3 anopheles g
162	40.5	50.6	231	2	Q86F16_ECHJA	Q86f16 schistosoma	235	39.5	49.4	1245	2	Q4FKK3_9TRYP	Q4fk3 trypanosoma
163	40.5	50.6	572	2	Q5B129_EMENI	Q5b129 aspergillus	236	39.5	49.4	48	2	Q7S0Q4_NEUCR	Q7s0q4 neurospora
164	40.5	50.6	652	2	Q4TB21_TETNG	Q4tb21 tetraodon n	237	39	48.8	58	2	Q4TDS6_TETNG	Q4tds6 tetraodon n
165	40	50.0	95	2	Q4Y583_PLACH	Q4y583 plasmodium	238	39	48.8	85	2	Q4YL80_PLABE	Q4yl80 plasmodium
166	40	50.0	101	2	Q802G5_9HIV1	Q802g5 human immun	239	39	48.8	104	1	YCP2_YEAST	YCP2347 saccharomyc
167	40	50.0	109	2	Q83921_ADEO7	Q83921 ovine adeno	240	39	48.8	109	2	Q8PYL6_METMA	Q8pyl6 methanosarc
168	40	50.0	110	2	Q5A662_CANAL	Q5a662 candida alb	241	39	48.8	148	2	Q5T418_HUMAN	Q5t418 homo sapien
169	40	50.0	183	2	Q81TG6_9VIRU	Q81tg6 streptococc	242	39	48.8	150	2	Q9H582_HUMAN	Q9h582 homo sapien
170	40	50.0	216	2	Q61K14_CAEBR	Q61k14 caenorhabdi	243	39	48.8	155	2	Q4Y6Y0_PLACH	Q4y6y0 plasmodium
171	40	50.0	216	2	Q21499_CAEBL	Q21499 caenorhabdi	244	39	48.8	161	2	Q48242_9NEOP	Q48242 denuvus som
172	40	50.0	219	2	Q4HM61_CAMLA	Q4hm61 campylobact	245	39	48.8	164	2	Q4S341_TETNG	Q4s341 tetraodon n
173	40	50.0	231	2	Q4N0N6_THEPA	Q4n0n6 theileria p	246	39	48.8	185	2	Q4TH70_TETNG	Q4th70 tetraodon n
174	40	50.0	239	2	Q9XW98_CAEBL	Q9xw98 caenorhabdi	247	39	48.8	204	2	Q5AKS2_CANAL	Q5aks2 candida alb
175	40	50.0	242	2	Q4P0F8_USTMA	Q4p0f8 ustilago ma	248	39	48.8	209	2	Q87MW5_VIBPA	Q87mw5 vibrio para
176	40	50.0	247	2	Q62493_CAEBL	Q62493 caenorhabdi	249	39	48.8	212	2	Q9A4W1_CAUCR	Q9a4w1 caulobacter
177	40	50.0	249	2	Q60SB0_CAEBR	Q60sb0 caenorhabdi	250	39	48.8				

251	39	48.8	214	2	Q6IPD7_HUMAN	Q6IPD7 homo sapien	324	2058	1	MYO10_HUMAN	Q9HDC7 homo sapien		
252	39	48.8	215	1	ERD2_ARATH	P35402 arabidopsis	325	2062	2	Q9JJY5_MOUSE	Q9JJY5 mus musculus		
253	39	48.8	238	2	Q531B5_9BACT	Q531B5 uncultured	326	2087	2	Q4RMH8_TETNG	Q4RMH8 tetraodon n		
254	39	48.8	240	2	Q6R7D3_9HERP	Q6R7D3 orestoid her	327	2111	2	O94893_HUMAN	O94893 homo sapien		
255	39	48.8	260	2	Q6EZA7_OREMO	Q6EZA7 oreochromis	328	38.5	48.1	2	O5RLP0_HCMV	O5RLP0 human cytom	
256	39	48.8	260	2	Q6EZA8_OREMO	Q6EZA8 oreochromis	329	38.5	48.1	2	O80JD6_HCMV	O80JD6 human cytom	
257	39	48.8	263	2	Q50MW3_ENTHI	Q50MW3 entameoba h	330	38.5	48.1	2	O52MF5_HCMV	O52MF5 human cytom	
258	39	48.8	275	2	Q4RIU2_TETNG	Q4RIU2 tetraodon n	331	38.5	48.1	2	O52MF7_HCMV	O52MF7 human cytom	
259	39	48.8	280	2	Q5CSK4_CRYPV	Q5CSK4 cryptospori	332	38.5	48.1	2	O68391_HCMV	O68391 human cytom	
260	39	48.8	280	2	Q5CMT5_CRYHO	Q5CMT5 cryptospori	333	38.5	48.1	2	O6SWW6_HCMV	O6SWW6 human cytom	
261	39	48.8	281	2	Q9VSH8_DROME	Q9VSH8 drosophila	334	38.5	48.1	2	O6SWR0_HCMV	O6SWR0 human cytom	
262	39	48.8	293	2	Q7YH67_CEST	Q7YH67 taenia asia	335	38.5	48.1	2	O5Q004_HCMV	O5Q004 human cytom	
263	39	48.8	306	2	Q7KLR0_DROME	Q7KLR0 drosophila	336	38.5	48.1	2	O80JD3_HCMV	O80JD3 human cytom	
264	39	48.8	315	2	Q4KT70_SNUCL	Q4KT70 chrysoideixi	337	38.5	48.1	2	O5Q000_HCMV	O5Q000 human cytom	
265	39	48.8	324	2	O45326_CABEL	O45326 caenorhabdi	338	38.5	48.1	2	O52MG2_HCMV	O52MG2 human cytom	
266	39	48.8	330	2	P90634_LEIDO	P90634 leishmania	339	38.5	48.1	2	O6SWT8_HCMV	O6SWT8 human cytom	
267	39	48.8	330	2	Q4Q914_LEIMA	Q4Q914 leishmania	340	38.5	48.1	2	O5P2X3_HCMV	O5P2X3 human cytom	
268	39	48.8	332	2	Q582U7_9TRYP	Q582U7 trypanosoma	341	38.5	48.1	2	O5P2X4_HCMV	O5P2X4 human cytom	
269	39	48.8	332	2	Q95207_9TRYP	Q95207 trypanosoma	342	38.5	48.1	2	O5P2Y1_HCMV	O5P2Y1 human cytom	
270	39	48.8	334	2	Q96615_CABEL	Q96615 caenorhabdi	343	38.5	48.1	2	O5P2Z8_HCMV	O5P2Z8 human cytom	
271	39	48.8	339	2	Q18807_CABEL	Q18807 caenorhabdi	344	38.5	48.1	2	O5RLF2_HCMV	O5RLF2 human cytom	
272	39	48.8	354	2	Q910D1_HCMV	Q910D1 human cytom	345	38.5	48.1	2	O805Q8_HCMV	O805Q8 human cytom	
273	39	48.8	367	1	MTC1_PBCVI	P36216 paramecium	346	38.5	48.1	2	O80JD2_HCMV	O80JD2 human cytom	
274	39	48.8	367	2	O41165_CHVP1	O41165 paramecium	347	38.5	48.1	2	O805Q6_HCMV	O805Q6 human cytom	
275	39	48.8	381	2	O86211_ENTFA	O86211 enterococcu	348	38.5	48.1	2	O5P2Z7_HCMV	O5P2Z7 human cytom	
276	39	48.8	381	2	Q831M5_ENTFA	Q831M5 enterococcu	349	38.5	48.1	2	O6SWZ5_HCMV	O6SWZ5 human cytom	
277	39	48.8	397	2	O5AI92_CANAL	O5AI92 candida alb	350	38.5	48.1	2	O5P2W4_HCMV	O5P2W4 human cytom	
278	39	48.8	406	2	O5AI35_CANAL	O5AI35 candida alb	351	38.5	48.1	2	O5P2W7_HCMV	O5P2W7 human cytom	
279	39	48.8	419	2	O4K7T1_PSEFS	O4K7T1 pseudomonas	352	38.5	48.1	2	O5P2X2_HCMV	O5P2X2 human cytom	
280	39	48.8	430	2	O6TVP3_PPOXV	O6TVF3 bovine papu	353	38.5	48.1	2	O80JD5_HCMV	O80JD5 human cytom	
281	39	48.8	430	2	O6TVV5_PPOXV	O6TVF5 orf virus.	354	38.5	48.1	2	O80JD0_HCMV	O80JD0 human cytom	
282	39	48.8	430	2	O6TW65_PPOXV	O6TW65 orf virus.	355	38.5	48.1	2	Q80JDU1_HCMV	Q80JDU1 human cytom	
283	39	48.8	435	2	Q8NJL7_ASFPU	Q8NJL7 aspergillus	356	38.5	48.1	2	O52MH1_HCMV	O52MH1 human cytom	
284	39	48.8	435	2	Q4WM50_ASFPU	O4WM50 aspergillus	357	38.5	48.1	2	O52MI0_HCMV	O52MI0 human cytom	
285	39	48.8	447	2	O73GB2_WOLPM	O73GB2 wolbachia p	358	38.5	48.1	2	O52MI3_HCMV	O52MI3 human cytom	
286	39	48.8	462	2	O5KBN3_CRYNE	O5KBN3 cryptococcu	359	38.5	48.1	2	O6RXI9_HCMV	O6RXI9 human cytom	
287	39	48.8	462	2	O55NA1_CRYNE	O55NA1 cryptococcu	360	38.5	48.1	2	Q40793_PETCR	Q40793 petroselinu	
288	39	48.8	472	2	O68ST7_9AGAR	Q68ST7 pleurotomy d	361	38.5	48.1	300	2	O4SMS9_TETNG	O4SMS9 tetraodon n
289	39	48.8	474	2	O6BHR2_DEBHA	Q6BHR2 debaryomyce	362	38.5	48.1	1222	2	O7KLG6_DROME	O7KLG6 drosophila
290	39	48.8	501	2	O6YXR9_PHYPA	O6YXR9 physcomitre	363	38.5	48.1	1694	2	O9VP76_DROME	O9VP76 drosophila
291	39	48.8	503	2	Q9NAR8_BRAFL	Q9NAR8 branchiosto	364	38.5	48.1	1718	2	O9Y1V0_DROME	O9Y1V0 drosophila
292	39	48.8	510	2	Q41608_GIBZE	Q41608 gibberella	365	38.5	48.1	1888	2	O4Q8R2_LEIMA	O4Q8R2 leishmania
293	39	48.8	515	2	Q4WRG5_ASFPU	Q4WRG5 aspergillus	366	38	47.5	12	1	UTS2A_CATCO	P04558 catostomus
294	39	48.8	538	2	Q76P04_DICDI	Q76P04 dictyosteli	367	38	47.5	12	1	UTS2B_CATCO	P04559 catostomus
295	39	48.8	552	2	Q41870_GIBZE	Q41870 gibberella	368	38	47.5	12	1	UTS2B_CYPCA	P04561 cyprinus ca
296	39	48.8	588	2	O97201_LEIMA	O97201 leishmania	369	38	47.5	12	1	UTS2_GILMI	P01147 gillichthys
297	39	48.8	612	2	O5WSF1_LEGPL	Q5WSF1 legionella	370	38	47.5	12	1	UTS2_POLSP	P81022 polyodon sp
298	39	48.8	612	2	O5X0M4_LEGPA	Q5X0M4 legionella	371	38	47.5	12	1	UTS2_SCYCA	P35490 scyllorhinu
299	39	48.8	612	2	O5ZR83_LEGPH	Q5ZR83 legionella	372	38	47.5	52	2	Q4XDG6_PLACH	Q4XDG6 plasmodium
300	39	48.8	618	2	O66835_AQUAE	O66835 aquifex aeo	373	38	47.5	59	2	O4TF36_TETNG	Q4TF36 tetraodon n
301	39	48.8	619	2	O4FBI3_PLAMG	O4FBI3 placopecten	374	38	47.5	59	2	O4THE1_TETNG	Q4THE1 tetraodon n
302	39	48.8	660	1	PRIA_BORBU	O45032 borrelia bu	375	38	47.5	65	2	O657W1_ORYSA	O657W1 oryza sativ
303	39	48.8	660	2	O662Z8_BORGA	O662Z8 borrelia ga	376	38	47.5	74	2	O5K4Y4_BABIN	O5K4Y4 barbus inte
304	39	48.8	707	2	Q95JUR7_MACFA	Q95JR7 macaca fasc	377	38	47.5	83	1	UTS2_PLAFA	P21857 platichthys
305	39	48.8	723	1	ZC11A_CHICK	Q5ZJ17 gallus gall	378	38	47.5	90	2	O5QTF8_SHIFL	O5QTF8 shigella fl
306	39	48.8	745	2	O4S190_TETNG	Q4S190 tetraodon n	379	38	47.5	95	2	O69C27_9REOV	O69C27 pulau reovi
307	39	48.8	748	2	O77066_CHOFU	O77066 choriostoneu	380	38	47.5	95	2	O9J1B2_9REOV	O9J1B2 nelson bay
308	39	48.8	789	2	O6BG16_PARTE	Q6BG16 paramecium	381	38	47.5	96	2	O4ROT8_TETNG	O4ROT8 tetraodon n
309	39	48.8	792	1	ZC11A_MOUSE	Q5NZFI mus musculu	382	38	47.5	102	2	O81OR0_DROME	O81OR0 drosophila
310	39	48.8	795	2	Q5B8S6_EMENI	Q5B8S6 aspergillus	383	38	47.5	109	2	O61HA8_DROME	O61HA8 drosophila
311	39	48.8	813	2	Q9BLJ2_CIOIN	Q9BLJ2 ciona intes	384	38	47.5	113	1	UTS2B_MOUSE	O76511 mus musculus
312	39	48.8	844	2	O81904_ARATH	O81904 arabidopsis	385	38	47.5	117	2	O9PBZ4_XYLPA	O9PBZ4 xylella fas
313	39	48.8	874	2	O4P330_USTWA	Q4P330 ustilago ma	386	38	47.5	118	1	UTS2B_RAT	O76512 rattus norv
314	39	48.8	965	1	YNC3_YEAST	P53971 saccharomyc	387	38	47.5	119	1	UTS2B_HUMAN	O76510 homo sapien
315	39	48.8	1068	2	Q54ZS5_DICDI	Q54ZS5 dictyosteli	388	38	47.5	121	1	UTS2_FIG	Q95J46 sus scrofa
316	39	48.8	1106	2	Q6CX17_KULUA	Q6CX17 kluveromyc	389	38	47.5	123	1	UTS2_MOUSE	Q9QZQ4 rattus norv
317	39	48.8	1642	2	O515F7_ENTHI	O515F7 entameoba h	390	38	47.5	123	1	UTS2_RAT	Q9QZQ4 rattus norv
318	39	48.8	1656	2	Q50S87_ENTHI	Q50S87 entameoba h	391	38	47.5	123	2	O541G7_MOUSE	O541G7 mus musculus
319	39	48.8	1912	2	O4T2F0_TETNG	Q4T2F0 tetraodon n	392	38	47.5	124	1	UTS2_HUMAN	O95399 homo sapien
320	39	48.8	1946	2	Q4RQW4_TETNG	Q4RQW4 tetraodon n	393	38	47.5	124	2	O6QJ36_CHICK	O6QJ36 gallus gall
321	39	48.8	2016	2	Q8TJ89_METAC	Q8TJ89 methanosarc	394	38	47.5	125	1	UTS2A_CYPCA	P04560 cyprinus ca
322	39	48.8	2052	1	MYO10_BOVIN	P79114 bos taurus	395	38	47.5	125	1	UTS2B_BRARE	P02298 brachydanio
323	39	48.8	2053	2	Q694W8_XENLA	Q694W8 xenopus lae	396	38	47.5	125	1	UTS2G_CYPCA	P06580 cyprinus ca

397	38	47.5	125	1	UTS2_MACMU	Qhyc2 macaca mula	470	38	47.5	525	2	Q8NJL1_ASPPU	Q8nj11 aspergillus
398	38	47.5	126	2	Q7SZC4_BRARE	Q7szc4 brachydanio	471	38	47.5	529	2	Q8GLE0_MACMU	Q8gle0 macaca mula
399	38	47.5	125	2	Q6Q273_CHICK	Q6q273 gallus gall	472	38	47.5	535	2	Q6CQ20_KLUJA	Q6cq20 kluyveromyc
400	38	47.5	127	1	UTS2_RANRI	P31715 rana ridibu	473	38	47.5	567	2	Q6BRE0_DEBHA	Q6brs0 debaryomyce
401	38	47.5	127	1	Q8C56_MOUSE	Q8c566 mus musculu	474	38	47.5	606	2	Q5AF79_CANAL	Q5af79 candida alb
402	38	47.5	129	2	Q7QWH4_PLAPE	Q7qwh4 platichthys	475	38	47.5	606	2	Q5AF65_CANAL	Q5af65 candida alb
403	38	47.5	129	2	Q7QWH5_PLAPE	Q7qwh5 platichthys	476	38	47.5	606	2	Q5AFV0_CANAL	Q5afv0 candida alb
404	38	47.5	148	1	V105_FOWPV	Q9j5b5 fowlpox vir	477	38	47.5	619	2	Q5A314_CANAL	Q5a314 candida alb
405	38	47.5	148	2	Q7QH50_FOWPV	Q7qh50 fowlpox vir	478	38	47.5	636	2	Q5KSS3_9ECHI	Q5ks33 luidia quini
406	38	47.5	165	2	Q8SY97_DROME	Q8sy97 drosophila	479	38	47.5	637	2	Q5B3G3_EMENI	Q5b3g3 aspergillus
407	38	47.5	189	2	Q581W3_3TRYP	Q581w3 trypanosoma	480	38	47.5	637	2	Q7VFX4_HELHP	Q7vfx4 helicobacte
408	38	47.5	190	2	Q5TUF4_ANOGA	Q5tuf4 anopheles g	481	38	47.5	650	2	Q6CMQ2_KLUJA	Q6cmq2 kluyveromyc
409	38	47.5	192	2	Q8V5Q5_9NUCL	Q8v5q5 helicoverpa	482	38	47.5	679	2	Q4XZH6_PLACH	Q4xzh6 plasmodium
410	38	47.5	192	2	Q91BU9_9NUCL	Q91bu9 helicoverpa	483	38	47.5	683	2	Q756N0_ASHGO	Q756n0 ashbysa goss
411	38	47.5	192	2	Q99GU2_9NUCL	Q99gu2 helicoverpa	484	38	47.5	686	2	Q7UIT9_RHORA	Q7uit9 rhodopitell
412	38	47.5	192	2	Q9E228_9NUCL	Q9e228 helicoverpa	485	38	47.5	692	2	Q6CUK6_KLUJA	Q6cuk6 kluyveromyc
413	38	47.5	203	2	Q4TD97_TETNG	Q4td97 tetraodon n	486	38	47.5	716	2	Q5KCD1_CRYNE	Q5kcd1 cryptococcu
414	38	47.5	204	2	Q52VH8_CIOIN	Q52vh8 ciona intes	487	38	47.5	719	2	Q55JC8_CRYNE	Q55jc8 cryptococcu
415	38	47.5	205	2	Q4TH99_TETNG	Q4th99 tetraodon n	488	38	47.5	796	2	Q4QDR7_LEIMA	Q4qdr7 leishmania
416	38	47.5	210	2	Q21981_CAEBL	Q21981 caenorhabdi	489	38	47.5	833	2	Q537F7_9VIRU	Q537f7 cotesia plu
417	38	47.5	220	2	Q5D306_9BACT	Q5d306 uncultured	490	38	47.5	997	1	CEBPZ_MOUSE	P53569 mus musculu
418	38	47.5	224	2	Q5D2U6_9BACT	Q5d2u6 uncultured	491	38	47.5	1030	2	Q9LHT5_ARATH	Q9lht5 arabidopsis
419	38	47.5	229	2	Q4THR7_TETNG	Q4thr7 tetraodon n	492	38	47.5	1089	2	Q19927_CAEBL	Q19927 caenorhabdi
420	38	47.5	237	2	Q7VFM5_HELHP	Q7vfm5 helicobacte	493	38	47.5	1143	2	Q4SP84_TETNG	Q4sp84 tetraodon n
421	38	47.5	242	2	Q60Z21_CAEBR	Q60z21 caenorhabdi	494	38	47.5	1188	2	Q9FG53_ARATH	Q9fg53 arabidopsis
422	38	47.5	242	2	Q9PU09_LATCH	Q9pu09 latimeria c	495	38	47.5	1265	2	Q7S9A7_NEUCR	Q7s9a7 neutropora
423	38	47.5	244	2	Q5CV15_CRYPV	Q5cv15 cryptospori	496	38	47.5	1442	2	Q7RCU7_PLAYO	Q7rcu7 plasmodium
424	38	47.5	244	2	Q5CMJ3_CRYHO	Q5cmj3 cryptospori	497	38	47.5	1487	2	Q15843_LEIMA	Q15843 leishmania
425	38	47.5	250	2	Q9XXK0_CAEBL	Q9xxk0 caenorhabdi	498	38	47.5	1628	2	Q584C7_9TRYP	Q584c7 trypanosoma
426	38	47.5	256	2	Q5C4C9_SCHJA	Q5c4c9 schistosoma	499	38	47.5	1683	2	Q86KY1_DICDI	Q86ky1 dictyosteli
427	38	47.5	279	1	HCE21_ORYLA	P31581 oryzias lat	500	38	47.5	1702	2	P97706_RAT	P97706 rattus norv
428	38	47.5	283	2	Q6AR06_DBSPS	Q6ar06 desulfotale	501	38	47.5	1864	2	Q8IHI6_BRUMA	Q8ihi6 bruglia mala
429	38	47.5	283	2	Q88W68_LACPL	Q88w68 lactobacill	502	38	47.5	1933	2	Q8IHI5_BRUMA	Q8ihi5 bruglia mala
430	38	47.5	284	2	Q8U327_PYRPU	Q8u327 pyrococcus	503	38	47.5	2105	1	POLR_ASGVP	P96309 apple stem
431	38	47.5	285	2	P74637_SYNY3	P74637 synechocyst	504	38	47.5	2722	2	Q86JN0_DICDI	Q86jn0 dictyosteli
432	38	47.5	289	2	Q4IN07_GIBZE	Q4in07 gibberella	505	38	47.5	2722	2	Q55A92_DICDI	Q55a92 dictyosteli
433	38	47.5	290	2	Q4Q155_LEIMA	Q4q155 leishmania	506	38	47.5	5890	2	Q8IK84_PLAF7	Q8ik84 plasmodium
434	38	47.5	291	2	Q16260_CAEBL	Q16260 caenorhabdi	507	37.5	46.9	60	1	CK3_NAJHA	P01459 najja baye a
435	38	47.5	303	2	Q5FR51_GLUOX	Q5fr51 gluconobact	508	37.5	46.9	106	2	Q500Y1_DROME	Q500y1 drosophila
436	38	47.5	315	2	Q61A89_CAEBR	Q61a89 caenorhabdi	509	37.5	46.9	123	2	Q25401_LITS1	Q25401 litomosoid
437	38	47.5	319	2	Q4LI20_9BURK	Q4li20 burkholderi	510	37.5	46.9	136	2	Q91IH2_HHV8	Q91ih2 human harpe
438	38	47.5	323	2	Q4MW36_BACCE	Q4mw36 bacillus ce	511	37.5	46.9	140	2	Q53CT8_9GAMA	Q53ct8 macaca fusc
439	38	47.5	328	2	Q90X89_BRARE	Q90x89 brachydanio	512	37.5	46.9	152	1	VE6_HPV03	P67399 human papil
440	38	47.5	328	2	Q6NYD5_BRARE	Q6nyd5 brachydanio	513	37.5	46.9	156	2	Q8BYD2_MOUSE	Q8byd2 mus musculu
441	38	47.5	329	2	Q9NAN9_CAEBL	Q9nan9 caenorhabdi	514	37.5	46.9	243	2	Q80LS1_NPVAH	Q80ls1 adoxophyes
442	38	47.5	329	2	Q6RUM6_PROSI	Q6rum6 cleome hase	515	37.5	46.9	284	2	Q91GW1_HHV8	Q91gw1 human herpe
443	38	47.5	330	2	Q61AB7_CAEBR	Q61ab7 caenorhabdi	516	37.5	46.9	354	2	Q25402_LITS1	Q25402 litomosoid
444	38	47.5	334	2	Q52V10_CIOIN	Q52v10 ciona intes	517	37.5	46.9	1551	1	VGLM_DUGBV	Q92004 dugbe virus
445	38	47.5	341	2	Q52V12_CIOIN	Q52v12 ciona intes	518	37	46.2	31	2	Q9DEW3_COTCO	Q9dew3 coturnix co
446	38	47.5	343	2	Q4T062_TETNG	Q4t062 tetraodon n	519	37	46.2	31	2	Q9DFH7_9SMRG	Q9dfh7 mastacembel
447	38	47.5	348	2	Q4HY24_GIBZE	Q4hy24 gibberella	520	37	46.2	31	2	Q9DFI2_BRACHYD	Q9dfi2 brachydanio
448	38	47.5	348	2	Q6L656_NEOP	Q6l656 hydropsyche	521	37	46.2	31	2	Q9DFI6_MONAL	Q9dfi6 monoterus
449	38	47.5	357	2	Q8IBW3_PLAF7	Q8ibw3 plasmodium	522	37	46.2	40	2	Q8CKA1_YERPE	Q8cka1 yersinia pe
450	38	47.5	357	2	Q4YNG9_PLAPE	Q4yng9 plasmodium	523	37	46.2	41	2	Q86GV4_CAEBL	Q86gv4 caenorhabdi
451	38	47.5	357	2	Q6MS30_MYCHI	Q6ms30 mycoplasma	524	37	46.2	41	2	Q8NVCO_STAAM	Q8nvco staphylococ
452	38	47.5	389	2	Q50TC8_NYTHI	Q50tc8 entamoeba h	525	37	46.2	41	2	Q8NVCO_STAAM	Q8nvco staphylococ
453	38	47.5	392	2	Q52V11_CIOIN	Q52v11 ciona intes	526	37	46.2	46	2	Q56BK4_9CAUD	Q56bk4 enterobacte
454	38	47.5	392	2	Q56N32_CIOIN	Q56n32 ciona intes	527	37	46.2	46	2	Q4ZH59_9SAUR	Q4zh59 eremitas bre
455	38	47.5	393	2	Q9K8R0_BACHD	Q9k8r0 bacillus ha	528	37	46.2	51	2	Q32975_PINTH	Q32975 pinus thunb
456	38	47.5	399	2	Q8ESG2_OCEIH	Q8esg2 oceanobacil	529	37	46.2	51	2	Q9DG17_ONCMY	Q9dg17 oncorhynch
457	38	47.5	402	2	Q6ALJ5_HELVI	Q6alj5 heliothis v	530	37	46.2	54	2	Q8X2D1_ECOS7	Q8x2d1 escherichia
458	38	47.5	421	2	Q8GMJ7_ECOLI	Q8gmj7 escherichia	531	37	46.2	54	2	Q92GE3_RICCN	Q92ge3 rickettsia
459	38	47.5	423	2	Q5VH36_PROSI	Q5vh36 podandrogyn	532	37	46.2	56	2	Q8MX11_CAEBL	Q8mx11 caenorhabdi
460	38	47.5	424	2	Q5N959_ORYSA	Q5n959 oryza sativ	533	37	46.2	56	2	Q4R413_MACFA	Q4r413 macaca fasc
461	38	47.5	428	2	Q5VH38_PROSI	Q5vh38 cleome pilo	534	37	46.2	58	2	Q64ZM8_BACFR	Q64zm8 bacteroides
462	38	47.5	470	2	Q6MMG4_BDEBA	Q6mmg4 bdellovibri	535	37	46.2	59	2	Q4XUD4_PLACH	Q4xud4 plasmodium
463	38	47.5	499	2	Q89BC4_BRAJA	Q89bc4 bradyrhizob	536	37	46.2	61	2	Q8X3H9_ECOS7	Q8x3h9 escherichia
464	38	47.5	500	2	Q7PG12_ANOGA	Q7pg12 anopheles g	537	37	46.2	74	2	Q5K4V7_BARIN	Q5k4v7 barbus inte
465	38	47.5	509	2	Q4RK29_TETNG	Q4rk29 tetraodon n	538	37	46.2	78	2	Q9QXJ3_RAT	Q9qxj3 rattus norv
466	38	47.5	510	2	Q50SH8_XENTR	Q50sh8 xenopus tro	539	37	46.2	84	2	Q51GC7_ENTHI	Q51gc7 entamoeba h
467	38	47.5	518	2	Q6C8R1_YARLI	Q6c8r1 yarrowia li	540	37	46.2	85	2	Q8FA94_ECOL6	Q8fa94 escherichia
468	38	47.5	520	2	Q59PB6_CANAL	Q59pb6 candida alb	541	37	46.2	86	2	Q5CM86_CRYHO	Q5cm86 cryptospori
469	38	47.5	525	2	Q4WM43_ASPPU	Q4wm43 aspergillus	542	37	46.2	88	2	Q8X216_ECOS7	Q8x216 escherichia

543	37	46.2	95	2	Q51Y35_MAGGR	Q51Y35 magnaporthae	616	37	46.2	220	2	Q9AP64_9BACT	Q9AP64 uncultured
544	37	46.2	97	2	Q3Y043_CABEL	Q3Y043 caenorhabdi	617	37	46.2	220	2	Q9AP62_9BACT	Q9AP62 uncultured
545	37	46.2	99	2	O70889_9HIV1	O70889 human immu	618	37	46.2	220	2	Q8RT16_9BACT	Q8RT16 uncultured
546	37	46.2	99	2	Q90217_9HIV1	Q90217 human immu	619	37	46.2	220	2	Q9AP63_9BACT	Q9AP63 uncultured
547	37	46.2	99	2	Q90276_9HIV1	Q90276 human immu	620	37	46.2	220	2	Q6X2Q5_9BACT	Q6X2Q5 uncultured
548	37	46.2	100	2	O8YLG1_ANASP	O8YLG1 anabaena sp	621	37	46.2	220	2	Q6X2Q2_9BACT	Q6X2Q2 uncultured
549	37	46.2	101	2	O8E6U9_9HIV1	O8E6U9 human immu	622	37	46.2	220	2	Q6X2Q0_9BACT	Q6X2Q0 uncultured
550	37	46.2	101	2	Q8E6W4_9HIV1	Q8E6W4 human immu	623	37	46.2	220	2	Q6X2P5_9BACT	Q6X2P5 uncultured
551	37	46.2	101	2	Q6H1Q3_9HIV1	Q6H1Q3 human immu	624	37	46.2	220	2	Q6X2P0_9BACT	Q6X2P0 uncultured
552	37	46.2	101	2	Q6H1R2_9HIV1	Q6H1R2 human immu	625	37	46.2	220	2	Q6X2N9_9BACT	Q6X2N9 uncultured
553	37	46.2	101	2	Q902M7_9HIV1	Q902M7 human immu	626	37	46.2	220	2	Q6X2N7_9BACT	Q6X2N7 uncultured
554	37	46.2	101	2	Q90819_9HIV1	Q90819 human immu	627	37	46.2	220	2	Q6X2N5_9BACT	Q6X2N5 uncultured
555	37	46.2	101	2	Q908K7_9HIV1	Q908K7 human immu	628	37	46.2	220	2	Q6X2N3_9BACT	Q6X2N3 uncultured
556	37	46.2	101	2	Q908L6_9HIV1	Q908L6 human immu	629	37	46.2	220	2	Q6X2N0_9BACT	Q6X2N0 uncultured
557	37	46.2	101	2	Q908M5_9HIV1	Q908M5 human immu	630	37	46.2	220	2	Q6X2M7_9BACT	Q6X2M7 uncultured
558	37	46.2	101	2	Q90MK8_9HIV1	Q90MK8 human immu	631	37	46.2	220	2	Q6X2M4_9BACT	Q6X2M4 uncultured
559	37	46.2	101	2	Q9QM86_9HIV1	Q9QM86 human immu	632	37	46.2	220	2	Q6VW19_9BACT	Q6VW19 uncultured
560	37	46.2	107	2	Q4RDL8_TFTNG	Q4RDL8 tetraodon n	633	37	46.2	220	2	Q6VW10_9BACT	Q6VW10 uncultured
561	37	46.2	108	2	Q59YU9_CNAL	Q59YU9 candida alb	634	37	46.2	220	2	Q6VUJ7_9BACT	Q6VUJ7 uncultured
562	37	46.2	116	2	Q6ZG05_ORISA	Q6ZG05 oryza sativ	635	37	46.2	220	2	Q6VUJ1_9BACT	Q6VUJ1 uncultured
563	37	46.2	119	2	Q656T0_ORISA	Q656T0 oryza sativ	636	37	46.2	220	2	Q6VUX9_9BACT	Q6VUX9 uncultured
564	37	46.2	130	1	Y1631_PYRHO	Q59297 pyrococcus	637	37	46.2	220	2	Q6VUX5_9BACT	Q6VUX5 uncultured
565	37	46.2	139	1	Y053_NPVAC	P41457 autographa	638	37	46.2	220	2	Q6VUW0_9BACT	Q6VUW0 uncultured
566	37	46.2	139	2	Q17261_BRUPA	Q17261 bugia paha	639	37	46.2	220	2	Q6VUW8_9BACT	Q6VUW8 uncultured
567	37	46.2	140	2	Q17176_BRUMA	Q17176 bugia mala	640	37	46.2	220	2	Q6VUW9_9BACT	Q6VUW9 uncultured
568	37	46.2	143	2	Q5EHY2_GECJA	Q5EHY2 gecko japon	641	37	46.2	220	2	Q6VUW7_9BACT	Q6VUW7 uncultured
569	37	46.2	149	2	Q4MGN1_BACCE	Q4MGN1 bacillus ce	642	37	46.2	220	2	Q6VUW6_9BACT	Q6VUW6 uncultured
570	37	46.2	150	2	Q6ZU01_HUMAN	Q6ZU01 homo sapien	643	37	46.2	220	2	Q6VUW1_9BACT	Q6VUW1 uncultured
571	37	46.2	154	1	MER2_EUPOC	O15825 eupletes oc	644	37	46.2	220	2	Q6VUW7_9BACT	Q6VUW7 uncultured
572	37	46.2	161	2	Q8BS55_MOUSE	Q8BS55 mus musculu	645	37	46.2	220	2	Q6X3P1_9BACT	Q6X3P1 uncultured
573	37	46.2	163	2	Q9LZ34_ARATH	Q9LZ34 arabidopsis	646	37	46.2	220	2	Q5D3J7_9BACT	Q5D3J7 uncultured
574	37	46.2	174	2	Q6GAM5_STAAS	Q6GAM5 staphylococ	647	37	46.2	220	2	Q5D3J6_9BACT	Q5D3J6 uncultured
575	37	46.2	180	2	Q6YPQ6_ONYPE	Q6YPQ6 onion yello	648	37	46.2	220	2	Q5D3J5_9BACT	Q5D3J5 uncultured
576	37	46.2	181	2	Q9Y996_AERPE	Q9Y996 aeropyrium p	649	37	46.2	220	2	Q5D319_9BACT	Q5D319 uncultured
577	37	46.2	188	1	RM32_HUMAN	Q8BYC8 homo sapien	650	37	46.2	220	2	Q5D318_9BACT	Q5D318 uncultured
578	37	46.2	189	2	Q5F617_HUMAN	Q5F617 homo sapien	651	37	46.2	222	2	Q6X2Q7_9BACT	Q6X2Q7 uncultured
579	37	46.2	209	2	Q5DEV3_SCHJA	Q5DEV3 schistosoma	652	37	46.2	222	2	Q6X2Q8_9BACT	Q6X2Q8 uncultured
580	37	46.2	216	2	Q9ZPR5_ARABID	Q9ZPR5 arabidopsis	653	37	46.2	222	2	Q6X2Q9_9BACT	Q6X2Q9 uncultured
581	37	46.2	220	2	Q5VUS3_9BACT	Q5VUS3 uncultured	654	37	46.2	222	2	Q6X2Q6_9BACT	Q6X2Q6 uncultured
582	37	46.2	220	2	Q5VUS7_9BACT	Q5VUS7 uncultured	655	37	46.2	224	2	Q6CMD5_KLULA	Q6CMD5 klyveromyc
583	37	46.2	220	2	Q5VUT0_9BACT	Q5VUT0 uncultured	656	37	46.2	224	2	Q5D3C7_9BACT	Q5D3C7 uncultured
584	37	46.2	220	2	Q6VUT1_9BACT	Q6VUT1 uncultured	657	37	46.2	224	2	Q5D3C9_9BACT	Q5D3C9 uncultured
585	37	46.2	220	2	Q6VUT4_9BACT	Q6VUT4 uncultured	658	37	46.2	224	2	Q5D3G1_9BACT	Q5D3G1 uncultured
586	37	46.2	220	2	Q6VUT3_9BACT	Q6VUT3 uncultured	659	37	46.2	224	2	Q5D3G4_9BACT	Q5D3G4 uncultured
587	37	46.2	220	2	Q5VUUS_9BACT	Q5VUUS uncultured	660	37	46.2	224	2	Q5D3G6_9BACT	Q5D3G6 uncultured
588	37	46.2	220	2	Q6VUV1_9BACT	Q6VUV1 uncultured	661	37	46.2	224	2	Q5D3G7_9BACT	Q5D3G7 uncultured
589	37	46.2	220	2	Q6VUV4_9BACT	Q6VUV4 uncultured	662	37	46.2	224	2	Q5D3G8_9BACT	Q5D3G8 uncultured
590	37	46.2	220	2	Q6VUV9_9BACT	Q6VUV9 uncultured	663	37	46.2	224	2	Q5D3H0_9BACT	Q5D3H0 uncultured
591	37	46.2	220	2	Q6VUW8_9BACT	Q6VUW8 uncultured	664	37	46.2	224	2	Q5D3H1_9BACT	Q5D3H1 uncultured
592	37	46.2	220	2	Q5VUY2_9BACT	Q5VUY2 uncultured	665	37	46.2	224	2	Q5D3H2_9BACT	Q5D3H2 uncultured
593	37	46.2	220	2	Q5VUY3_9BACT	Q5VUY3 uncultured	666	37	46.2	224	2	Q5D3H3_9BACT	Q5D3H3 uncultured
594	37	46.2	220	2	Q5VUY6_9BACT	Q5VUY6 uncultured	667	37	46.2	224	2	Q5D3H4_9BACT	Q5D3H4 uncultured
595	37	46.2	220	2	Q6VUZ7_9BACT	Q6VUZ7 uncultured	668	37	46.2	224	2	Q5D3H7_9BACT	Q5D3H7 uncultured
596	37	46.2	220	2	Q6VUZ9_9BACT	Q6VUZ9 uncultured	669	37	46.2	224	2	Q5D3H9_9BACT	Q5D3H9 uncultured
597	37	46.2	220	2	Q6VW03_9BACT	Q6VW03 uncultured	670	37	46.2	224	2	Q5D3I1_9BACT	Q5D3I1 uncultured
598	37	46.2	220	2	Q6VW04_9BACT	Q6VW04 uncultured	671	37	46.2	224	2	Q5D3I4_9BACT	Q5D3I4 uncultured
599	37	46.2	220	2	Q6VW11_9BACT	Q6VW11 uncultured	672	37	46.2	224	2	Q5D316_9BACT	Q5D316 uncultured
600	37	46.2	220	2	Q6VW13_9BACT	Q6VW13 uncultured	673	37	46.2	224	2	Q5D317_9BACT	Q5D317 uncultured
601	37	46.2	220	2	Q6VW17_9BACT	Q6VW17 uncultured	674	37	46.2	224	2	Q5U344_9BACT	Q5U344 uncultured
602	37	46.2	220	2	Q6VW20_9BACT	Q6VW20 uncultured	675	37	46.2	224	2	Q5D3J4_9BACT	Q5D3J4 uncultured
603	37	46.2	220	2	Q6VW23_9BACT	Q6VW23 uncultured	676	37	46.2	224	2	Q5D3J3_9BACT	Q5D3J3 uncultured
604	37	46.2	220	2	Q6X2M8_9BACT	Q6X2M8 uncultured	677	37	46.2	224	2	Q5D3J2_9BACT	Q5D3J2 uncultured
605	37	46.2	220	2	Q6X2M9_9BACT	Q6X2M9 uncultured	678	37	46.2	224	2	Q5D3J1_9BACT	Q5D3J1 uncultured
606	37	46.2	220	2	Q6X2N1_9BACT	Q6X2N1 uncultured	679	37	46.2	224	2	Q5D3J0_9BACT	Q5D3J0 uncultured
607	37	46.2	220	2	Q6X2N2_9BACT	Q6X2N2 uncultured	680	37	46.2	224	2	Q5D3I3_9BACT	Q5D3I3 uncultured
608	37	46.2	220	2	Q6X2N6_9BACT	Q6X2N6 uncultured	681	37	46.2	224	2	Q5D3D1_9BACT	Q5D3D1 uncultured
609	37	46.2	220	2	Q6X2N8_9BACT	Q6X2N8 uncultured	682	37	46.2	224	2	Q5D3D0_9BACT	Q5D3D0 uncultured
610	37	46.2	220	2	Q6X2P4_9BACT	Q6X2P4 uncultured	683	37	46.2	224	2	Q5D3C8_9BACT	Q5D3C8 uncultured
611	37	46.2	220	2	Q6X2P6_9BACT	Q6X2P6 uncultured	684	37	46.2	233	2	Q4ZG05_9BACT	Q4ZG05 unidentifie
612	37	46.2	220	2	Q6X2P9_9BACT	Q6X2P9 uncultured	685	37	46.2	233	2	Q4ZG09_9BACT	Q4ZG09 unidentifie
613	37	46.2	220	2	Q8RT26_9BACT	Q8RT26 uncultured	686	37	46.2	233	2	Q4ZG82_9BACT	Q4ZG82 unidentifie
614	37	46.2	220	2	Q9AP60_9BACT	Q9AP60 uncultured	687	37	46.2	233	2	Q4ZG82_9BACT	Q4ZG82 unidentifie
615	37	46.2	220	2	Q9AP61_9BACT	Q9AP61 uncultured	688	37	46.2	233	2	Q4ZG89_9BACT	Q4ZG89 unidentifie

835	37	46.2	531	2	Q8CFB8_MOUSE	Q8cff8 mus musculus	36.5	45.6	105	1	VORD_PYRHO	O58412 pyrococcus
836	37	46.2	536	2	Q6URK0_BACFO	Q6ukm0 bacteroides	36.5	45.6	105	2	Q5JIK1_PYRKO	Q5jik1 pyrococcus
837	37	46.2	543	2	Q5K839_CRYNE	Q5k839 cryptococcus	36.5	45.6	113	2	Q50VE5_ENTHI	Q50ve5 entamoeba h
838	37	46.2	559	2	Q4SNK3_TETNG	Q4snk3 tetradon n	36.5	45.6	148	1	VE6_HPV10	P36802 human papil
839	37	46.2	564	2	Q8MQ12_DROME	Q8mq12 drosophila	36.5	45.6	149	2	Q4SZ37_TETNG	Q4sz37 tetradon n
840	37	46.2	569	2	Q3VEY2_DROME	Q3vey2 drosophila	36.5	45.6	150	2	Q98004_PAPI	Q98004 human papil
841	37	46.2	574	2	Q4H3F8_CIOIN	Q4h3f8 ciona intes	36.5	45.6	216	2	Q67MQ3_SYMTH	P37mq3 symbiobacte
842	37	46.2	590	2	Q4RR34_TETNG	Q4rr34 tetradon n	36.5	45.6	271	1	PEX2_YEAST	P32800 saccharomyc
843	37	46.2	594	2	Q4Y835_PLACH	Q4y835 plasmodium	36.5	45.6	276	2	Q9F733_CHLTE	Q9f733 chlorobium
844	37	46.2	602	2	Q4V707_DROME	Q4v707 drosophila	36.5	45.6	350	2	Q8WU63_HUMAN	Q8wu63 homo sapien
845	37	46.2	622	2	Q7P1X6_CHRVO	Q7p1x6 chromobacte	36.5	45.6	367	2	Q750R7_ASHGO	Q750r7 ashbysa goss
846	37	46.2	624	2	Q4S289_TETNG	Q4s289 tetradon n	36.5	45.6	376	2	Q57ND7_SALCH	Q57nd7 salmonella
847	37	46.2	626	2	Q551J9_CRYNE	Q551j9 cryptococcus	36.5	45.6	376	2	Q5PM2_SALFA	Q5pm2 salmonella
848	37	46.2	639	1	NOSZ_RHIME	Q59746 rhizobium m	36.5	45.6	376	2	Q8Z648_SALTI	Q8z648 salmonella
849	37	46.2	640	2	Q6ORL8_CAEBR	Q6orl8 caenorhabdi	36.5	45.6	489	2	Q8WTR8_HUMAN	Q8wtr8 homo sapien
850	37	46.2	642	2	Q4N7H3_THEPA	Q4n7h3 theileria p	36.5	45.6	517	2	Q50P46_ENTHI	Q50p46 entamoeba h
851	37	46.2	645	2	Q6N843_RHOPA	Q6n843 rhodopseudo	36.5	45.6	525	2	Q4SIG2_TETNG	Q4sig2 tetradon n
852	37	46.2	650	1	NOSZ_BEAJA	Q89xj6 bradyrhizob	36.5	45.6	542	2	Q50LW2_ENTHI	Q50lw2 entamoeba h
853	37	46.2	655	2	Q9FJ84_ARATH	Q9fj84 arabidopsis	36.5	45.6	578	2	Q50V82_ENTHI	Q50v82 entamoeba h
854	37	46.2	681	2	Q5P0L0_AZOSE	Q5p0l0 azoarcus sp	36.5	45.6	586	2	Q50PH5_ENTHI	Q50ph5 entamoeba h
855	37	46.2	683	2	Q61U03_CAEBR	Q61u03 caenorhabdi	36.5	45.6	672	2	Q4WGB4_ASFFU	Q4wgb4 aspergillus
856	37	46.2	686	2	Q5TX25_ANOGA	Q5tx25 anopheles g	36.5	45.6	870	2	Q96376_CLABR	Q96376 clarkia bre
857	37	46.2	696	2	Q61834_CAEBL	Q61834 caenorhabdi	36.5	45.6	871	2	Q9ZPN5_CLACO	Q9zpn5 clarkia con
858	37	46.2	697	2	Q7RN38_PLAYO	Q7rn38 plasmodium	36.5	45.6	1030	2	Q9BY89_HUMAN	Q9by89 homo sapien
859	37	46.2	710	2	Q8W2D2_ARATH	Q8w2d2 arabidopsis	36.5	45.6	1700	2	Q41IR0_GIBZE	Q41ir0 gibberella
860	37	46.2	724	2	Q4YZ69_PLABE	Q4yz69 plasmodium	36	45.0	31	2	Q4Z7E2_PLABE	Q4z7e2 plasmodium
861	37	46.2	732	2	Q5KMT2_CRYNE	Q5kmt2 cryptococcus	36	45.0	33	2	Q4YVK6_PLABE	Q4yvk6 plasmodium
862	37	46.2	732	2	Q5X5X0_CRYNE	Q5x5x0 cryptococcus	36	45.0	46	2	Q4X3H7_PLACH	Q4x3h7 plasmodium
863	37	46.2	765	2	Q5QU35_IDILO	Q5qu35 idiomarina	36	45.0	50	2	Q64X18_BACFR	Q64x18 bacteroides
864	37	46.2	770	2	Q8CDK4_MOUSE	Q8cdk4 mus musculus	36	45.0	60	1	CK1_NAJMO	P01467 naja mossam
865	37	46.2	773	2	Q7QRF9_GIALA	Q7qrf9 giardia lam	36	45.0	60	1	CK1_NAJHA	P01468 naja pallid
866	37	46.2	781	2	Q414V5_GIBZE	Q414v5 gibberella	36	45.0	60	1	CK2_NAJHA	P01462 naja haje a
867	37	46.2	823	2	Q517A3_ENTHI	Q517a3 entamoeba h	36	45.0	60	1	CK2_NAJMO	P01469 naja mossam
868	37	46.2	827	2	Q537F8_9VIRU	Q537f8 cotesia plu	36	45.0	60	1	CK2_NAJNI	P01463 naja nivea
869	37	46.2	871	2	Q7Q1V7_ANOGA	Q7q1v7 anopheles g	36	45.0	60	1	CK3_NAJMO	P01470 naja mossam
870	37	46.2	887	2	Q8XVW5_BALSO	Q8xvw5 ralstonia s	36	45.0	60	1	CK3_NAJNI	P01458 naja nivea
871	37	46.2	895	2	Q8ZGM5_BURMA	Q8zgm5 burkholderi	36	45.0	60	1	CK4_NAJHA	P01461 naja haje a
872	37	46.2	895	2	Q63QK2_BURPS	Q63qk2 burkholderi	36	45.0	60	1	CK5_NAJHA	P01464 naja haje a
873	37	46.2	1006	2	Q5U4R2_XENLA	Q5u4r2 xenopus lae	36	45.0	60	1	CK5_NAJHH	P01457 naja haje h
874	37	46.2	1045	2	Q6Z1W9_ORYSA	Q6z1w9 oryza sativ	36	45.0	60	1	CK6_NAJHA	P01465 naja haje a
875	37	46.2	1076	2	Q5ZMV4_CHICK	Q5zmv4 gallus gall	36	45.0	60	1	CK7_NAJHA	P01466 naja haje a
876	37	46.2	1076	2	Q5Z1O7_CHICK	Q5z1o7 gallus gall	36	45.0	60	1	CK8_NAJHA	P01460 naja haje a
877	37	46.2	1090	2	Q4UI35_THEAN	Q4ui35 theileria a	36	45.0	66	2	Q9LBZ3_STAAU	Q9lbz3 staphylococ
878	37	46.2	1122	2	Q6PU69_FRIPA	Q6pu69 pristinonchu	36	45.0	72	2	Q98XM9_9HIV1	Q98xm9 human immu
879	37	46.2	1161	2	Q7QJQ7_ANOGA	Q7qjq7 anopheles g	36	45.0	73	2	Q4Z1L0_PLABE	Q4z1l0 plasmodium
880	37	46.2	1198	2	Q5CUP9_CRYPV	Q5cup9 cryptocospori	36	45.0	76	2	Q91LC2_WSSV	Q91lc2 white spot
881	37	46.2	1279	2	Q54112_DICDI	Q54112 dictyosteli	36	45.0	76	2	Q91LC3_WSSV	Q91lc3 white spot
882	37	46.2	1293	2	Q7R6A1_GIALA	Q7r6a1 giardia lam	36	45.0	81	1	TRGS_TACTR	P81281 tachypleus
883	37	46.2	1317	2	Q7RH57_PLAYO	Q7rh57 plasmodium	36	45.0	83	2	Q4PN14_IXOSC	Q4pn14 ixodes scap
884	37	46.2	1340	2	Q8NDA2_HUMAN	Q8nda2 homo sapien	36	45.0	88	2	Q4PN13_IXOSC	Q4pn13 ixodes scap
885	37	46.2	1365	1	SUZ2_DROME	P25172 drosophila	36	45.0	102	2	Q8AX97_FUGRU	Q8ax97 fugu rubrip
886	37	46.2	1368	2	Q9V630_DROME	Q9v630 drosophila	36	45.0	105	2	Q8C775_MOUSE	Q8c775 mus musculu
887	37	46.2	1392	2	Q4T9K3_TETNG	Q4t9k3 tetradon n	36	45.0	108	2	Q5VX84_HUMAN	Q5vx84 homo sapien
888	37	46.2	1519	2	Q6Q193_RAT	Q6q193 rattus norv	36	45.0	108	2	Q8CA52_MOUSE	Q8ca52 mus musculu
889	37	46.2	1557	2	Q4H3F1_CIOIN	Q4h3f1 ciona intes	36	45.0	114	2	Q9D8K6_MOUSE	Q9d8k6 mus musculu
890	37	46.2	1652	2	Q9VC36_DROME	Q9vc36 drosophila	36	45.0	125	2	Q54KP3_DICDI	Q54kp3 dictyosteli
891	37	46.2	1654	2	Q7YU13_DROME	Q7yu13 drosophila	36	45.0	131	2	Q92PC2_RHIME	Q92pc2 rhizobium m
892	37	46.2	1748	1	POLR_ELV	P35928 erysimum la	36	45.0	132	2	Q6Z212_ORYSA	Q6z212 oryza sativ
893	37	46.2	1748	2	Q549T0_ELV	Q549t0 erysimum la	36	45.0	133	2	Q6HI99_BACHK	Q6hi99 bacillus th
894	37	46.2	1787	2	Q8FW32_CANGA	Q8fw32 candida gla	36	45.0	138	2	Q02107_CAEBL	Q02107 caenorhabdi
895	37	46.2	1844	2	Q8IKX2_PLAF7	Q8ikx2 plasmodium	36	45.0	139	2	Q7YX35_CRYPV	Q7yx35 cryptospori
896	37	46.2	1947	2	Q4N896_THEPA	Q4n896 theileria p	36	45.0	139	2	Q4Z7B0_PLABE	Q4z7b0 plasmodium
897	37	46.2	2053	2	Q5XL62_TETTH	Q5xl62 tetrahymena	36	45.0	146	2	Q5CWM4_CRYHO	Q5cwm4 cryptospori
898	37	46.2	2073	2	Q94LW0_ORYSA	Q94lw0 oryza sativ	36	45.0	143	2	Q9DE52_CHICK	Q9de52 gallus gall
899	37	46.2	2155	1	TECTA_HUMAN	Q75443 homo sapien	36	45.0	144	2	Q9ZPR8_ARATH	Q9zpr8 arabidopsis
900	37	46.2	2155	1	TECTA_MOUSE	Q08523 mus musculu	36	45.0	144	2	Q8RDZ6_FUSNN	Q8rdz6 fusobacteri
901	37	46.2	2429	2	Q4PAD1_USTMA	Q4pad1 ustilago ma	36	45.0	146	2	Q8CA58_MOUSE	Q8ca58 mus musculu
902	37	46.2	2531	2	Q6TXE7_RAT	Q6txe7 rattus norv	36	45.0	148	2	Q7VPX6_CHLEPN	Q7vpx6 chlamydia p
903	37	46.2	3182	2	Q7QV55_GIALA	Q7qv55 giardia lam	36	45.0	149	2	Q9NVK6_HUMAN	Q9nvk6 homo sapien
904	37	46.2	3283	2	Q7RP14_PLAYO	Q7rp14 plasmodium	36	45.0	153	1	VIBG_ECOLI	P32106 escherichia
905	36.5	45.6	67	1	BD09_MOUSE	Q8z1c6 mus musculu	36	45.0	153	2	Q9BUZ2_HUMAN	Q9bu22 homo sapien
906	36.5	45.6	105	1	VORD_PYRAB	Q9uyz0 pyrococcus	36	45.0	153	2	Q93AB0_YERPE	Q93abo yersinia pe
907	36.5	45.6	105	1	VORD_PYRFU	Q51800 pyrococcus	36	45.0	153	2	Q8XDH3_ECO57	Q8xdh3 escherichia

981 36 45.0 154 2 Q9K271 CHLPPN
 982 36 45.0 154 2 Q4K001_STRPN
 983 36 45.0 155 2 Q5VX85_HUMAN
 984 36 45.0 163 2 Q8VB89_WSSV
 985 36 45.0 164 2 Q8BQR9_MOUSE
 986 36 45.0 169 2 Q59VN3_CANAL
 987 36 45.0 171 2 Q928K4_CHLPPN
 988 36 45.0 171 2 Q8CKK6_CHLTE
 989 36 45.0 172 2 Q5BNF2_SCHJA
 990 36 45.0 174 2 Q6ZGF0_ORISA
 991 36 45.0 179 2 Q8ZV24_PYRAE
 992 36 45.0 180 2 Q7D3B8_AGR75
 993 36 45.0 180 2 Q9Z1Z4_BORBU
 994 36 45.0 183 2 Q9PVD6_BRARE
 995 36 45.0 186 2 Q9BZ94_HUMAN
 996 36 45.0 186 2 Q91XW7_HEPC
 997 36 45.0 201 2 Q503B7_BRARE
 998 36 45.0 204 2 Q9UPN9_HUMAN
 999 36 45.0 204 2 Q864T3_SHEEP
 1000 36 45.0 204 2 Q9R1S0_MOUSE

ALIGNMENTS

RESULT 1
 Q22426 CABEL PRELIMINARY; PRT; 1302 AA.
 ID Q22426 CABEL PRELIMINARY; PRT; 1302 AA.
 AC Q22426;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Twik family of potassium channels protein 2.
 GN Name=twk-2; ORFNames=TI2C9.3;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RC MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; U41104; AAK18976.2; -; Genomic DNA.
 DR Ensembl; TI2C9.3; Caenorhabditis elegans.
 DR WormBase; WBGene0000657; twk-2.
 DR WormPep; TI2C9.3; CE36894.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0005267; P:potassium channel activity; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR005560; DUF326.
 DR InterPro; IPR001622; K-channel_pore.
 DR Pfam; PF03860; DUF326; 3.
 KW Complete proteome; Ionic channel.
 SQ SEQUENCE 1302 AA; 148653 MW; DA737D251C81548A CRC64;

Query Match 62.5%; Score 50; DB 2; Length 1302;
 Best Local Similarity 77.8%; Pred. No. 75;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTCT 11
 :|:|:|:|:|
 Db 814 FYSEFWKTCT 822

RESULT 2
 Q84MY4 ORISA
 ID Q84MY4 ORISA PRELIMINARY; PRT; 370 AA.
 AC Q84MY4;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative initiation factor 2 alpha kinase.
 GN ORFNames=O803G04000;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.,
 Buell C., Tsirlin T., Kim M., Bera J., Jin S., Padrosh D.,
 Tallon L., Koo H., Ziemann V., Hsiiao J., Blunt S., Vanaken S.,
 Riedmuller S., Utterback T., Feidblyum T., Yang Q., Haas B., Suh B.,
 Peterson J., Quackenbush J., White O., Salzberg S., Fraser C.;
 Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell R.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AC092778; AAP12907.1; -; Genomic DNA.
 DR Gramene; Q84MY4; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Initiation factor; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 370 AA; 42462 MW; F18D0871C3B3F504 CRC64;
 Query Match 60.0%; Score 48; DB 2; Length 370;
 Best Local Similarity 55.6%; Pred. No. 46;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 CYCFWKTCT 10
 :|:|:|:|:|
 Db 14 CYFCLWPSC 22
 RESULT 3
 Q7MNB7 VIBVY
 ID Q7MNB7_VIBVY PRELIMINARY; PRT; 507 AA.
 AC Q7MNB7;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Hypothetical protein VV0800.
 GN OrderedLocustNames=VV0800;
 OS Vibrio vulnificus (strain YJ016).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=196600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=1465965; DOI=10.1101/gr.1295503;
 RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
 Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
 Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
 "Comparative genome analysis of Vibrio vulnificus, a marine
 pathogen.";
 RL Genome Res. 13:2577-2587(2003).
 DR EMBL; BA000037; BAC93564.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.

```

SQ SEQUENCE 507 AA; 58254 MW; FPFCAE282CC756EA CRC64;
Query Match 60.0%; Score 48; DB 2; Length 507;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
Db 394 YCFWKSC 400
|||||:|
|:|:|:|

RESULT 4
O6G3K0 BARHE
ID O6G3K0 BARHE PRELIMINARY; PRT; 117 AA.
AC O6G3K0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BH07670;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=38323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 49882 / Houston 1;
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Almark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canback B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scola B., Holmberg M., Andersson S.G.E.;
RT "The house-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAP27568.1; -; Genomic_DNA.
DR InterPro; IPR002696; DUF37.
DR Pfam; PF01809; DUF37; 1.
DR ProDom; PD04225; DUF37; 1.
DR TIGRFAMs; TIGR00278; DUF37; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 117 AA; 13758 MW; 3393CBD2947B0C83 CRC64;

Query Match 56.9%; Score 45.5; DB 2; Length 117;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 7; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 1 YCYT---CFWKTC 11
Db 100 YCFKPCWCKIST 113
|||||:|
|:|:|:|

RESULT 5
Q4W5B9 HUMAN
ID Q4W5B9 HUMAN PRELIMINARY; PRT; 92 AA.
AC Q4W5B9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein UGT2B11 (Fragment).
GN Name=UGT2B11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holmes A., Haglund K.;
RT "The sequence of Homo sapiens BAC clone RP13-644M16.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;

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RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC111000; AAY41046.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 92 AA; 10894 MW; D479BBF2D398A475 CRC64;

Query Match 56.2%; Score 45; DB 2; Length 92;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYTCFWK 8
Db 74 FCLFCFWK 81
|||||
|:|:|:|

RESULT 6
YKQ3 SCHPO
ID YKQ3 SCHPO STANDARD; PRT; 204 AA.
AC Q9P6M2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein C688.03c in chromosome I.
GN ORFNames=SPAC688.03c;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoeft A., Fritze C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Leirach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Botashkin J.,
RA Shpakowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- SIMILARITY: Contains 1 ANMECR1 domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not

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CC removed.
CC -----
DR EMBL; AL355632; CAB90770.1; -; Genomic_DNA.
DR GeneDB Spombe; SPAC688.03c; -.
DR InterPro; IPR002733; AMMECR1.
DR PANTHER; PTHR13016; DUF51; 1.
DR Pfam; PF01871; AMMECR1; 1.
DR ProDom; PD009671; DUF51; 1.
DR TIGRFAMs; TIGR00296; AMMECR1; 1.
DR PROSITE; PS51112; AMMECR1; 1.
DR Complete proteome; Hypothetical protein.
FT DOMAIN 6 200 AMMECR1.
SQ SEQUENCE 204 AA; 23565 MW; 1CF3B044CDD9C858 CRC64;

Query Match 56.2%; Score 45; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YCYVCF 6
Db 17 YCYVCF 22

RESULT 7
Q52TG4_9POAL PRELIMINARY; PRT; 515 AA.
ID Q52TG4_9POAL PRELIMINARY; PRT; 515 AA.
AC Q52TG4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Maturase K.
GN Name=matK;
OS Cyperus alternifolius.
OC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Cyperaceae; Cyperus.
CC NCBI_TaxID=4611;
RW [1]
RP NUCLEOTIDE SEQUENCE.
RA Li X.X., Zhou Z.K.;
RT "Monocotyledons phylogeny based on three genes (matK, rbcL and 18S
RT xDNA sequences.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probably assists in splicing chloroplast group II
CC -1- Introns (by similarity).
DR EMBL; AY952421; AAX84503.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0008380; P:RNA splicing; IEA.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
DR Chloroplast; mRNA processing.
SQ SEQUENCE 515 AA; 62095 MW; 9CD01D4E837D2866 CRC64;

Query Match 56.2%; Score 45; DB 2; Length 515;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYVCFWK 8
Db 307 YCFVCFWQ 314

RESULT 8
UDB11 HUMAN
ID UDB11 HUMAN STANDARD; PRT; 529 AA.
AC U75310;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE UDP-glucuronosyltransferase 2B11 precursor (EC 2.4.1.17) (UDPGT).
GN Name=UGT2B11;

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98340847; PubMed=9675083; DOI=10.1006/bbrc.1998.8908;
RA Beaulieu M., Levesque E., Hum D.W., Belanger A.;
RT "Isolation and characterization of a human orphan UDP-
RL glucuronosyltransferase, UGT2B11.";
RN Biochem. Biophys. Res. Commun. 248:44-50 (1998).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: UDPGT is of major importance in the conjugation and
CC subsequent elimination of potentially toxic xenobiotics and
CC endogenous compounds.
CC -1- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
CC beta-D-glucuronoside.
CC -1- SUBCELLULAR LOCATION: Microsomal.
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF016492; AAC27891.1; -; mRNA.
DR EMBL; BC069441; AAH69441.1; -; mRNA.
DR Ensembl; ENSG00000198277; Homo sapiens.
DR HGNC; HGNC:12545; UGT2B11.
DR MIM; 603064; -.
DR GO; GO:0008210; P:estrogen metabolism; TAS.
DR GO; GO:0006805; P:xenobiotic metabolism; TAS.
DR InterPro; IPR002213; UDP_glucos_trans.
DR PANTHER; PTHR11926; UDP_Glucos_trans; 1.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
DR Endoplasmic reticulum; Glycoprotein; Glycosyltransferase; Microsome;
KW Multigene family; Signal; Transferase; Transmembrane.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 529 UDP-glucuronosyltransferase 2B11.
FT TRANSMEM 493 513 Potential.
FT CARBOHYD 315 315 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 529 AA; 61038 MW; CB4AC3C71CFC2AB4 CRC64;

Query Match 56.2%; Score 45; DB 1; Length 529;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 YCYCFWK 8
Db      511 FCLFCFWK 518

RESULT 9
UDB28_HUMAN
ID   UDB28_HUMAN STANDARD; PRT; 529 AA.
AC   Q9BY64; Q9BY62; Q9BY63;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   UDP-glucuronosyltransferase 2B28 precursor (EC 2.4.1.17) (UDPGT).
GN   Name=UGT2B28;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE, ALTERNATIVE SPLICING, AND CHARACTERIZATION.
RX      MEDLINE=21197745; PubMed=11300766; DOI=10.1021/bi002607y;
RA      Lyesque E., Turgeon D., Carrier J.-S., Montminy V., Beaulieu M.,
RA      Belanger A.;
RT      "Isolation and characterization of the UGT2B28 cDNA encoding a novel
RL      human steroid conjugating UDP-glucuronosyltransferase.";
CC      Biochemistry 40:3869-3881(2001).
CC      -1- FUNCTION: UDPGTs are of major importance in the conjugation and
CC      subsequent elimination of potentially toxic xenobiotics and
CC      endogenous compounds. This isozyme has glucuronidating capacity
CC      with steroid substrates such as 5-beta-androstane 3-alpha,17-beta-
CC      diol, estradiol, ADT, eugenol and bile acids. Only isoform 1 seems
CC      to be active.
CC      -1- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
CC      beta-D-glucuronoside.
CC      -1- SUBCELLULAR LOCATION: Microsomal.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=1; Synonym=I;
CC      IsoId=Q9BY64-1; Sequence=Displayed;
CC      Name=2; Synonym=II;
CC      IsoId=Q9BY64-2; Sequence=VSP_006710, VSP_006711;
CC      Name=3; Synonym=III;
CC      IsoId=Q9BY64-3; Sequence=VSP_006712;
CC      -1- TISSUE SPECIFICITY: Expressed in the liver, breast and kidney.
CC      -1- SIMILARITY: Belongs to the UDP-glycosyltransferase family.

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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DR   EMBL; AF177272; AAK31807.1; -; mRNA.
DR   EMBL; AF177273; AAK31808.1; -; mRNA.
DR   EMBL; AF177274; AAK31809.1; -; mRNA.
DR   Ensembl; ENSG00000135226; Homo sapiens.
DR   HGNC; HGNC:13479; UGT2B28.
DR   MIM; 606497; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0008152; P:metabolism; IDA.
DR   GO; GO:0006805; P:xenobiotic metabolism; IDA.
DR   InterPro; IPR002213; UDP_Glucos_trans.
DR   PANTHER; PTHR11926; UDP_Glucos_trans; 1.
DR   Pfam; PF00201; UDPGT; 1.
DR   PROSITE; PS00375; UDPGT; 1.
KW   Alternative splicing; Endoplasmic reticulum; Glycoprotein;
KW   Glycosyltransferase; Microsome; Multigene family; Signal; Transferase;
KW   Transmembrane.
FT   SIGNAL      1      24      Potential.
FT   CHAIN       25     529     UDP-glucuronosyltransferase 2B28.
FT   TRANSMEM    495     517     Potential.
FT   CARBOHYD    315     315     N-linked (GlcNAc... ) (Potential).

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FT   VARSPLIC   105    221    Missing (in isoform 3).
FT   VARSPLIC   335    335    V -> I (in isoform 2).
FT   VARSPLIC   336    529    /FTId=VSP_006710.
FT   VARSPLIC   529    529    Missing (in isoform 2).
FT   VARSPLIC   529    529    /FTId=VSP_006711.
SQ   SEQUENCE 529 AA; 60906 MW; 8C75277E964690C1 CRC64;
Query Match
Best Local Similarity 56.2%; Score 45; DB 1; Length 529;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy      1 YCYCFWK 8
Db      511 FCLFCFWK 518

RESULT 10
Q5CR06_CRYPV PRELIMINARY; PRT; 814 AA.
AC   Q5CR06;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Oxyesterol binding protein 1A-like pleckstrin homology (PH) domain
DE   containing protein.
GN   ORFNames=cg44_2580;
OS   Cryptosporidium parvum.
OC   Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC   Cryptosporidiidae; Cryptosporidium.
OX   NCBI_TaxID=5807;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      STRAIN=Iowa type II;
RX      PubMed=15044751; DOI=10.1126/science.1094786;
RA      Abrahamson M.S., Templeton T.J., Enomoto S., Abrahamante J.E., Zhu G.,
RA      Lantzo C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
RA      Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
RA      Anantharaman V., Aravind L., Kapur V.;
RT      "Complete genome sequence of the apicomplexan, Cryptosporidium
RT      parvum.";
RL      Science 304:441-445(2004).
CC      -1- SIMILARITY: Contains 1 PH domain.
DR   EMBL; AAEE01000008; EAK87842.1; -; Genomic_DNA.
DR   GO; GO:0008202; P:steroid metabolism; IEA.
DR   InterPro; IPR000648; Oxyesterol_bd.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011993; PH type.
DR   Pfam; PF01237; Oxyesterol_BP; 1.
DR   Pfam; PF00169; PH; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
SQ   SEQUENCE 814 AA; 95280 MW; E47061C4F2A020C8 CRC64;
Query Match
Best Local Similarity 55.2%; Score 45; DB 2; Length 814;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      2 CYCCFWK 8
Db      345 CYCCFWK 351

RESULT 11
Q96CY8_HUMAN
ID   Q96CY8_HUMAN PRELIMINARY; PRT; 96 AA.
AC   Q96CY8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   MAX protein, isoform d.
GN   Name=MAX;
OS   Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Director MGC Project;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; BC013669; AAH13669.1; -; mRNA.
 DR HSSP; P61244; 1HLO.
 DR SRS; Q96CV8; 13-57.
 DR Ensembl; ENSG00000125952; Homo sapiens.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR002418; TF_Myc.
 DR Pfam; PF00010; HLH; 1.
 DR PRINTS; PR00044; LEUZIPRMYC.
 DR SMART; SM00353; HLH; 1.
 DR PROSITE; PS08888; HLH; 1.
 SQ SEQUENCE 96 AA; 11455 MW; D380F721DCF2D6C8 CRC64;
 Query Match 55.0%; Score 44; DB 2; Length 96;
 Best Local Similarity 66.7%; Pred. No. 51;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 YYCFWKTC 11
 Db 59 YFLFWKLC 67
 RESULT 12
 ID Q800X8 CHESE PRELIMINARY; PRT; 107 AA.
 AC Q800X8
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE GABA transporter GAT-3 (Fragment).
 OS Chelydra serpentina serpentina (common snapping turtle).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
 OX NCBI_TaxID=134619;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21876906; PubMed=11882478;
 RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
 RT "Octylphenol (OP) alters the expression of members of the amyloid
 protein family in the hypothalamus of the snapping turtle, Chelydra
 serpentina serpentina".
 RL Environ. Health Perspect. 110:269-275(2002).
 DR EMBL; AF469182; AA048729.1; -; mRNA.
 DR GO; GO:0005887; C:integral to plasma membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005328; F:neurotransmitter:sodium symporter activity; IEA.
 DR GO; GO:0015293; F:symporter activity; IEA.
 DR GO; GO:0006836; P:neurotransmitter transport; IEA.
 DR InterPro; IPR000175; Na/nttran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PROSITE; PS0267; NA_NEUROTRAN_SYM_3; 1.
 FT NON_TER 1 107
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 12175 MW; 5592D41B90F18579 CRC64;
 Query Match 55.0%; Score 44; DB 2; Length 107;
 Best Local Similarity 71.4%; Pred. No. 56;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 CYCFWFK 8
 Db 71 CYFCIWK 77
 RESULT 13
 ID Q4TB59 TETNG PRELIMINARY; PRT; 108 AA.
 AC Q4TB59;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF7196, whole genome shotgun sequence.
 GN (Fragment).
 DN ORFNames=GSTENG0003901001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontoidea; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Luthalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., Mesirov J.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Kahn D., Robinson-Rechavi M.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Scarpelli C.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Mincker P., Lander E.S., Weissenbach J., Roest Croliius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype".
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; CAAS01007196; CAF89873.1; -; Genomic_DNA.
 FT NON_TER 1 108
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11968 MW; 62FBA62PDF7A4D06 CRC64;
 Query Match 55.0%; Score 44; DB 2; Length 108;


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Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFCWK 8
Db 68 CYFCWK 74

RESULT 14
Q6TLC5.APIME
ID Q6TLC5.APIME PRELIMINARY; PRT; 203 AA.
AC Q6TLC5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE GABA neurotransmitter transporter-1A (Fragment).
GN Name=GAT-A;
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dutton P.J.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY395073; AAC96729.1; -; mRNA.
DR Ensembl; ENSAPMG0000002726; Apis mellifera.
DR GO; GO:0005887; C:integral to plasma membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005328; F:symporter activity; IEA.
DR GO; GO:0015293; F:symporter activity; IEA.
DR GO; GO:0006836; P:neurotransmitter transport; IEA.
DR InterPro; IPR00175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00209; NANEUSMPORT.
DR PROSITE; PS00610; NA_NEUOTRAN_SYMP_1; 1.
DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
KW Symport; Transmembrane; Transport.
FT NON_TER 1 203
FT NON_TER 203 203
SQ SEQUENCE 203 AA; 23346 MW; 772C2D635E1A2C9C CRC64;

Query Match 55.0%; Score 44; DB 2; Length 203;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFCWK 8
Db 187 CYFCWK 193

RESULT 15
DMA_SQUAC
ID DMA_SQUAC STANDARD; PRT; 245 AA.
AC P36963;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Proteolipid protein DM alpha.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hypnosqualea; Squaliformes; Squaloidei;
OC Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TSSUS=Brain;
RC MEDLINE=9400810; PubMed=8398138; DOI=10.1016/0896-6273(93)90148-K;
RA Kitagawa K., Sinoway M.P., Yang C., Gould R.M., Colman D.R.;
RT "A proteolipid protein gene family: expression in sharks and rays and
possible evolution from an ancestral gene encoding a pore-forming
RT polypeptide.";
```

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Neuron 11:433-448(1993).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- TISSUE SPECIFICITY: Highly expressed in white matter in
myelinating shark brain.
-1- SIMILARITY: Belongs to the myelin proteolipid protein family.
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-----
EMBL; U02973; AAC59639.1; -; mRNA.
DR PIR; I51323; I51323.
DR InterPro; IPR001614; Myelin_PLP.
DR PANTHER; PTHR11683; Myelin_PLP; 1.
DR Pfam; PF01275; Myelin_PLP_1.
DR PRINTS; PR00214; MYELINPLP.
DR SMART; SM00002; PLP; 1.
DR PROSITE; PS00575; MYELIN_PLP_1; 1.
DR PROSITE; PS01004; MYELIN_PLP_2; 1.
KW Myelin; Transmembrane.
FT TRANSMEM 19 35 Potential.
FT TRANSMEM 71 87 Potential.
FT TRANSMEM 117 133 Potential.
FT TRANSMEM 204 220 Potential.
SQ SEQUENCE 245 AA; 26910 MW; 521B0A11076B16CS CRC64;

Query Match 55.0%; Score 44; DB 1; Length 245;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YCYCFWK 10
Db 140 YIYTWSTC 149

RESULT 16
Q4TB60.TETNG
ID Q4TB60.TETNG PRELIMINARY; PRT; 253 AA.
AC Q4TB60;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF195, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG000390001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lufalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Carra G., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
```

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; CAAB01007195; CAF89872.1; -; Genomic_DNA.

DR InterPro; IPR000175; Na/ntran_sympor.

DR Pfam; PF00209; SNF; 1.

DR PRINTS; PR00176; NAMEUSMPORT.

DR PROSITE; PS0267; NA NEUROTRAN SYMP_3; 1.

DR SYMPOR; Transmembrane; Transport.

KW Non_Ter 1

FT Non_Ter 253

SQ SEQUENCE 253 AA; 28323 MW; F26C0C519DE0F3BF CRC64;

Query Match 55.0%; Score 44; DB 2; Length 253;

Best Local Similarity 71.4%; Pred. No. 1.2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8

Db 160 CYCFWK 166

RESULT 17

HTPX_METH

ID_HTPX_METH STANDARD; PRT; 258 AA.

AC 026659;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Probable protease htpx homolog (EC 3.4.24.-).

GN Name=htpx; OrderedLocNames=MTS569;

OS Methanobacterium thermoautotrophicum.

OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;

OC Methanobacteriaceae; Methanothermobacter.

OX NCBI_TaxID=187420;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Delta H;

RX MEDLINE=98037514; PubMed=9371463;

RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

RA Jivani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,

RA Daniele C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

RT "Complete genome sequence of Methanobacterium thermoautotrophicum

deltaH: functional analysis and comparative genomics.";

RL J. Bacteriol. 179:7135-7155(1997).

CC -!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the peptidase M48 family.

CC -----

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CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

DR EMBL; AE000839; AAB85075.1; -; Genomic_DNA.

DR PIR; C69175; C69175.

DR HAMAP; MF_00188; atypical; 1.

DR InterPro; IPR006025; Pept_M_Zn_BS.

DR Pfam; PF01435; Peptidase M48.

DR PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.

KW Complete proteome; Hydrolase; Metal-binding; Metalloprotease;

KW Protease; Transmembrane; Zinc

FT TRANSMEM 24 44 Potential.

FT TRANSMEM 45 65 Potential.

FT TRANSMEM 157 177 Potential.

FT TRANSMEM 186 206 Potential.

FT ACT SITE 147 147 By similarity.
 FT METAL 146 146 Zinc (catalytic) (By similarity).
 FT METAL 150 150 Zinc (catalytic) (By similarity).
 SQ SEQUENCE 258 AA; 28605 MW; DBD9884292ABFAL3 CRC64;

Query Match 55.0%; Score 44; DB 1; Length 258;

Best Local Similarity 75.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CYCFWK 9

Db 169 CYCFWK 176

RESULT 18

Q9SDR9_PRUDU

ID_Q9SDR9_PRUDU PRELIMINARY; PRT; 266 AA.

AC Q9SDR9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Lecithin-cholesterol acyl transferase (Fragment).

GN Name=LCA1;

OS Prunus dulcis (Almond) (Prunus amygdalus).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.

OX NCBI_TaxID=3755;

RN NUCLEOTIDE SEQUENCE.

RP Ma R.C., Oliveira M.M.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF209309; AAF22841.1; -; Genomic DNA.

DR GO; GO:0004607; P:phosphatidylcholine-sterol O-acyltransferase.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006629; P:lipid metabolism; IEA.

DR InterPro; IPR003386; LACT.

DR InterPro; IPR000379; Ser_estra.

DR Pfam; PF02450; LACT; 1.

KW Transferase.

FT NON_TER 1

SQ SEQUENCE 266 AA; 29613 MW; 057533E294332F37 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 266;

Best Local Similarity 75.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YYCFWKTC 10

Db 166 YLCFWKWC 173

RESULT 19

Q9UIK8_HUMAN

ID_Q9UIK8_HUMAN PRELIMINARY; PRT; 269 AA.

AC Q9UIK8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE HRIHP2063 protein (Fragment).

GN Name=HRIHP2063;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Brain;

RA Ueki N.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB015349; BAA08120.1; -; mRNA.

FT NON_TER 1

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SQ SEQUENCE 269 AA; 28713 MW; 083196F0BA9CCFAD CRC64;
Query Match 55.0%; Score 44; DB 2; Length 269;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YCYICFWKTC 10
    |||||
Db 79 YCYPCTWGDC 88

RESULT 20
Q8Y800 LISMO
ID Q8Y800 LISMO PRELIMINARY; PRT; 285 AA.
AC Q8Y800;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lmol119 protein.
GN OrderedLocusNames=lmol119;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Donann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fshli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Varquez-Boland J.-A., Voss H., Wehlend J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591977; CAC99197.1; -, Genomic_DNA.
DR PIR; AG1214; AG1214.
DR Litolist; LMol119; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR InterPro; IPR002294; D12N6 mtfase.
DR PRINTS; PR00505; D12N6MTFRASE.
KW Complete proteome.
SQ SEQUENCE 285 AA; 33446 MW; AAD3BA211F7C15AD CRC64;
Query Match 55.0%; Score 44; DB 2; Length 285;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYICFWKTC 9
    |||||
Db 61 YSIICFWKS 69

RESULT 21
Q6ATD1 ORYSA
ID Q6ATD1 ORYSA PRELIMINARY; PRT; 342 AA.
AC Q6ATD1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative peroxisome assembly protein 2.
GN Name=OSJNBa0018H09.15;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.

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OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I. C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F., *McCombie W.R., *de la Bastide M., *Spiegel L.,
RA *Zutavern T., *Muller S., *Nascimento L., *Balija V., *Bell M.,
RA *Miller B., *Katzenberger F., *Andrade M.V., *Dike S.,
RA *O'Shaughnessy A., *Palmer L.;
RT "Oryza sativa (japonica cultivar-group) chromosome 5 BAC clone
RT OSJNBa0018H09, complete sequence.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Peroxisomal; membrane-associated (By
CC similarity).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AC137610; AAT85132.1; -, Genomic_DNA.
DR Gramene; Q6ATD1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005777; C:peroxisome; IEA.
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR006845; Pex2_Pex12_N.
DR InterPro; IPR001841; Znf_RING.
DR Pfam; PF04757; Pex2_Pex12; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PSS0089; ZF_RING_2; 1.
KW Membrane; Metal-binding; Peroxisome; Zinc; Zinc-finger.
SQ SEQUENCE 342 AA; 39939 MW; B2E1A04C68B463E0 CRC64;
Query Match 55.0%; Score 44; DB 2; Length 342;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YCYICFWKTC 10
    |||||
Db 309 YCYICQTRC 318

RESULT 22
Q8BP26 MOUSE
ID Q8BP26 MOUSE PRELIMINARY; PRT; 355 AA.
AC Q8BP26;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 12 days embryo male wolffian duct includes surrounding
DE region cDNA, RIKEN full-length enriched library, clone:672040BE06
DE product:gamma-aminobutyric acid (GABA-A) transporter 3, full insert
DE sequence.
GN Name=Slc6a13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Wolffian duct includes surrounding region;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Wolffian duct includes surrounding region;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

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Db      257 CYFCIWK 263
||:| ||
RESULT 24
Q4RXE3_TETNG PRELIMINARY; PRT; 450 AA.
AC Q4RXE3;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 11 SCAP14979, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00027448001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Parra G., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., McEwan P., Bosak S.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crallius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014979; CAG06939.1; -; Genomic_DNA.
DR InterPro; IPR000175; Na/nttran_sympot.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPOT.
DR ProDom; PD000448; Na/nttran_sympot; 1.
DR PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
KW Symport; Transmembrane; Transport.
FT NON_TER 1 450
FT NON_TER 450 450
SQ SEQUENCE 450 AA; 51087 MW; 11E84E30B57F1813 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 450;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYTCFWK 8
Db 175 CYFCIWK 181
||:| ||

RESULT 25
Q7Q1J2_ANOQA PRELIMINARY; PRT; 484 AA.
AC Q7Q1J2;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ENSANGP00000014339 (Fragment).
GN ORFNames=GSTENG00007038001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Parra G., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., McEwan P., Bosak S.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crallius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014979; CAG06939.1; -; Genomic_DNA.
DR InterPro; IPR000175; Na/nttran_sympot.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPOT.
DR ProDom; PD000448; Na/nttran_sympot; 1.
DR PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
KW Symport; Transmembrane; Transport.
FT NON_TER 1 450
FT NON_TER 450 450
SQ SEQUENCE 450 AA; 51087 MW; 11E84E30B57F1813 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 450;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYTCFWK 8
Db 175 CYFCIWK 181
||:| ||

RESULT 26
Q4T522_TETNG PRELIMINARY; PRT; 491 AA.
AC Q4T522;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome undetermined SCAP9468, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00007038001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Parra G., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,

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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier P., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01009468; CAF92010.1; -; Genomic_DNA.
 DR InterPro; IPR000175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR PROSITE; PS00754; NA_NEUOTRAN_SYMP_2; 1.
 DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
 KW Symport; Transmembrane; Transport.
 FT NON_TER 491 491
 FT NON_TER 1 1
 SQ SEQUENCE 491 AA; 54917 MW; 825271642F3D1177 CRC64;
 Query Match 55.0%; Score 44; DB 2; Length 491;
 Best Local Similarity 71.4%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CYCFWK 8
 DB 152 CYFCWK 158
 ID Q6ZMW8 HUMAN PRELIMINARY; PRT; 501 AA.
 AC Q6ZMW8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLJ16816.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG TISSUE-THYMUS;
 RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 RA Yanahita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H.,
 RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
 RA Isegai T.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK131564; BAD18697.1; -; mRNA.
 DR GO; GO:0005887; C:integral to plasma membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005328; F:neurotransmitter:sodium symporter activity; IEA.
 DR GO; GO:0015293; F:symporter activity; IEA.
 DR GO; GO:0006836; P:neurotransmitter transport; IEA.
 DR InterPro; IPR00175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR PRODOM; PD000448; Na/ntran_symport; 1.
 DR PROSITE; PS00754; NA_NEUOTRAN_SYMP_2; 1.
 DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
 KW Symport; Transmembrane; Transport.
 SQ SEQUENCE 501 AA; 56343 MW; 3E90337635B79DC1 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 501;
 Best Local Similarity 71.4%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CYCFWK 8
 DB 160 CYFCWK 166
 ID Q4ST51 TETNG PRELIMINARY; PRT; 504 AA.
 AC Q4ST51;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 19 SCAF14302, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames-GSTENG00013119001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99893;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulin J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier P., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01014302; CAF96181.1; -; Genomic_DNA.
 DR InterPro; IPR000175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
 KW Symport; Transmembrane; Transport.
 FT NON_TER 504 504
 FT NON_TER 1 1
 SQ SEQUENCE 504 AA; 57180 MW; 12DA8DA2A2642731 CRC64;
 Query Match 55.0%; Score 44; DB 2; Length 504;
 Best Local Similarity 71.4%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CYCFWK 8
 DB 153 CYFCWK 159
 ID Q8IMC1 DROME PRELIMINARY; PRT; 508 AA.
 AC Q8IMC1;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CG1732-PB, isoform B.
 GN Name=CG1732; ORFNames=CG1732;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Mecoptera; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE
 RX MEDLINE=20196005; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foulke C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.J., Pacle B.J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-P., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537569;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacle B.J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., M.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacle B.J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003843; AAN06506.2; -; Genomic DNA.
 DR Ensembl; CG1732; Drosophila melanogaster.
 DR FlyBase; FBgn0039915; CG1732.
 DR GO; GO:0005887; C:integral to plasma membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005328; F:neurotransmitter:sodium symporter activity; IEA.
 DR GO; GO:0015293; F:symporter activity; IEA.
 DR GO; GO:0006836; P:neurotransmitter transport; IEA.
 DR InterPro; IPR001175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR PRODOM; PD000448; Na/ntran_symport; 1.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1; 1.
 DR PROSITE; PS0267; NA_NEUROTRAN_SYMPT_3; 1.
 DR SymPort; Transmembrane; Transport.
 DR SQ SEQUENCE 508 AA; 56774 MW; 026564B624CEFA CRC64;
 Query Match 55.0%; Score 44; DB 2; Length 508;
 Best Local Similarity 71.4%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CYTCFWK 8
 Db 263 CYFCWIK 269
 RESULT 30
 Q4T523 TETNG
 ID Q4T523 TETNG PRELIMINARY; PRT; 535 AA.
 AC Q4T523;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF9468, whole genome shotgun sequence.
 DE (Fragment).
 OS ORFNames=GSTENG0007037001;
 GN Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

```
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
```

```
CC EMBL; CAAE01014979; CAG07063.1; -; Genomic_DNA.
```

```
DR InterPro; IPR000175; Na/ntran_symport.
```

```
DR Pfam; PF00209; SNF_1
```

```
DR PRINTS; PR00176; NANEUSMPORT.
```

```
DR ProDom; PD000448; Na/ntran_symport; 1.
```

```
DR PROSITE; PS00610; NA_NEUOTRAN_SYMP_1; 1.
```

```
DR PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; 1.
```

```
DR PROSITE; PS00267; NA_NEUROTRAN_SYMP_3; 2.
```

```
KW Symport; Transmembrane; TransPort.
```

```
KW NON_TER
```

```
FT NON_TER 1
```

```
SQ SEQUENCE 565 AA; 63378 MW; EC90FB9D9457A016 CRC64;
```

```
Query Match 55.0%; Score 44; DB 2; Length 565;
```

```
Best Local Similarity 71.4%; Pred.No. 2.6e+02;
```

```
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 2 CYCYCFWK 8  
||:|||  
Db 209 CYFCIWK 215
```

```
RESULT 32
```

```
S6A13 HUMAN
```

```
ID SGA13 HUMAN STANDARD; PRT; 569 AA.
```

```
AC Q9NSD5;
```

```
DT 16-OCT-2001 (Rel. 40, Created)
```

```
DT 16-OCT-2001 (Rel. 40, Last sequence update)
```

```
DT 10-MAY-2005 (Rel. 47, Last annotation update)
```

```
DE Sodium- and chloride-dependent GABA transporter 2.
```

```
GN Names=SLC6A13;
```

```
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.
```

```
NCBI_TaxID=9606;
```

```
[1]
```

```
RN NUCLEOTIDE SEQUENCE.
```

```
RP TISSUE=Liver;
```

```
RC MEDLINE=21682564; PubMed=11824941; DOI=10.1139/cjpp-79-12-977;  
RA Gong Y., Zhang M., Cui L., Minuk G.Y.;
```

```
RT "Sequence and chromosomal assignment of a human novel cDNA: similarity  
to gamma-aminobutyric acid transporter.";
```

```
RL Can. J. Physiol. Pharmacol. 79:977-984(2001).
```

```
CC -1 FUNCTION: Terminates the action of GABA by its high affinity  
sodium-dependent reuptake into presynaptic terminals (By  
similarity).
```

```
CC -1 SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1 TISSUE SPECIFICITY: Expressed strongly in the kidney and to a  
lesser extent in the liver and brain.
```

```
CC -1 SIMILARITY: Belongs to the sodium:neurotransmitter symporter (SNP)  
family.
```

```
-----  
This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on it's  
use as long as its content is in no way modified and this statement is not  
removed.
```

```
EMBL; U76343; AAF64247.1; -; mRNA.  
Ensembl; ENSG0000010379; Homo sapiens.  
HGNC; HGNC:11046; SLC6A13.  
InterPro; IPR000175; Na/ntran_symport.  
PANTHER; PTHR11616; Na/ntran_symport; 1.  
Pfam; PF00209; SNF; 1.  
PRINTS; PR00176; NANEUSMPORT.  
ProDom; PD000448; Na/ntran_symport; 1.  
PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.  
PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; 1.  
PROSITE; PS00267; NA_NEUROTRAN_SYMP_3; 1.  
KW Glycoprotein; Multigene family; Neurotransmitter transport;  
KW Polypeptidism; Symport; Transmembrane; Transport.
```


FT TOPO DOM 1 22 Cytoplasmic (Potential).
 FT TRANSMEM 23 40 1 (Potential).
 FT TRANSMEM 51 70 2 (Potential).
 FT TRANSMEM 95 115 3 (Potential).
 FT TOPO DOM 116 187 Extracellular (Potential).
 FT TRANSMEM 188 206 4 (Potential).
 FT TRANSMEM 215 232 5 (Potential).
 FT TRANSMEM 268 285 6 (Potential).
 FT TRANSMEM 293 308 7 (Potential).
 FT TRANSMEM 341 360 8 (Potential).
 FT TRANSMEM 390 408 9 (Potential).
 FT TRANSMEM 425 445 10 (Potential).
 FT TRANSMEM 466 485 11 (Potential).
 FT TRANSMEM 505 523 12 (Potential).
 FT TOPO DOM 524 569 Cytoplasmic (Potential).
 FT CARBOHYD 151 151 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 155 155 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 160 160 N-linked (GlcNAc. .) (Potential).
 FT VARIANT 398 398 V-> I (in dBSNP:577294).
 FT SEQUENCE 569 AA; 63747 MW; EACD717A65A92563 CRC64;
 FT /FTid=VAR_011594.

Query Match 55.0%; Score 44; DB 1; Length 569;
 Best Local Similarity 71.4%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CYCFWK 8
 |||||
 Db 201 CYCFWK 207

RESULT 33

ID Q8BKGO MOUSE PRELIMINARY; PRT; 586 AA.
 AC Q8BKGO;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched
 DE library, clone:E13002N21 product:SODIUM- AND CHLORIDE-DEPENDENT GABA
 DE TRANSPORTER 3 homolog (Fragment).
 GN Name=gab4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Scambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guetincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuke S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RA The FANTOM Consortium,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitasuna T., Tashiro H., Itoh A.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada M.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multicapillary sequencer";
 RN Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Scambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guetincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,

Query Match

55.0%; Score 44; DB 2; Length 586;

Best Local Similarity 71.4%; Pred. No. 2.7e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8
Db 193 CYFCWK 199

RESULT 34
Q6TLC6 APIME
ID Q6TLC6 APIME PRELIMINARY; PRT; 593 AA.
AC Q6TLC6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE GABA neurotransmitter transporter-1B (Fragment).
GN Name=GAT-1B;
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY395072; AAQ96728.1; -; mRNA.
DR Ensembl; ENSAPMG0000008948; Apis mellifera.
DR GO; GO:0005887; C: integral to plasma membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0005328; F: neurotransmitter: sodium symporter activity; IEA.
DR GO; GO:0015233; F: symporter activity; IEA.
DR GO; GO:0006836; P: neurotransmitter transport; IEA.
DR GO; GO:0006836; P: symporter activity; IEA.
DR InterPro; IPR000175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR PROSITE; PS00610; NA_NEUROTRAN_SYM_1; 1.
DR PROSITE; PS00610; NA_NEUROTRAN_SYM_1; 1.
DR PROSITE; PS0267; NA_NEUROTRAN_SYM_3; 1.
DR Symport; Transmembrane; Transport.
FT NON_TER 1
SQ SEQUENCE 593 AA; 66885 MW; C1194BB039B2028E CRC64;

Query Match 55.0%; Score 44; DB 2; Length 593;
Best Local Similarity 71.4%; Pred. No. 2.7e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8
Db 220 CYFCWK 226

RESULT 35
Q25512 MANSE
ID Q25512 MANSE PRELIMINARY; PRT; 597 AA.
AC Q25512;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GABA neurotransmitter transporter.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Spingolidea;
OC Spingidae; Spinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RL Tissue=Embryo;
RC MEDLINE=95251402; PubMed=7733681; DOI=10.1006/abbi.1995.1258;
RX Mbungu D., Ross L.S., Gill S.S.;
RA "Cloning, functional expression, and pharmacology of a GABA transporter from Manduca sexta.";
RT Arch. Biochem. Biophys. 318:489-497(1995).
RN NUCLEOTIDE SEQUENCE.

DR EMBL; L40373; AAA92342.1; -; mRNA.
DR PIR; S65673; S65673.
DR GO; GO:0005887; C: integral to plasma membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0005328; F: neurotransmitter: sodium symporter activity; IEA.
DR GO; GO:0015233; F: symporter activity; IEA.
DR GO; GO:0006836; P: neurotransmitter transport; IEA.
DR InterPro; IPR000175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR PROSITE; PS00610; NA_NEUROTRAN_SYM_1; 1.
DR PROSITE; PS0267; NA_NEUROTRAN_SYM_3; 1.
DR Symport; Transmembrane; Transport.
SQ SEQUENCE 597 AA; 67720 MW; DBP6B9DF1AB58165 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 597;
Best Local Similarity 71.4%; Pred. No. 2.7e+02; Mismatches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8
Db 238 CYFCWK 244

RESULT 36
Q6PA82 XENLA
ID Q6PA82 XENLA PRELIMINARY; PRT; 600 AA.
AC Q6PA82;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68654 protein.
GN Name=MGC68654;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RC Tissue=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RA NUCLEOTIDE SEQUENCE.
RC Tissue=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
RT Dev. Dyn. 225:384-391(2002).
RN [3]
RA NUCLEOTIDE SEQUENCE.

RC TISSUE=Kidney;
RA Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC060418.1; -, mRNA.
DR GO; GO:0005887; C:integral to plasma membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005328; F:neurotransmitter:sodium symporter activity; IEA.
DR GO; GO:0015293; F:symporter activity; IEA.
DR GO; GO:0006836; P:neurotransmitter transport; IEA.
DR InterPro; IPR000175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom; PD000448; Na/ntran_symport; 1.
DR PROSITE; PS00610; NA NEUROTRAN SYMP 1; 1.
DR PROSITE; PS00754; NA NEUROTRAN SYMP 2; 1.
DR PROSITE; PS0267; NA NEUROTRAN SYMP_3; 1.
KW Symport; Transmembrane; Transport.
SQ SEQUENCE 600 AA; 67342 MW; 58749B524A8B930 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 600;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYFCFWK 8
||| ||
Db 222 CYFCIWK 228

RESULT 37
S6A13 MOUSE
ID S6A13_MOUSE STANDARD; PRT; 602 AA.
AC P31649;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sodium- and chloride-dependent GABA transporter 3 (GAT3).
GN Name=Sic6a13; Synonyms=Gabt3, Gab-3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney, and Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Aleschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smal M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-1- FUNCTION: Terminates the action of GABA by its high affinity
sodium-dependent reuptake into presynaptic terminals. Can also
transport beta-alanine and taurine.
-1- BIOPHYSICO-CHEMICAL PROPERTIES:
Kinetic parameters:
KM=18 uM for GABA;
KM=28 uM for beta-alanine;
KM=540 uM for taurine;
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: Brain, liver and kidney.
-1- DEVELOPMENTAL STAGE: Abundant in neonatal brain but not in adult
brain.
-1- SIMILARITY: Belongs to the sodium:neurotransmitter symporter (SNF)
family.

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use as long as its content is in no way modified and this statement is not
removed.

DR EMBL; L04663; -, NOT ANNOTATED_CDS; mRNA.
DR EMBL; BC023117; AAH23117.1; -, mRNA.
DR EMBL; BC029637; AAH29637.1; -, mRNA.
DR PIR; A44409; A44409.
DR Ensembl; ENSMUSG0000030108; Mus musculus.
DR MGI; MGI:95629; Slc6a13.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002981; GAT2 transporter.
DR InterPro; IPR000175; Na/ntran_symport.
DR PANTHER; PTHR11616; Na/ntran_symport; 1.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR01196; GAT2TRANSPORT.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom; PD000448; Na/ntran_symport; 1.
DR PROSITE; PS00610; NA NEUROTRAN SYMP 1; 1.
DR PROSITE; PS00754; NA NEUROTRAN SYMP 2; 1.
DR PROSITE; PS0267; NA NEUROTRAN SYMP 3; 1.
KW Glycoprotein; Multigene family; Neurotransmitter transport; Symport;
Transmembrane; Transport.
FT TOPO_DOM 1 40 Cytoplasmic (Potential).
FT TRANSMEM 41 61 1 (Potential).
FT TRANSMEM 69 88 2 (Potential).
FT TRANSMEM 113 133 3 (Potential).
FT TOPO_DOM 134 205 Extracellular (Potential).
FT TRANSMEM 206 224 4 (Potential).
FT TRANSMEM 233 250 5 (Potential).
FT TRANSMEM 286 303 6 (Potential).
FT TRANSMEM 315 336 7 (Potential).
FT TRANSMEM 369 388 8 (Potential).
FT TRANSMEM 418 436 9 (Potential).
FT TRANSMEM 453 473 10 (Potential).
FT TRANSMEM 494 513 11 (Potential).
FT TRANSMEM 533 551 12 (Potential).
FT TOPO_DOM 552 602 Cytoplasmic (Potential).
FT CARBOHYD 169 169 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 602 AA; 68285 MW; 372FE77F3126ABEA CRC64;
Query Match 55.0%; Score 44; DB 1; Length 602;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYFCFWK 8
||| ||
Db 219 CYFCIWK 225

RESULT 38
S6A13 RAT
ID S6A13_RAT STANDARD; PRT; 602 AA.

AC P31646;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Sodium- and chloride-dependent GABA transporter 2.
 DB Names=Slc6a13; Synonyms=Gabt2, Gat-2;
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Sprague-Dawley; TISSUE=Brain;
 RC MEDLINE=93016029; PubMed=1400419;
 RX Borden L.A., Smith K.E., Hartig P.R., Branchek T.A., Weinshank R.L.;
 RA "Molecular heterogeneity of the gamma-aminobutyric acid (GABA)
 RT transport system. Cloning of two novel high affinity GABA transporters
 RT from rat brain".
 RL J. Biol. Chem. 267:21098-21104(1992).
 CC -1- FUNCTION: Terminates the action of GABA by its high affinity
 CC sodium-dependent reuptake into presynaptic terminals.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Brain, retina, and peripheral tissues.
 CC -1- SIMILARITY: Belongs to the sodium:neurotransmitter symporter (SNF)
 CC family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR ENBL; M95762; AAA40602.1; -; mRNA.
 DR PIR; A45078; A45078.
 DR Ensembl; ENSRNOG00000012876; Rattus norvegicus.
 DR RGD; 620788; Slc6a13.
 DR GO; GO:0005332; F:gamma-aminobutyric acid:sodium symporter ac. . ; IDA.
 DR GO; GO:0042165; F:neurotransmitter binding; IDA.
 DR GO; GO:0006836; P:neurotransmitter transport; IDA.
 DR InterPro; IPR002981; GAT2 transporter.
 DR InterPro; IPR000175; Na/ntran_symport.
 DR PANTHER; PTHR11616; Na/ntran_symport; 1.
 DR Pfam; PF00209; SNF, 1.
 DR PRINTS; PR01196; GAT2TRNSPORT.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntran_symport; 1.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1; 1.
 DR PROSITE; PS00754; NA_NEUROTRAN_SYMPT_2; 1.
 DR PROSITE; PS50267; NA_NEUROTRAN_SYMPT_3; 1.
 DR Glycoprotein; Multigene family; Neurotransmitter transport; Symport;
 KW Transmembrane; Transport.
 KM TOPO_DOM 1 40 Cytoplasmic (Potential).
 KM FT 1 40
 KM TRANSMEM 41 88 1 (Potential).
 KM FT TRANSMEM 69 88 2 (Potential).
 KM FT TRANSMEM 113 133 3 (Potential).
 KM TOPO_DOM 134 205 Extracellular (Potential).
 KM FT TRANSMEM 206 224 4 (Potential).
 KM FT TRANSMEM 233 250 5 (Potential).
 KM FT TRANSMEM 286 303 6 (Potential).
 KM FT TRANSMEM 315 336 7 (Potential).
 KM FT TRANSMEM 369 388 8 (Potential).
 KM FT TRANSMEM 418 436 9 (Potential).
 KM FT TRANSMEM 453 473 10 (Potential).
 KM FT TRANSMEM 494 513 11 (Potential).
 KM FT TRANSMEM 533 551 12 (Potential).
 KM TOPO_DOM 552 602 Cytoplasmic (Potential).
 KM FT CARBOHYD 169 169 N-linked (GlcNAc. . .) (Potential).
 KM FT CARBOHYD 173 173 N-linked (GlcNAc. . .) (Potential).
 KM FT CARBOHYD 178 178 N-linked (GlcNAc. . .) (Potential).
 KM SQ SEQUENCE 602 AA; 68263 MW; CB7510BFA6ABF8C CRC64;

Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYTCFWK 8
|||
DB 219 CYFCWK 225

RESULT 39
Q8TCC2 HUMAN
ID ID Q8TCC2 HUMAN PRELIMINARY; PRT; 602 AA.
AC Q8TCC2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Solute carrier family 6 (Neurotransmitter transporter, GABA), member
DE 13.
DE NCBI_TaxID=9606;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TSSUE=Kidney;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshnyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney;
RC Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC022392; AAH22392.1; -; mRNA.
DR Ensembl: ENSG0000010379; Homo sapiens.
DR GO: GO:0005887; C:integral to plasma membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005332; F:gamma-aminobutyric acid:sodium symporter ac.; IEA.
DR GO: GO:0005328; F:neurotransmitter:sodium symporter activity; IEA.
DR GO: GO:0015293; F:symporter activity; IEA.
DR GO: GO:0006836; P:neurotransmitter transport; IEA.
DR InterPro: IPR002981; GAT2_transporter.
DR InterPro: IPR00175; Na/ntran_symport.
DR Pfam: PF00209; SNF; 1.
DR PRINTS: PR01196; GAT2TRNSPORT.
DR PRODOM: PD000176; NANEUSMPORT.
DR PROSITE: PD000448; Na/Ktrap_symport; 1.
DR PROSITE: PS00754; NA_NEUROTRAN_SYMPT_2; 1.
DR PROSITE: PSS0267; NA_NEUROTRAN_SYMPT_3; 1.
DR PROSITE: Transmembrane; TRANS.
SQ SEQUENCE 602 AA; 68008 MW; 3BA3AB4BABDC980 CRC64;

Query Match	55.0%	Score 44:	DB 2:	Length 602:

```

Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYTCFWK 8
Db 219 CYFCWK 225

RESULT 40
Q9NJ10.TRINI
ID Q9NJ10.TRINI PRELIMINARY; PRT; 608 AA.
AC Q9NJ10;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE High affinity GABA transporter.
GN Name=GAT;
OS Trichoplusia ni (Cabbage looper);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Noctuidae; Plusiinae; Trichoplusia.
OX NCBI_TaxID=7111;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99365990; PubMed=10436937; DOI=10.1016/S0965-1748(99)00039-9;
RA Gao X., McLean H., Caveney S., Donly C.;
RT "Molecular cloning and functional characterization of a GABA
RT transporter from the CNS of the cabbage looper, Trichoplusia ni.";
RL Insect Biochem. Mol. Biol. 29:609-623(1999).
DR EMBL; AF141930; AAF70819.1; -; mRNA.
DR GO; GO:0005887; C:integral to plasma membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005328; F:neurotransmitter:sodium symporter activity; IEA.
DR GO; GO:0015293; F:symporter activity; IEA.
DR GO; GO:0006836; P:neurotransmitter transport; IEA.
DR InterPro; IPR000175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom; PD000448; Na/ntran_symport; 1.
DR PROSITE; PS00610; NA_NEUROTRAN_SYM_1; 1.
DR PROSITE; PS00267; NA_NEUROTRAN_SYM_3; 1.
KW Symport; Transmembrane; Transport.
SQ SEQUENCE 608 AA; 68991 MW; 865ABFADE63991EA CRC64;

Query Match 55.0%; Score 44; DB 2; Length 608;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYTCFWK 8
Db 237 CYFCWK 243

RESULT 41
S6A12.CANFA
ID S6A12.CANFA STANDARD; PRT; 614 AA.
AC P27799;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Sodium- and chloride-dependent betaine transporter (Na+/Cl-
DE betaine/GABA transporter).
GN Name=SLC6A12;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1];
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Cocker spaniel; TISSUE=Kidney;
RX MEDLINE=92112724; PubMed=1370453;
RA Yamauchi A., Uchida S., Kwon H.M., Preston A.S., Robey R.B.,

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RA Garcia-Perez A., Burg M.B., Handler J.S.;
RT "Cloning of a Na(+)- and Cl(-)-dependent betaine transporter that is
RT regulated by hypertonicity.";
RL J. Biol. Chem. 267:649-652(1992).
[2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=95166770; PubMed=7862636;
RA Takenaka M., Bagnasco S.M., Preston A.S., Uchida S., Yamauchi A.,
RA Kwon H.M., Handler J.S.;
RT "The canine betaine gamma-amino-n-butyric acid transporter gene:
RT diverse mRNA isoforms are regulated by hypertonicity and are expressed
RT in a tissue-specific manner.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:1072-1076(1995).
[3]
RN INTERACTION WITH LIN7C.
RX PubMed=10710551;
RA Straight S.W., Karnak D., Borg J.-P., Kamberov E., Dare H.,
RA Margolis B., Wade J.B.;
RT "Lin-7 is localized to the basolateral surface of renal epithelia via
RT its NH(2) terminus.";
RL Am. J. Physiol. 278:F464-F475(2000).
CC -I- FUNCTION: Transports betaine and GABA. May have a role in
CC regulation of GABAergic transmission in the brain through the
CC reuptake of GABA into presynaptic terminals, as well as in osmotic
CC regulation.
CC -I- SUBUNIT: Interacts with LIN7C.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Kidney.
CC -I- SIMILARITY: Belongs to the sodium:neurotransmitter symporter (SNF)
CC family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M80403; AAA30877.1; -; mRNA.
CC EMBL; D42037; BAA22547.1; -; Genomic_DNA.
CC PIR; A41757; A41757.
CC Ensembl; ENSCARG00000015756; Canis familiaris.
CC InterPro; IPR002983; Bet_transporter.
CC InterPro; IPR000175; Na/ntran_symport.
CC PANTHER; PTHR11616; Na/ntran_symport; 1.
CC Pfam; PF00209; SNF; 1.
CC PRINTS; PR01198; BETTRANSPORT.
CC PRINTS; PR00176; NANEUSMPORT.
CC ProDom; PD000448; Na/ntran_symport; 1.
CC PROSITE; PS00610; NA_NEUROTRAN_SYM_1; 1.
CC PROSITE; PS00754; NA_NEUROTRAN_SYM_2; 1.
CC PROSITE; PS0267; NA_NEUROTRAN_SYM_3; 1.
KW Glycoprotein; Neurotransmitter transport; Symport; Transmembrane;
KW Transport.
FT TOPO_DOM 1 44 Cytoplasmic (Potential).
FT TRANSMEM 45 65 1 (Potential).
FT TRANSMEM 73 92 2 (Potential).
FT TRANSMEM 117 137 3 (Potential).
FT TOPO_DOM 138 210 Extracellular (Potential).
FT TRANSMEM 211 229 4 (Potential).
FT TRANSMEM 238 255 5 (Potential).
FT TRANSMEM 291 308 6 (Potential).
FT TRANSMEM 320 341 7 (Potential).
FT TRANSMEM 374 393 8 (Potential).
FT TRANSMEM 423 441 9 (Potential).
FT TRANSMEM 458 478 10 (Potential).
FT TRANSMEM 499 518 11 (Potential).
FT TRANSMEM 538 556 12 (Potential).
FT TOPO_DOM 557 614 Cytoplasmic (Potential).
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 614 AA; 69292 MW; B19A9589843183CC CRC64;

Query Match 55.0%; Score 44; DB 1; Length 614;

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CC ----- NOT_ANNOTATED_CDS; mRNA.
DR PIR; A43390.
DR Ensembl; ENSMUSG00000030109; Mus musculus.
DR MGI; MGI:95628; Slc6a12.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR InterPro; IPR002983; Bet_transporter.
DR PANTHER; PTHR11616; Na/ntran_symport; 1.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR01198; BETTRANSPORT.
DR ProDom; PD000448; Na/ntran_symport; 1.
DR PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1; 1.
DR PROSITE; PS00754; NA_NEUROTRAN_SYMPT_2; 1.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMPT_3; 1.
KW Glycoprotein; Multigene family; Neurotransmitter transport; Symport;
KW Transmembrane; Transport.
FT TOPO_DOM 1 44 Cytoplasmic (Potential).
FT TRANSMEM 45 65 1 (Potential).
FT TRANSMEM 73 92 2 (Potential).
FT TRANSMEM 117 137 3 (Potential).
FT TOPO_DOM 138 210 Extracellular (Potential).
FT TRANSMEM 211 229 4 (Potential).
FT TRANSMEM 238 255 5 (Potential).
FT TRANSMEM 291 308 6 (Potential).
FT TRANSMEM 320 341 7 (Potential).
FT TRANSMEM 374 393 8 (Potential).
FT TRANSMEM 423 441 9 (Potential).
FT TRANSMEM 458 478 10 (Potential).
FT TRANSMEM 499 518 11 (Potential).
FT TOPO_DOM 557 614 Cytoplasmic (Potential).
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 614 AA; 69614 MW; 9A6B49EA3503725B CRC64;

Query Match 55.0%; Score 44; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYICFWK 8
Db 224 CYICWK 230

RESULT 44
S6A12_RABIT STANDARD; PRT; 614 AA.
AC P48055;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sodium- and chloride-dependent betaine transporter (Na+/Cl-
DE betaine/GABA transporter).
GN Name=SLC6A12;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ferraris J.D., Burg M.B., Williams C.K., Peters E.M., Garcia-Perez A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transports betaine and GABA. May have a role in
CC regulation of GABAergic transmission in the brain through the
CC reuptake of GABA into presynaptic terminals, as well as in osmotic
CC regulation (By similarity).
CC -!- SUBUNIT: Interacts with LIN7C (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the sodium:neurotransmitter symporter (SNF)
CC family.

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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U26341; AAA67953.1; -; mRNA.
DR InterPro; IPR002983; Bet_transporter.
DR PANTHER; PTHR11616; Na/ntran_symport; 1.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR01198; BETTRANSPORT.
DR ProDom; PD000448; Na/ntran_symport; 1.
DR PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1; 1.
DR PROSITE; PS00754; NA_NEUROTRAN_SYMPT_2; 1.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMPT_3; 1.
KW Glycoprotein; Neurotransmitter transport; Symport; Transmembrane;
KW Transport.
FT TOPO_DOM 1 44 Cytoplasmic (Potential).
FT TRANSMEM 45 65 1 (Potential).
FT TRANSMEM 73 92 2 (Potential).
FT TRANSMEM 117 137 3 (Potential).
FT TOPO_DOM 138 210 Extracellular (Potential).
FT TRANSMEM 211 229 4 (Potential).
FT TRANSMEM 238 255 5 (Potential).
FT TRANSMEM 291 308 6 (Potential).
FT TRANSMEM 320 341 7 (Potential).
FT TRANSMEM 374 393 8 (Potential).
FT TRANSMEM 423 441 9 (Potential).
FT TRANSMEM 458 478 10 (Potential).
FT TRANSMEM 499 518 11 (Potential).
FT TOPO_DOM 557 614 Cytoplasmic (Potential).
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 614 AA; 69111 MW; 70B175DD218BEEA5 CRC64;

Query Match 55.0%; Score 44; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYICFWK 8
Db 224 CYICWK 230

RESULT 45
S6A12_RAT STANDARD; PRT; 614 AA.
AC P48056;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sodium- and chloride-dependent betaine transporter (Na+/Cl-
DE betaine/GABA transporter).
GN Name=SLC6A12;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=97019277; PubMed=8865807; DOI=10.1016/0005-2736(96)00118-6;
RA Burnham C.E., Buerk B., Schmidt C., Bucuvalas J.C.;
RT "A liver-specific isoform of the betaine/GABA transporter in the rat:
RT cDNA sequence and organ distribution."
RL Biochim. Biophys. Acta 1284:4-8(1996).
CC -!- FUNCTION: Transports betaine and GABA. May have a role in
CC regulation of GABAergic transmission in the brain through the

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CC CC reuptake of GABA into presynaptic terminals, as well as in osmotic
CC CC regulation (By similarity).
CC CC -1- SUBUNIT: Interacts with LIN7C (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC CC -1- SIMILARITY: Belongs to the sodium:neurotransmitter symporter (SNF)
CC CC family.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC CC EMBL; U28927; AAC52867.1; ALT INIT; mRNA.
CC CC Ensembl; ENSNOCG00000013547; Rattus norvegicus.
CC CC InterPro; IPR002983; Bet transporter.
CC CC InterPro; IPR000175; Na/ntran_symport.
CC CC PANTHER; PTHR11616; Na/ntran_symport; 1.
CC CC Pfam; PF00209; SNF; 1.
CC CC PRINTS; PR01198; BETTRANSPORT.
CC CC ProDom; PD000448; Na/ntran_symport; 1.
CC CC PROSITE; PS00610; NA_NEUOTRAN_SYMP_1; 1.
CC CC PROSITE; PS00754; NA_NEUOTRAN_SYMP_2; 1.
CC CC PROSITE; PS50267; NA_NEUOTRAN_SYMP_3; 1.
CC CC Glycoprotein; Neurotransmitter transport; Symport; Transmembrane;
CC CC Transport.
CC CC TOPO_DOM 1 44 Cytoplasmic (Potential).
CC CC TRANSMEM 45 65 1 (Potential).
CC CC TRANSMEM 73 92 2 (Potential).
CC CC TRANSMEM 117 137 3 (Potential).
CC CC TOPO_DOM 138 210 Extracellular (Potential).
CC CC TRANSMEM 211 229 4 (Potential).
CC CC TRANSMEM 238 255 5 (Potential).
CC CC TRANSMEM 291 308 6 (Potential).
CC CC TRANSMEM 320 341 7 (Potential).
CC CC TRANSMEM 374 393 8 (Potential).
CC CC TRANSMEM 423 441 9 (Potential).
CC CC TRANSMEM 458 478 10 (Potential).
CC CC TRANSMEM 499 518 11 (Potential).
CC CC TRANSMEM 537 556 12 (Potential).
CC CC TOPO_DOM 558 614 Cytoplasmic (Potential).
CC CC CARBOHYD 171 171 N-linked (GLCNAC...) (Potential).
CC CC CARBOHYD 183 183 N-linked (GLCNAC...) (Potential).
CC CC SEQUENCE 614 AA; 69749 MW; 14C78DE51ED808B CRC64;

Query Match 55.0%; Score 44; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYCFCWK 8
Db 224 CYFCWK 230
|||||

RESULT 46
Q8VCS9_MOUSE PRELIMINARY; PRT; 614 AA.
AC Q8VCS9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Solute carrier family 6 (Neurotransmitter transporter, betaine/GABA),
DE member 12.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Liver;

Query Match 55.0%; Score 44; DB 2; Length 614;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYCFCWK 8
Db 224 CYFCWK 230
|||||

RESULT 47
Q91503_TORMA PRELIMINARY; PRT; 622 AA.
AC Q91503;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GABA/beta-alanine transporter.
OS Torpedo marmorata (Marbled electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hypnosquala; Pristiogaster; Batoidae;
OC Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.
CC NCBI_TaxID=7788;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lobus electricus;
RX MEDLINE=96163462; PubMed=8575437;
RA Guimbal C., Klostermann A., Killmann M.W.;
RT "Phylogenetic conservation of 4-aminobutyric acid (GABA) transporter
RT isoforms: Cloning and pharmacological characterization of a GABA/beta-
RT alanine transporter from Torpedo."
RL Eur. J. Biochem. 234:794-800(1995).
DR EMBL; X87170; CAA60635.1; -; mRNA.
DR PIR; S63539; S63539.

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derje J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uadin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gay L.J., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2].
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL EMBL; BC019211; AAH19211.1; -; mRNA.
DR MGI; MGI:95628; Slc6a12.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR InterPro; IPR002983; Bet transporter.
DR InterPro; IPR000175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR01198; BETTRANSPORT.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom; PD000448; Na/ntran_symport; 1.
DR PROSITE; PS00610; NA_NEUOTRAN_SYMP_1; 1.
DR PROSITE; PS00754; NA_NEUOTRAN_SYMP_2; 1.
DR PROSITE; PS50267; NA_NEUOTRAN_SYMP_3; 1.
DR SEQUENCE 614 AA; 69641 MW; F876F7E57717D7B5 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 614;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYCFCWK 8
Db 224 CYFCWK 230
|||||

RESULT 47
Q91503_TORMA PRELIMINARY; PRT; 622 AA.
AC Q91503;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GABA/beta-alanine transporter.
OS Torpedo marmorata (Marbled electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hypnosquala; Pristiogaster; Batoidae;
OC Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.
CC NCBI_TaxID=7788;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lobus electricus;
RX MEDLINE=96163462; PubMed=8575437;
RA Guimbal C., Klostermann A., Killmann M.W.;
RT "Phylogenetic conservation of 4-aminobutyric acid (GABA) transporter
RT isoforms: Cloning and pharmacological characterization of a GABA/beta-
RT alanine transporter from Torpedo."
RL Eur. J. Biochem. 234:794-800(1995).
DR EMBL; X87170; CAA60635.1; -; mRNA.
DR PIR; S63539; S63539.

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DR GO: GO:0005887; C: integral to plasma membrane; IEA.
 DR GO: GO:0016020; C: membrane; IEA.
 DR GO: GO:0005328; P: neurotransmitter: sodium symporter activity; IEA.
 DR GO: GO:0015293; P: symporter activity; IEA.
 DR GO: GO:0006836; P: neurotransmitter transport; IEA.
 DR InterPro: IPR000175; Na/ntran_symport.
 DR Pfam: PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom: PD000448; Na/ntran_symport; 1.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
 DR PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; 1.
 DR PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
 DR Symport; Transmembrane; Transport.
 KW SEQUENCE 622 AA; 70348 MW; 579478786CDP4BD4 CRC64;
 Query Match 55.0%; Score 44; DB 2; Length 622;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CYCFWK 8
 DB 227 CYCFWK 233
 RESULT 48
 S6all MOUSE
 ID S6all MOUSE STANDARD; PRT; 627 AA.
 AC P31650;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Sodium- and chloride-dependent GABA transporter 4 (GAT4).
 GN Name=Slc6all; Synonyms=Gabt4, Gat-4, Gat4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93131969; PubMed=8420981;
 RT Liu Q.-R., Lopez-Coequera B., Mandiyan S., Nelson H., Nelson N.;
 RT "Molecular characterization of four pharmacologically distinct gamma-aminobutyric acid transporters in mouse brain.";
 RL J. Biol. Chem. 268:2106-2112(1993).
 CC -1- FUNCTION: Terminates the action of GABA by its high affinity sodium-dependent reuptake into presynaptic terminals. Can also transport beta-alanine and taurine.
 CC -1- BIOPHYSICOCHEMICAL PROPERTIES:
 CC Kinetic parameters:
 CC KM=0.8 uM for GABA;
 CC KM=99 uM for beta-alanine;
 CC KM=1.4 mM for taurine;
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Brain.
 CC -1- SIMILARITY: Belongs to the sodium:neurotransmitter symporter (SNF) family.

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 CC EMBL; L04662; -; NOT_ANNOTATED_CDS; mRNA.
 DR PIR; B44409; B44409.
 DR Ensembl; ENSMUSG00000030307; Mus musculus.
 DR MGI; MGI:95630; Gabt4.
 DR InterPro; IPR002982; GAT3 transporter.
 DR InterPro; IPR000175; Na/ntran_symport.
 DR PANTHER; PTHR11616; Na/ntran_symport; 1.
 DR Pfam; PF00209; SNF; 1.

DR PRINTS; PR01197; GAT3TRANSPORT.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom: PD000448; Na/ntran_symport; 1.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
 DR PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; 1.
 DR PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
 KW Glycoprotein; Multigene family; Neurotransmitter transport; Symport;
 KW Transmembrane; Transport.
 FT TOPO_DOM 1 53 Cytoplasmic (Potential).
 FT TRANSMEM 54 74 1 (Potential).
 FT TRANSMEM 82 101 2 (Potential).
 FT TRANSMEM 126 146 3 (Potential).
 FT TOPO_DOM 147 220 Extracellular (Potential).
 FT TRANSMEM 221 239 4 (Potential).
 FT TRANSMEM 248 265 5 (Potential).
 FT TRANSMEM 301 318 6 (Potential).
 FT TRANSMEM 330 351 7 (Potential).
 FT TRANSMEM 384 403 8 (Potential).
 FT TRANSMEM 433 451 9 (Potential).
 FT TRANSMEM 468 488 10 (Potential).
 FT TRANSMEM 509 528 11 (Potential).
 FT TRANSMEM 548 566 12 (Potential).
 FT TOPO_DOM 567 627 Cytoplasmic (Potential).
 FT CARBOHYD 182 182 N-linked (GLNAC...) (Potential).
 FT CARBOHYD 185 185 N-linked (GLNAC...) (Potential).
 FT CARBOHYD 193 193 N-linked (GLNAC...) (Potential).
 SQ SEQUENCE 627 AA; 69889 MW; B6D4E45FC92C4CB7 CRC64;
 Query Match 55.0%; Score 44; DB 1; Length 627;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CYCFWK 8
 DB 234 CYCFWK 240
 RESULT 49
 S6all RAT
 ID S6all RAT STANDARD; PRT; 627 AA.
 AC P31647;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Sodium- and chloride-dependent GABA transporter 3.
 GN Name=Slc6all; Synonyms=Gabt3, Gat-3, Gat-b;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=93016029; PubMed=1400419;
 RA Borden L.A., Smith K.B., Hartig P.R., Branchek T.A., Weinschenk R.L.;
 RT "Molecular heterogeneity of the gamma-aminobutyric acid (GABA) transport system. Cloning of two novel high affinity GABA transporters from rat brain."
 RT J. Biol. Chem. 267:21098-21104(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92360310; PubMed=1497897; DOI=10.1016/0896-6273(92)90172-A;
 RA Clark J.A., Deutch A.Y., Gallipoli P.Z., Amara S.G.;
 RT "Functional expression and CNS distribution of a beta-alanine-sensitive neuronal GABA transporter."
 RL Neuron 9:337-348(1992).
 CC -1- FUNCTION: Terminates the action of GABA by its high affinity sodium-dependent reuptake into presynaptic terminals.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Brain and retina.
 CC -1- SIMILARITY: Belongs to the sodium:neurotransmitter symporter (SNF) family.

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CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
DR DR EMBL; M95738; AAA41183.1; -; mRNA.
DR DR EMBL; M95763; AAA40607.1; -; mRNA.
DR DR EMBL; J42358; AAB22850.1; -; mRNA.
DR DR F1R; JH0695; JH0695.
DR DR RGD; ENSRNOG00000005697; Rattus norvegicus.
DR DR RGD; G28737; S1C6a11.
DR DR GO; GO:0005332; P:gamma-aminobutyric acid:sodium symporter ac. . . ; IDA.
DR DR GO; GO:0042165; P:neurotransmitter binding; IDA.
DR DR GO; GO:0006836; P:neurotransmitter transport; IDA.
DR DR InterPro; IPR002982; GAT3 transporter.
DR DR InterPro; IPR00175; Na/ntran symport.
DR DR PANTHER; PTHR11616; Na/ntran_symport; 1.
DR DR Pfam; PF00209; SNF; 1.
DR DR PRINTS; PR01197; GAT3TNSPORT.
DR DR PRINTS; PR00176; NANEUSPORT.
DR DR PRODOM; PD000448; Na/ntran symport; 1.
DR DR PROSITE; PS00610; NA_NEUROTRAN_SYM_1; 1.
DR DR PROSITE; PS00754; NA_NEUROTRAN_SYM_2; 1.
DR DR PROSITE; PS00754; NA_NEUROTRAN_SYM_3; 1.
DR DR Glycoprotein; Multigene family; Neurotransmitter transport; Symport;
DR KW transmembrane; transport.
FT FT TOPO_DOM 1 53 Cytoplasmic (Potential).
FT FT TRANSMEM 54 74 1 (Potential).
FT FT TRANSMEM 82 101 2 (Potential).
FT FT TRANSMEM 126 146 3 (Potential).
FT FT TOPO_DOM 147 220 Extracellular (Potential).
FT FT TRANSMEM 221 239 4 (Potential).
FT FT TRANSMEM 248 265 5 (Potential).
FT FT TRANSMEM 301 318 6 (Potential).
FT FT TRANSMEM 330 351 7 (Potential).
FT FT TRANSMEM 384 403 8 (Potential).
FT FT TRANSMEM 433 451 9 (Potential).
FT FT TRANSMEM 468 488 10 (Potential).
FT FT TRANSMEM 509 528 11 (Potential).
FT FT TRANSMEM 548 566 12 (Potential).
FT FT TOPO_DOM 567 627 Cytoplasmic (Potential).
FT FT CARBOHYD 182 182 N-linked (GlcNAc. .) (Potential).
FT FT CARBOHYD 185 185 N-linked (GlcNAc. .) (Potential).
FT FT CARBOHYD 193 193 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 627 AA; 69947 MW; B0B3C2F8B6D4327 CRC64;

Query Match 55.0%; Score 44; DB 1; Length 627;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CYPCFWK 8
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RESULT 50
Q8BWA7 MOUSE
AC Q8BWA7 MOUSE PRELIMINARY; PRT; 627 AA.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
DE library, clone:D930045G19 product:SODIUM- AND CHLORIDE-DEPENDENT GABA
DE TRANSPORTER 3 homolog.
GN Name=Gabtg4;
OS Mus musculus (Mouse);
OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279233; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guncinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20493974; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara B., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
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RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
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RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakazume N., Sano H.,

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RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK053078; BAC35259.1; -, mRNA.
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 DR GO: GO:0005887; C: integral to plasma membrane; IEA.
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 DR GO: GO:0005328; F: neurotransmitter:sodium symporter activity; IEA.
 DR GO: GO:0015293; F: symporter activity; IEA.
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Query Match 55.0%; Score 44; DB 2; Length 627;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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 Db 234 CYICWK 240

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:05:44 ; Search time 14.6667 Seconds
(without alignments)
62.007 Million cell updates/sec

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Perfect score: 80
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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986 32 40.0 8 1 US-08-287-957-5 Sequence 5, Appl
987 32 40.0 8 2 US-09-144-991B-2 Sequence 2, Appl
988 32 40.0 8 2 US-09-144-991B-8 Sequence 8, Appl
989 32 40.0 8 2 US-10-175-833-2 Sequence 2, Appl
990 32 40.0 8 2 US-10-175-833-8 Sequence 8, Appl
991 32 40.0 9 1 US-08-287-957-26 Sequence 26, Appl
992 32 40.0 9 1 US-08-287-957-32 Sequence 32, Appl
993 32 40.0 9 2 US-09-144-991B-32 Sequence 32, Appl
994 32 40.0 9 2 US-09-144-991B-33 Sequence 33, Appl
995 32 40.0 9 2 US-09-144-991B-34 Sequence 34, Appl
996 32 40.0 9 2 US-09-144-991B-56 Sequence 56, Appl
997 32 40.0 9 2 US-09-144-991B-57 Sequence 57, Appl
998 32 40.0 9 2 US-09-144-991B-58 Sequence 58, Appl
999 32 40.0 9 2 US-09-144-991B-61 Sequence 61, Appl
1000 32 40.0 9 2 US-10-175-833-32 Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-528-200-158 Application US/09528200
; Sequence 158, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHIA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFGANG
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSENIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR FILING DATE: DE 199 17 713.9
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-158

Query Match 66.2%; Score 53; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4 YCFWKTCCT 11
Db 1 PCFWKTCCT 8

RESULT 2
US-09-734-583B-4
; Sequence 4, Application US/09734583B
; Patent No. 6930088

; GENERAL INFORMATION:
; APPLICANT: Hornik, Vered
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOG
; FILE REFERENCE: 87534-3000
; CURRENT APPLICATION NUMBER: US/09/734,583B
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Phe residue is a D isomer
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: The Thr residue ends with CH2OH
; FEATURE:
; NAME/KEY: DISULFIDE BRIDGE
; LOCATION: (2)..(2)
; OTHER INFORMATION: A disulfide bridge is formed between Cys residues 2 and 7
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: The Trp residue is a D isomer
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-734-583B-4

Query Match 66.2%; Score 53; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4 YCFWKTCCT 11
Db 1 PCFWKTCCT 8

RESULT 3
US-08-586-670A-16
; Sequence 16, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000

```

; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2..5
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Phe is in the D conformation; the Trp
; OTHER INFORMATION: is in the D conformation;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7..9
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The sulfur atom of the cysteine is
; OTHER INFORMATION: methylated; the carboxyl group of the C-
; OTHER INFORMATION: terminal Thr is reduced to an alcohol;
; US-08-586-670A-16

Query Match 66.2%; Score 53; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTKT 11
DB 2 FCFWKTKT 9
:|||||
:|||||

RESULT 4
US-09-484-318-1
; Sequence 1, Application US/09484318
; Patent No. 6180085
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,318
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
; US-09-484-318-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTKT 11
DB 1 FCFWKTKT 8
:|||||
:|||||

RESULT 6
US-09-484-319-1
; Sequence 1, Application US/09484319
; Patent No. 6180086
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,319
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
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```

RESULT 5
US-09-484-318-8
; Sequence 8, Application US/09484318
; Patent No. 6180085
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,318
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTKT 11
DB 1 FCFWKTKT 8
:|||||
:|||||

RESULT 6
US-09-484-319-1
; Sequence 1, Application US/09484319
; Patent No. 6180086
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,319
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
```

; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-319-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|:|||||
Db 1 FCYWKTCCT 8

RESULT 7

US-09-484-319-8

; Sequence 8, Application US/09484319
; Patent No. 6180086

GENERAL INFORMATION:

; APPLICANT: Achilefu, Samuel

; APPLICANT: Rajagopalan, Raghavan

; APPLICANT: Dorshow, Richard B

; APPLICANT: Bugaj, Joseph E.

; TITLE OF INVENTION: NEW HYDROPHILIC CVANINE DYES

; FILE REFERENCE: DNA STRING

; CURRENT APPLICATION NUMBER: US/09/484,319

; CURRENT FILING DATE: 2000-01-18

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence:Octreotate

; NAME/KEY: SITE

; LOCATION: (1)

; OTHER INFORMATION: This is D-phenylalanine

; NAME/KEY: DISULFID

; LOCATION: (2)..(7)

; NAME/KEY: SITE

; LOCATION: (4)

; OTHER INFORMATION: This is D-tryptophan

US-09-484-319-8

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|:|||||
Db 1 FCYWKTCCT 8

RESULT 8

US-09-484-320-1

; Sequence 1, Application US/09484320

; Patent No. 6180087

GENERAL INFORMATION:

; APPLICANT: Achilefu, Samuel

; APPLICANT: Rajagopalan, Raghavan

; APPLICANT: Dorshow, Richard B

; APPLICANT: Bugaj, Joseph E.

; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications

; FILE REFERENCE: dnastring

; CURRENT APPLICATION NUMBER: US/09/484,320

; CURRENT FILING DATE: 2000-01-18

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Octreotide

; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-320-1

Query Match 62.5%; Score 50; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|:|||||
Db 1 FCYWKTCCT 8

RESULT 9

US-09-484-320-8

; Sequence 8, Application US/09484320

; Patent No. 6180087

GENERAL INFORMATION:

; APPLICANT: Achilefu, Samuel

; APPLICANT: Rajagopalan, Raghavan

; APPLICANT: Dorshow, Richard B

; APPLICANT: Bugaj, Joseph E.

; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications

; FILE REFERENCE: dnastring

; CURRENT APPLICATION NUMBER: US/09/484,320

; CURRENT FILING DATE: 2000-01-18

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Octreotate

; NAME/KEY: SITE

; LOCATION: (1)

; OTHER INFORMATION: This is D-phenylalanine

; NAME/KEY: DISULFID

; LOCATION: (2)..(7)

; NAME/KEY: SITE

; LOCATION: (4)

; OTHER INFORMATION: This is D-tryptophan

US-09-484-320-8

Query Match 62.5%; Score 50; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|:|||||
Db 1 FCYWKTCCT 8

RESULT 10

US-09-484-321-1

; Sequence 1, Application US/09484321

; Patent No. 6183726

GENERAL INFORMATION:

; APPLICANT: Achilefu, Samuel

; APPLICANT: Rajagopalan, Raghavan

; APPLICANT: Dorshow, Richard B

; APPLICANT: Bugaj, Joseph E.

; TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES

; FILE REFERENCE: DNA STRING

; CURRENT APPLICATION NUMBER: US/09/484,321
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-321-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
:|:|:|:|
Db 1 FCYWKTKT 8

RESULT 11

US-09-484-321-8
; Sequence 8, Application US/09484321
; Patent No. 6183726
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,321
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-484-321-8

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
:|:|:|:|
Db 1 FCYWKTKT 8

RESULT 12

US-09-484-323-1
; Sequence 1, Application US/09484323
; Patent No. 6190641
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,323
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-323-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
:|:|:|:|
Db 1 FCYWKTKT 8

RESULT 13

US-09-484-323-8
; Sequence 8, Application US/09484323
; Patent No. 6190641
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,323
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-484-323-8

```
Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
Db 1 FCYWKTKCT 8

RESULT 14
US-09-325-769-1
; Sequence 1, Application US/09325769
; Patent No. 6217848
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Dorshow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; APPLICANT: Rajagopalan, Raghavan
; TITLE OF INVENTION: NOVEL CYANINE AND INDOCYANINE DYE BIOCONJUGATES FOR
; TITLE OF INVENTION: BIOMEDICAL APPLICATIONS
; FILE REFERENCE: 1668-286
; CURRENT APPLICATION NUMBER: US/09/325,769
; CURRENT FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: ATTY DOCKET 1668-284
; EARLIER FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine.
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide.
US-09-325-769-2
Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
Db 1 FCYWKTKCT 8

RESULT 15
US-09-325-769-2
; Sequence 2, Application US/09325769
; Patent No. 6217848
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Dorshow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; APPLICANT: Rajagopalan, Raghavan
; TITLE OF INVENTION: NOVEL CYANINE AND INDOCYANINE DYE BIOCONJUGATES FOR
; TITLE OF INVENTION: BIOMEDICAL APPLICATIONS
; FILE REFERENCE: 1668-286
; CURRENT APPLICATION NUMBER: US/09/325,769
; CURRENT FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: ATTY DOCKET 1668-284
; EARLIER FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine.
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide.
US-09-325-769-1
; Sequence 1, Application US/09636170
; Patent No. 6264919
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/636,170
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue has had the terminal COOH
; OTHER INFORMATION: reduced to CH2OH.
US-09-325-769-2
Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
Db 1 FCYWKTKCT 8

RESULT 16
US-09-636-170-1
; Sequence 1, Application US/09636170
; Patent No. 6264919
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/636,170
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
; OTHER INFORMATION:
US-09-636-170-1
Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
Db 1 FCYWKTKCT 8
```



```
Db      1 FCYWKTC 8

RESULT 17
US-09-636-170-8
; Sequence 8, Application US/09636170
; Patent No. 6264919
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/636,170
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-636-170-8

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTC 11
       :|:|||||
Db      1 FCYWKTC 8

RESULT 18
US-09-637-518-1
; Sequence 1, Application US/09637518
; Patent No. 6264920
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastrng
; CURRENT APPLICATION NUMBER: US/09/637,518
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-637-518-1

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTC 11
       :|:|||||
Db      1 FCYWKTC 8

RESULT 19
US-09-637-518-8
; Sequence 8, Application US/09637518
; Patent No. 6264920
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastrng
; CURRENT APPLICATION NUMBER: US/09/637,518
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-637-518-8

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTC 11
       :|:|||||
Db      1 FCYWKTC 8

RESULT 20
US-09-528-200-159
; Sequence 159, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARTSEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
```

```
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-637-518-1

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTC 11
       :|:|||||
Db      1 FCYWKTC 8

RESULT 19
US-09-637-518-8
; Sequence 8, Application US/09637518
; Patent No. 6264920
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastrng
; CURRENT APPLICATION NUMBER: US/09/637,518
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-637-518-8

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTC 11
       :|:|||||
Db      1 FCYWKTC 8

RESULT 20
US-09-528-200-159
; Sequence 159, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARTSEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
```

; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-159

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||
Db 1 FCYWKVCT 8

RESULT 21

US-09-528-200-156
; Sequence 156, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-156

Query Match 60.0%; Score 48; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||
Db 1 FCYWKVCT 8

RESULT 22

US-09-734-583B-2
; Sequence 2, Application US/09734583B
; Patent No. 6930088
; GENERAL INFORMATION:
; APPLICANT: Hornik, Vered
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOG
; FILE REFERENCE: 87534-3000
; CURRENT APPLICATION NUMBER: US/09/734,583B
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: DISULFIDE BRIDGE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Cys residues at amino acid positions 1 and 6 form a disulfide bridge
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Trp residue is the D isomer
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-734-583B-2

Query Match 56.2%; Score 45; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
:|||||
Db 1 CFWKTC 6

RESULT 23

US-09-528-200-157
; Sequence 157, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR FILING DATE: 1999-09-04
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-157

Query Match 56.2%; Score 45; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||
Db 1 FCYWKVCT 8

RESULT 24

US-08-985-526-15
; Sequence 15, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY

```
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-985-526-15

Query Match 56.2%; Score 45; DB 2; Length 34;
Best Local Similarity 33.3%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 1; Indels 8; Gaps 1;

Qy 1 YCYVCFWK 10
   :||:|:|:|
Db 2 FCYWKVCKGKSFYKVC 19

RESULT 25
US-09-813-918-3
; Sequence 3, Application US/09813918
; Patent No. 6383789
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001175
; CURRENT APPLICATION NUMBER: US/09/813,918
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Human
US-09-813-918-3

Query Match 56.2%; Score 45; DB 2; Length 288;
Best Local Similarity 62.5%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

Qy 1 YCYVCFWK 8
   :||:|:|:|
Db 270 FCLFCFWK 277

RESULT 26
US-10-060-311-3
; Sequence 3, Application US/10060311
; Patent No. 6713295
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001175DIV
; CURRENT APPLICATION NUMBER: US/10/060,311
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-060-311-3

Query Match 56.2%; Score 45; DB 2; Length 288;
Best Local Similarity 62.5%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYVCFWK 8
   :||:|:|:|
Db 270 FCLFCFWK 277

RESULT 27
US-10-778-300-3
; Sequence 3, Application US/10778300
; Patent No. 6846661
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001175DIV II
; CURRENT APPLICATION NUMBER: US/10/778,300
; CURRENT FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-778-300-3

Query Match 56.2%; Score 45; DB 2; Length 288;
Best Local Similarity 62.5%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYVCFWK 8
   :||:|:|:|
Db 270 FCLFCFWK 277

RESULT 28
US-09-813-918-2
; Sequence 2, Application US/09813918
; Patent No. 6383789
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001175
; CURRENT APPLICATION NUMBER: US/09/813,918
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 454
```

```
; TYPE: PRT
; ORGANISM: Human
US-09-813-918-2

Query Match      56.2%; Score 45; DB 2; Length 454;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYCFWK 8
Db 436 FCLFCFWK 443

RESULT 29
US-10-060-311-2
; Sequence 2, Application US/10060311
; Patent No. 6713295
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; FILE REFERENCE: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-060-311-2

Query Match      56.2%; Score 45; DB 2; Length 454;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYCFWK 8
Db 436 FCLFCFWK 443

RESULT 30
US-10-778-300-2
; Sequence 2, Application US/10778300
; Patent No. 6946661
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; FILE REFERENCE: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
; CURRENT FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-778-300-2

Query Match      56.2%; Score 45; DB 2; Length 454;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYCFWK 8
Db 436 FCLFCFWK 443

RESULT 31
US-09-270-767-60201
```

```
; Sequence 60201, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60201
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60201

Query Match      55.0%; Score 44; DB 2; Length 217;
Best Local Similarity 55.6%; Pred. No. 67;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CYCYCFWKTC 10
Db 153 CYCYCYVXC 161

RESULT 32
US-09-270-767-32343
; Sequence 32343, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32343
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32343

Query Match      55.0%; Score 44; DB 2; Length 350;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCYCFWK 8
Db 250 CYPCFWK 256

RESULT 33
US-09-270-767-44745
; Sequence 44745, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44745
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44745
```

```
Query Match      55.0%; Score 44; DB 2; Length 361;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CYCFCWKC 10
Db      297 CYCYTYXC 305

RESULT 34
US-09-815-923-14
; Sequence 14, Application US/09815923
; Patent No. 6787642
; GENERAL INFORMATION:
; APPLICANT: Gill, Sarjeet S.
; APPLICANT: Ross, Linda S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. 6787642el
; TITLE OF INVENTION: Target Sites for Insecticides
; FILE REFERENCE: 023070-093800US
; CURRENT APPLICATION NUMBER: US/09/815,923
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; OTHER INFORMATION: GABA transporter
; US-09-815-923-14

Query Match      55.0%; Score 44; DB 2; Length 597;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFCWK 8
Db      238 CYFCWK 244

RESULT 35
US-08-295-814E-2
; Sequence 2, Application US/08295814E
; Patent No. 5658786
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Borden, Laurence A.
; APPLICANT: Hartig, Paul R.
; APPLICANT: Weinschank, Richard L.
; TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA
; TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,814E
; FILING DATE: DECEMBER 19, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John
; REGISTRATION NUMBER: 28,678

Query Match      55.0%; Score 44; DB 1; Length 602;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFCWK 8
Db      219 CYFCWK 225

RESULT 36
US-08-291-299-9
; Sequence 9, Application US/08291299
; Patent No. 5766848
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA
; TITLE OF INVENTION: TRANSPORTER AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,299
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John F.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42897-A/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-291-299-9

Query Match      55.0%; Score 44; DB 1; Length 602;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFCWK 8
Db      219 CYFCWK 225

RESULT 37
US-09-343-361-2
```

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; REFERENCE/DOCKET NUMBER: 40558-B-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-295-814E-2

Query Match      55.0%; Score 44; DB 1; Length 602;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFCWK 8
Db      219 CYFCWK 225

RESULT 36
US-08-291-299-9
; Sequence 9, Application US/08291299
; Patent No. 5766848
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA
; TITLE OF INVENTION: TRANSPORTER AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,299
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John F.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42897-A/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-291-299-9

Query Match      55.0%; Score 44; DB 1; Length 602;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFCWK 8
Db      219 CYFCWK 225

RESULT 37
US-09-343-361-2
```

```
; Sequence 2, Application US/09343361
; Patent No. 6225115
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E. et al
; TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses
; FILE REFERENCE: 40558-D
; CURRENT APPLICATION NUMBER: US/09/343,361
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-343-361-2

Query Match          55.0%; Score 44; DB 2; Length 602;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFWK 8
Db      219 CYCINW 225

RESULT 38
US-10-009-693-1
; Sequence 1, Application US/10009693
; Patent No. 6906177
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: No. 6906177el Protein and its DNA
; FILE REFERENCE: 2613WOOP
; CURRENT APPLICATION NUMBER: US/10/009,693
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: JP 11-163924
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Human
US-10-009-693-1

Query Match          55.0%; Score 44; DB 2; Length 602;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFWK 8
Db      219 CYCINW 225

RESULT 39
PCT-US93-01959-2
; Sequence 2, Application PC/TUS9301959
; GENERAL INFORMATION:
; APPLICANT: Smith, E. Kelli
; APPLICANT: Borden, A. Laurence
; APPLICANT: Hartig, R. Paul
; APPLICANT: Weishank, L. Richard
; TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:

Query Match          55.0%; Score 44; DB 4; Length 602;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFWK 8
Db      219 CYCINW 225

RESULT 40
PCT-US95-10579-9
; Sequence 9, Application PC/TUS9510579
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA
; TITLE OF INVENTION: TRANSPORTER AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10579
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42897-A-PCT/JPW/MAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-10579-9

Query Match          55.0%; Score 44; DB 4; Length 602;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFWK 8
Db      219 CYCINW 225

RESULT 41
PCT-US93-01959-2
; Sequence 2, Application PC/TUS9301959
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E. et al
; TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses
; FILE REFERENCE: 40558-D
; CURRENT APPLICATION NUMBER: US/09/343,361
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-343-361-2

Query Match          55.0%; Score 44; DB 2; Length 602;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFWK 8
Db      219 CYCINW 225

RESULT 42
PCT-US95-10579-9
; Sequence 9, Application PC/TUS9510579
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA
; TITLE OF INVENTION: TRANSPORTER AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10579
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42897-A-PCT/JPW/MAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-10579-9

Query Match          55.0%; Score 44; DB 4; Length 602;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFWK 8
Db      219 CYCINW 225
```

Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8
Db 219 CYFCWK 225

RESULT 41

US-08-295-814E-12
Sequence 12, Application US/08295814E
Patent No. 5658786
GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Borden, Laurence A.
APPLICANT: Hartig, Paul R.
APPLICANT: Weinschank, Richard L.
TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA
TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295.814E
FILING DATE: DECEMBER 19, 1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40558-B-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 614 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-295-814E-12

Query Match 55.0%; Score 44; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8
Db 224 CYFCWK 230

RESULT 42

US-08-543-881-2
Sequence 2, Application US/08543881
Patent No. 5712148
GENERAL INFORMATION:
APPLICANT: Borden, Laurence A.
APPLICANT: Smith, Kelli E.
APPLICANT: Weinschank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HUMAN BETAININE/GABA
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
CITY: NEW YORK
STATE: NEW YORK
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,881
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/334,858
FILING DATE:
APPLICATION NUMBER: US/08/001,738
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: White, P. John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42897/JPW/KEK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 614 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-543-881-2

Query Match 55.0%; Score 44; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CYCFWK 8
Db 224 CYFCWK 230

RESULT 43

US-08-291-299-2
Sequence 2, Application US/08291299
Patent No. 5768648
GENERAL INFORMATION:
APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: DNA ENCODING A HUMAN BETAININE/GABA
TITLE OF INVENTION: TRANSPORTER AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,299
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42897-A/JPW/TEP

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-291-299-2

Query Match          55.0%; Score 44; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYTCFWK 8
Db      224 CYFCIMK 230

RESULT 44
US-08-291-299-7
; Sequence 7, Application US/08291299
; Patent No. 5766848
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,299
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42897-A/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-291-299-7

Query Match          55.0%; Score 44; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYTCFWK 8
Db      224 CYFCIMK 230

RESULT 45
US-08-291-299-8
; Sequence 7, Application US/08291299
; Patent No. 5766848
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,299
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42897-A/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-291-299-8

Query Match          55.0%; Score 44; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYTCFWK 8
Db      224 CYFCIMK 230

RESULT 46
US-09-343-361-12
; Sequence 12, Application US/09343361
; Patent No. 6225115
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E. et al
; TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses
; FILE REFERENCE: 40558-D
; CURRENT APPLICATION NUMBER: US/09/343,361
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 12
; LENGTH: 614
; TYPE: PRT
; ORGANISM: dog
; US-09-343-361-12

Query Match          55.0%; Score 44; DB 2; Length 614;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYTCFWK 8
Db      224 CYFCIMK 230

```

```

; Sequence 8, Application US/08291299
; Patent No. 5766848
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,299
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42897-A/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-291-299-8

Query Match          55.0%; Score 44; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYTCFWK 8
Db      224 CYFCIMK 230

RESULT 46
US-09-343-361-12
; Sequence 12, Application US/09343361
; Patent No. 6225115
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E. et al
; TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses
; FILE REFERENCE: 40558-D
; CURRENT APPLICATION NUMBER: US/09/343,361
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 12
; LENGTH: 614
; TYPE: PRT
; ORGANISM: dog
; US-09-343-361-12

Query Match          55.0%; Score 44; DB 2; Length 614;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYTCFWK 8
Db      224 CYFCIMK 230

```


Db 224 CYFCIWK 230

RESULT 47

US-09-919-039-378 Application US/09919039

Sequence 378, Patent No. 6727066

GENERAL INFORMATION:

APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES

FILE REFERENCE: PA-0035 US

CURRENT APPLICATION NUMBER: US/09/919,039

PRIOR FILING DATE: 2002-09-09

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SEQ ID NO 378

LENGTH: 614

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6727066 5834958CD1

US-09-919-039-378

Query Match 55.0%; Score 44; DB 2; Length 614;

Best Local Similarity 71.4%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYFCWK 8

Db 224 CYFCIWK 230

RESULT 48

PCT-US94-00119-2

Sequence 2, Application PC/TUS9400119

GENERAL INFORMATION:

APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION

TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/00119

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Covert, Robert J.

REGISTRATION/DOCKET NUMBER: 42897-PCT/JPW/TEP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 614 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 55.0%; Score 44; DB 2; Length 614;

Best Local Similarity 71.4%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYFCWK 8

Db 224 CYFCIWK 230

RESULT 49

PCT-US95-10579-2

Sequence 2, Application PC/TUS9510579

GENERAL INFORMATION:

APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION

TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10579

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION/DOCKET NUMBER: 42897-A-PCT/JPW/NAT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 614 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-10579-2

Query Match 55.0%; Score 44; DB 4; Length 614;

Best Local Similarity 71.4%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYFCWK 8

Db 224 CYFCIWK 230

RESULT 50

PCT-US95-10579-7

Sequence 7, Application PC/TUS9510579

GENERAL INFORMATION:

APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION

TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

PCT-US94-00119-2

Query Match 55.0%; Score 44; DB 4; Length 614;

Best Local Similarity 71.4%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYFCWK 8

Db 224 CYFCIWK 230

RESULT 49

PCT-US95-10579-2

Sequence 2, Application PC/TUS9510579

GENERAL INFORMATION:

APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION

TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10579

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION/DOCKET NUMBER: 42897-A-PCT/JPW/NAT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 614 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-10579-2

Query Match 55.0%; Score 44; DB 4; Length 614;

Best Local Similarity 71.4%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYFCWK 8

Db 224 CYFCIWK 230

RESULT 50

PCT-US95-10579-7

Sequence 7, Application PC/TUS9510579

GENERAL INFORMATION:

APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION

TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINE/GABA

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

```
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/
/  ZIP: 10036
/  COMPUTER READABLE FORM:
/  MEDIUM TYPE: Floppy disk
/  COMPUTER: IBM PC compatible
/  OPERATING SYSTEM: PC-DOS/MS-DOS
/  SOFTWARE: PatentIn Release #1.24
/  CURRENT APPLICATION DATA:
/  APPLICATION NUMBER: PCT/US95/10579
/  FILING DATE:
/  CLASSIFICATION:
/  ATTORNEY/AGENT INFORMATION:
/  NAME: White, John P.
/  REGISTRATION NUMBER: 28,678
/  REFERENCE/DOCKET NUMBER: 42897-A-PCT/JPW/MAT
/  TELECOMMUNICATION INFORMATION:
/  TELEPHONE: (212) 278-0400
/  TELEFAX: (212) 391-0525
/  INFORMATION FOR SEQ ID NO: 7:
/  SEQUENCE CHARACTERISTICS:
/  LENGTH: 614 amino acids
/  TYPE: amino acid
/  TOPOLOGY: linear
/  MOLECULE TYPE: protein
PCT-US95-10579-7

Query Match      55.0%; Score 44; DB 4; Length 614;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CYCFCWK 8
Db      224 CYFCIWK 230
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Search completed: May 9, 2006, 12:09:16
Job time : 18.6667 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:10:26 ; Search time 99.3333 Seconds
(without alignments)
46.270 Million cell updates/sec

Title: US-10-796-158-5
Perfect score: 80
Sequence: 1 YCYCFWKVCT 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA Main.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	11	5	US-10-796-158-5
2	64	80.0	11	5	US-10-796-158-6
3	64	80.0	15	5	US-10-490-326-25
4	64	80.0	20	5	US-10-490-326-27
5	64	80.0	20	5	US-10-490-326-37
6	64	80.0	20	5	US-10-490-326-38
7	64	80.0	20	5	US-10-490-326-45
8	64	80.0	22	5	US-10-490-326-22
9	64	80.0	25	5	US-10-490-326-43
10	64	80.0	25	5	US-10-490-326-46
11	64	80.0	30	5	US-10-490-326-44
12	62.5	78.1	11	5	US-10-796-158-7
13	59	73.8	12	5	US-10-490-326-24
14	55	68.8	12	5	US-10-490-326-30
15	55	68.8	12	5	US-10-490-326-31
16	55	68.8	12	5	US-10-490-326-32
17	55	68.8	12	5	US-10-490-326-41
18	55	68.8	12	5	US-10-490-326-21
19	55	68.8	15	5	US-10-490-326-23
20	55	68.8	15	5	US-10-490-326-35
21	55	68.8	15	5	US-10-490-326-36
22	55	68.8	15	5	US-10-490-326-47
23	55	68.8	15	5	US-10-490-326-48
24	55	68.8	15	5	US-10-490-326-49
25	55	68.8	15	5	US-10-490-326-51
26	55	68.8	15	5	US-10-490-326-52
27	55	68.8	15	5	US-10-490-326-53

28	55	68.8	15	5	US-10-490-326-55	Sequence 55, Appl
29	55	68.8	16	5	US-10-490-326-50	Sequence 50, Appl
30	55	68.8	16	5	US-10-490-326-54	Sequence 54, Appl
31	55	68.8	18	5	US-10-490-326-56	Sequence 56, Appl
32	55	68.8	19	5	US-10-490-326-26	Sequence 26, Appl
33	55	68.8	19	5	US-10-490-326-58	Sequence 58, Appl
34	55	68.8	20	5	US-10-490-326-40	Sequence 40, Appl
35	55	68.8	21	5	US-10-490-326-29	Sequence 29, Appl
36	55	68.8	21	5	US-10-490-326-39	Sequence 39, Appl
37	55	68.8	22	5	US-10-490-326-57	Sequence 57, Appl
38	53	66.2	8	3	US-09-781-980-5	Sequence 5, Appl
39	53	66.2	8	3	US-10-818-246-1	Sequence 1, Appl
40	53	66.2	8	5	US-10-473-721A-15	Sequence 15, Appl
41	53	66.2	8	5	US-10-473-721A-16	Sequence 16, Appl
42	53	66.2	8	5	US-10-916-522A-4	Sequence 4, Appl
43	53	66.2	8	5	US-10-505-239-12	Sequence 12, Appl
44	53	66.2	9	6	US-11-006-071-7	Sequence 7, Appl
45	52	65.0	14	4	US-10-258-766A-1	Sequence 1, Appl
46	52	65.0	14	4	US-10-258-766A-6	Sequence 6, Appl
47	52	65.0	14	4	US-10-258-766A-7	Sequence 7, Appl
48	52	65.0	14	4	US-10-258-766A-8	Sequence 8, Appl
49	52	65.0	14	4	US-10-258-766A-13	Sequence 13, Appl
50	52	65.0	14	4	US-10-258-766A-14	Sequence 14, Appl
51	50	62.5	7	5	US-10-490-326-34	Sequence 34, Appl
52	50	62.5	7	5	US-10-796-158-4	Sequence 4, Appl
53	50	62.5	8	3	US-09-781-980-6	Sequence 6, Appl
54	50	62.5	9	4	US-10-427-160A-22	Sequence 22, Appl
55	50	62.5	9	4	US-10-444-853A-515	Sequence 515, App
56	50	62.5	9	5	US-10-780-447-22	Sequence 22, Appl
57	50	62.5	9	5	US-10-757-803-515	Sequence 515, App
58	50	62.5	9	5	US-10-826-966-515	Sequence 515, App
59	50	62.5	15	5	US-10-490-326-42	Sequence 42, Appl
60	49	61.3	21	4	US-10-058-053A-234	Sequence 234, App
61	49	61.3	21	4	US-10-838-226-234	Sequence 234, App
62	49	61.3	40	4	US-10-058-053A-231	Sequence 231, App
63	49	61.3	40	4	US-10-838-226-231	Sequence 231, App
64	49	61.3	78	4	US-10-424-599-150178	Sequence 150178, A
65	49	61.3	93	4	US-10-058-053A-116	Sequence 116, App
66	49	61.3	93	4	US-10-838-226-116	Sequence 116, App
67	48	60.0	7	5	US-10-775-180-845	Sequence 845, App
68	48	60.0	9	3	US-09-758-128-2	Sequence 2, Appl
69	48	60.0	9	3	US-09-758-426-2	Sequence 2, Appl
70	48	60.0	9	3	US-09-758-198-2	Sequence 2, Appl
71	48	60.0	9	3	US-09-861-661-2	Sequence 2, Appl
72	48	60.0	58	4	US-10-424-599-222430	Sequence 222430, A
73	48	60.0	240	5	US-10-450-763-50712	Sequence 50712, A
74	47	58.8	7	4	US-10-258-766A-5	Sequence 5, Appl
75	47	58.8	7	4	US-10-258-766A-10	Sequence 10, Appl
76	47	58.8	7	4	US-10-258-766A-12	Sequence 12, Appl
77	47	58.8	45	4	US-10-058-053A-280	Sequence 280, App
78	47	58.8	45	4	US-10-838-226-280	Sequence 280, App
79	47	58.8	95	4	US-10-058-053A-89	Sequence 89, Appl
80	47	58.8	95	4	US-10-838-226-89	Sequence 89, Appl
81	47	58.8	123	3	US-09-864-761-45509	Sequence 45509, A
82	46	57.5	8	3	US-09-758-128-3	Sequence 3, Appl
83	46	57.5	8	3	US-09-758-426-3	Sequence 3, Appl
84	46	57.5	8	3	US-09-758-198-3	Sequence 3, Appl
85	46	57.5	8	3	US-09-861-661-3	Sequence 3, Appl
86	45	56.2	6	5	US-10-916-522A-2	Sequence 2, Appl
87	45	56.2	6	5	US-10-490-326-33	Sequence 33, Appl
88	45	56.2	7	3	US-09-758-128-1	Sequence 1, Appl
89	45	56.2	7	3	US-09-758-426-1	Sequence 1, Appl
90	45	56.2	7	3	US-09-758-198-1	Sequence 1, Appl
91	45	56.2	7	3	US-09-861-661-1	Sequence 1, Appl
92	45	56.2	8	5	US-10-399-542-5	Sequence 5, Appl
93	45	56.2	34	4	US-10-036-869-15	Sequence 15, Appl
94	45	56.2	62	3	US-09-764-855-136	Sequence 136, App
95	45	56.2	62	4	US-10-072-349-136	Sequence 136, App
96	45	56.2	288	4	US-10-060-311-3	Sequence 3, Appl
97	45	56.2	288	4	US-10-778-300-3	Sequence 3, Appl
98	45	56.2	288	6	US-11-013-907-3	Sequence 3, Appl
99	45	56.2	454	4	US-10-060-311-2	Sequence 2, Appl
100	45	56.2	454	4	US-10-778-300-2	Sequence 2, Appl

977 40 50.0 445 4 US-10-202-471-148 Sequence 148, App
 978 40 50.0 445 4 US-10-207-915-148 Sequence 148, App
 979 40 50.0 445 4 US-10-219-538-177 Sequence 177, App
 980 40 50.0 445 4 US-10-197-709-148 Sequence 148, App
 981 40 50.0 445 4 US-10-206-915-148 Sequence 148, App
 982 40 50.0 445 4 US-10-199-670-148 Sequence 148, App
 983 40 50.0 445 4 US-10-201-858-148 Sequence 148, App
 984 40 50.0 445 4 US-10-205-890-148 Sequence 148, App
 985 40 50.0 445 4 US-10-208-024-148 Sequence 148, App
 986 40 50.0 445 4 US-10-201-853-148 Sequence 148, App
 987 40 50.0 445 4 US-10-063-745-32 Sequence 32, Appl
 988 40 50.0 445 4 US-10-206-916-148 Sequence 148, App
 989 40 50.0 445 5 US-10-972-317-32 Sequence 32, Appl
 990 40 50.0 445 5 US-10-183-001-148 Sequence 148, App
 991 40 50.0 445 5 US-10-950-374-177 Sequence 177, App
 992 40 50.0 445 5 US-10-175-749-148 Sequence 148, App
 993 40 50.0 445 5 US-10-180-554-148 Sequence 148, App
 994 40 50.0 621 3 US-09-845-908-6 Sequence 6, Appl
 995 40 50.0 640 4 US-10-437-963-110124 Sequence 110124,
 996 40 50.0 653 4 US-10-062-937B-5 Sequence 5, Appl
 997 40 50.0 653 4 US-10-391-399-73 Sequence 73, Appl
 998 40 50.0 790 4 US-10-437-963-180919 Sequence 180919,
 999 40 50.0 1456 4 US-10-437-963-180908 Sequence 180908,
 1000 40 50.0 1546 4 US-10-437-963-180917 Sequence 180917,

ALIGNMENTS

RESULT 1
 US-10-796-158-5
 ; Sequence 5, Application US/10796158
 ; Publication No. US20050118099A1
 ; GENERAL INFORMATION:
 ; APPLICANT: IDEC Pharmaceuticals
 ; APPLICANT: Braslawsky, Gary
 ; APPLICANT: Chinn, Paul
 ; APPLICANT: Hanna, Nabil
 ; TITLE OF INVENTION: THIOL-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
 ; FILE REFERENCE: 037003-0308678
 ; CURRENT APPLICATION NUMBER: US/10/796,158
 ; CURRENT FILING DATE: 2004-03-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic SST analog
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (1)..(4)
 ; OTHER INFORMATION: D stereoisomer
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (11)..(11)
 ; OTHER INFORMATION: AMIDATION OR ALCOHOL
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (11)..(11)
 ; OTHER INFORMATION: AMIDE OR ALCOHOL
 ; FEATURE:
 ; NAME/KEY: DISULFID
 ; LOCATION: (5)..(10)
 ; OTHER INFORMATION:
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (7)..(7)
 ; OTHER INFORMATION: D stereoisomer
 ; US-10-796-158-5
 Query Match 100.0%; Score 80; DB 5; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00083;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YCYCFWKTKT 11
 |||||
 Db 1 YCYCFWKTKT 11
 |||||
 RESULT 2
 US-10-796-158-6
 ; Sequence 6, Application US/10796158
 ; Publication No. US20050118099A1
 ; GENERAL INFORMATION:
 ; APPLICANT: IDEC Pharmaceuticals
 ; APPLICANT: Braslawsky, Gary
 ; APPLICANT: Chinn, Paul
 ; APPLICANT: Hanna, Nabil
 ; TITLE OF INVENTION: THIOL-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
 ; FILE REFERENCE: 037003-0308678
 ; CURRENT APPLICATION NUMBER: US/10/796,158
 ; CURRENT FILING DATE: 2004-03-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic SST analog
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (1)..(4)
 ; OTHER INFORMATION: D stereoisomer
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (7)..(7)
 ; OTHER INFORMATION: D stereoisomer
 ; FEATURE:
 ; NAME/KEY: DISULFID
 ; LOCATION: (5)..(10)
 ; OTHER INFORMATION:
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (11)..(11)
 ; OTHER INFORMATION: AMIDE OR ALCOHOL
 ; US-10-796-158-6
 Query Match 80.0%; Score 64; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.093;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 YCYCFWKTKT 11
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 Db 3 YCYCFWKTKT 11
 |||||
 RESULT 3
 US-10-490-326-25
 ; Sequence 25, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; Bombesin Analog Conjugates and Uses Thereof
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851

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; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-25

Query Match      80.0%; Score 64; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 YYCFWKTCCT 11
Db      7 YYCFWKTCCT 15

RESULT 4
US-10-490-326-27
; Sequence 27, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
US-10-490-326-27

Query Match      80.0%; Score 64; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 YYCFWKTCCT 11
Db      7 YYCFWKTCCT 15

RESULT 5
US-10-490-326-37
; Sequence 37, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
US-10-490-326-37

Query Match      80.0%; Score 64; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 YYCFWKTCCT 11
Db      7 YYCFWKTCCT 15

RESULT 6
US-10-490-326-38
; Sequence 38, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 14, 19
; OTHER INFORMATION: Cys at positions 14 and 19 are circularized
US-10-490-326-38

Query Match      80.0%; Score 64; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 YYCFWKTCCT 11
Db      12 YYCFWKTCCT 20

RESULT 7
US-10-490-326-45
; Sequence 45, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
```

APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: 14_19
OTHER INFORMATION: Cys at positions 14 and 19 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-45

Query Match 80.0%; Score 64; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0

Qy 3 YYCFWKTC 11
Db 12 YYCFWKTC 20

RESULT 8
US-10-490-326-22
Sequence 22, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: 16_21
OTHER INFORMATION: Cys at positions 16 and 21 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-22

Query Match 80.0%; Score 64; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0

Qy 3 YYCFWKTC 11
Db 14 YYCFWKTC 22

RESULT 9
US-10-490-326-43
Sequence 43, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: 19_24
OTHER INFORMATION: Cys at positions 19 and 24 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-43

Query Match 80.0%; Score 64; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0

Qy 3 YYCFWKTC 11
Db 17 YYCFWKTC 25

RESULT 10
US-10-490-326-46
Sequence 46, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: 19_24
OTHER INFORMATION: Cys at positions 19 and 24 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-46

Query Match 80.0%; Score 64; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0

Qy 3 YYCFWKTC 11
Db 14 YYCFWKTC 22

US-10-490-326-46

Query Match 80.0%; Score 64; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YCYCFWKTCCT 11
| | | | | | | | | |
Db 17 YCYCFWKTCCT 25

RESULT 11

US-10-490-326-44
; Sequence 44, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 24, 29
; OTHER INFORMATION: Cys at positions 24 and 29 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-44

Query Match 80.0%; Score 64; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YCYCFWKTCCT 11
| | | | | | | | | |
Db 22 YCYCFWKTCCT 30

RESULT 12

US-10-796-158-7
; Sequence 7, Application US/10796158
; Publication No. US20050118099A1
; GENERAL INFORMATION:
; APPLICANT: IDEC Pharmaceuticals
; APPLICANT: Braslawsky, Gary
; APPLICANT: Chinn, Paul
; APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: THIOL-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
; FILE REFERENCE: 037003-0308678
; CURRENT APPLICATION NUMBER: US/10/796,158
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic SST analog

; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: D stereoisomer
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: D stereoisomer
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (5)..(10)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDE OR ALCOHOL
US-10-796-158-7

Query Match 78.1%; Score 62.5; DB 5; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 YCYCFWKTCCT 11
| | | | | | | | | |
Db 2 YCYCFWKTCCT 11

RESULT 13

US-10-490-326-24
; Sequence 24, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-24

Query Match 73.8%; Score 59; DB 5; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYCFWKTCCT 11
| | | | | | | | | |
Db 2 YKYCFWKTCCT 12

RESULT 14

US-10-490-326-30
; Sequence 30, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun

; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; TITLE OF INVENTION: Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa = Sar
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 6, 11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-490-326-30

Query Match 68.8%; Score 55; DB 5; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKT 11
| | | | |
Db 4 YSCFWKTKT 12

RESULT 15
US-10-490-326-31
; Sequence 31, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fusellier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; TITLE OF INVENTION: Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 6, 11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-490-326-31

Query Match 68.8%; Score 55; DB 5; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKT 11
| | | | |
Db 4 YSCFWKTKT 12

RESULT 16
US-10-490-326-32
; Sequence 32, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fusellier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; TITLE OF INVENTION: Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa = OH-Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 6, 11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-490-326-32

Query Match 68.8%; Score 55; DB 5; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKT 11
| | | | |
Db 4 YSCFWKTKT 12

RESULT 17
US-10-490-326-41
; Sequence 41, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fusellier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; TITLE OF INVENTION: Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; US-10-490-326-41

;; PRIOR FILING DATE: 2002-09-20
;; PRIOR APPLICATION NUMBER: 60/323,851
;; PRIOR FILING DATE: 2001-09-21
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 41
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: VARIANT
;; LOCATION: 1
;; OTHER INFORMATION: Xaa = Sar
;; NAME/KEY: VARIANT
;; LOCATION: 3
;; OTHER INFORMATION: Xaa = Nle
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-490-326-41

Query Match 68.8%; Score 55; DB 5; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTCT 11
| | | | |
Db 4 YSCFWKTCT 12

RESULT 18
US-10-490-326-21
;; Sequence 21, Application US/10490326
;; Publication No. US20050070470A1
;; GENERAL INFORMATION:
;; APPLICANT: Coy, David H.
;; APPLICANT: Fuselier, Joseph A.
;; APPLICANT: Murphy, William A.
;; APPLICANT: Sun, Lichun
;; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
;; Bombesin Analog Conjugates and Uses Thereof
;; FILE REFERENCE: 07005/005002
;; CURRENT APPLICATION NUMBER: US/10/490,326
;; CURRENT FILING DATE: 2004-03-19
;; PRIOR APPLICATION NUMBER: PCT/US02/30143
;; PRIOR FILING DATE: 2002-09-20
;; PRIOR APPLICATION NUMBER: 60/323,851
;; PRIOR FILING DATE: 2001-09-21
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 21
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: VARIANT
;; LOCATION: 6
;; OTHER INFORMATION: Xaa = Nle
;; NAME/KEY: MOD RES
;; LOCATION: 9, 14
;; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-490-326-21

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTCT 11
| | | | |
Db 7 YSCFWKTCT 15

RESULT 19
US-10-490-326-23
;; Sequence 23, Application US/10490326
;; Publication No. US20050070470A1
;; GENERAL INFORMATION:
;; APPLICANT: Coy, David H.
;; APPLICANT: Fuselier, Joseph A.
;; APPLICANT: Murphy, William A.
;; APPLICANT: Sun, Lichun
;; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
;; Bombesin Analog Conjugates and Uses Thereof
;; FILE REFERENCE: 07005/005002
;; CURRENT APPLICATION NUMBER: US/10/490,326
;; CURRENT FILING DATE: 2004-03-19
;; PRIOR APPLICATION NUMBER: PCT/US02/30143
;; PRIOR FILING DATE: 2002-09-20
;; PRIOR APPLICATION NUMBER: 60/323,851
;; PRIOR FILING DATE: 2001-09-21
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 23
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: MOD RES
;; LOCATION: 9, 14
;; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-490-326-23

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTCT 11
| | | | |
Db 7 YSCFWKTCT 15

RESULT 20
US-10-490-326-35
;; Sequence 35, Application US/10490326
;; Publication No. US20050070470A1
;; GENERAL INFORMATION:
;; APPLICANT: Coy, David H.
;; APPLICANT: Fuselier, Joseph A.
;; APPLICANT: Murphy, William A.
;; APPLICANT: Sun, Lichun
;; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
;; Bombesin Analog Conjugates and Uses Thereof
;; FILE REFERENCE: 07005/005002
;; CURRENT APPLICATION NUMBER: US/10/490,326
;; CURRENT FILING DATE: 2004-03-19
;; PRIOR APPLICATION NUMBER: PCT/US02/30143
;; PRIOR FILING DATE: 2002-09-20
;; PRIOR APPLICATION NUMBER: 60/323,851
;; PRIOR FILING DATE: 2001-09-21
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 35
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: VARIANT
;; LOCATION: 6
;; OTHER INFORMATION: Xaa = Nle
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-490-326-35

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 7 YSCFWKTKCT 15

RESULT 21

US-10-490-326-36
; Sequence 36, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD_RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-36

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 7 YSCFWKTKCT 15

RESULT 22

US-10-490-326-47
; Sequence 47, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 47
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa = 4Pal
; NAME/KEY: MOD_RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-47

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 7 YSCFWKTKCT 15

RESULT 23

US-10-490-326-48
; Sequence 48, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-48

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 7 YSCFWKTKCT 15

RESULT 24

US-10-490-326-49
; Sequence 49, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.

APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or Bombesin Analog Conjugates and Uses Thereof
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: 9, 14
OTHER INFORMATION: Cys at positions 9 and 14 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-49

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSCFWKTCT 11
| | | | |
Db 7 YSCFWKTCT 15

RESULT 25
US-10-490-326-51
Sequence 51, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or Bombesin Analog Conjugates and Uses Thereof
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: 9, 14
OTHER INFORMATION: Cys at positions 9 and 14 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-51

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSCFWKTCT 11
| | | | |
Db 7 YSCFWKTCT 15

RESULT 26
US-10-490-326-52
Sequence 52, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or Bombesin Analog Conjugates and Uses Thereof
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: 6
OTHER INFORMATION: Xaa = Abu
NAME/KEY: MOD_RES
LOCATION: 9, 14
OTHER INFORMATION: Cys at positions 9 and 14 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-52

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSCFWKTCT 11
| | | | |
Db 7 YSCFWKTCT 15

RESULT 27
US-10-490-326-53
Sequence 53, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or Bombesin Analog Conjugates and Uses Thereof
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: 9, 14
OTHER INFORMATION: Cys at positions 9 and 14 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-53

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
,
;
; OTHER INFORMATION: Synthetic
US-10-490-326-53

Query Match      68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 YYCFWKTCCT 11
Db      7 YSCFWKTCCT 15

RESULT 28
US-10-490-326-55
; Sequence 55, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa = hSer
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at position 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-55

Query Match      68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 YYCFWKTCCT 11
Db      7 YSCFWKTCCT 15

RESULT 29
US-10-490-326-50
; Sequence 50, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 10, 15
; OTHER INFORMATION: Cys at positions 10 and 15 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-54

Query Match      68.8%; Score 55; DB 5; Length 16;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 YYCFWKTCCT 11
Db      8 YSCFWKTCCT 16

RESULT 30
US-10-490-326-54
; Sequence 54, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 10, 15
; OTHER INFORMATION: Cys at positions 10 and 15 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-54

Query Match      68.8%; Score 55; DB 5; Length 16;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 YYCFWKTCCT 11
Db      8 YSCFWKTCCT 16

RESULT 31
US-10-490-326-56
; Sequence 56, Application US/10490326
; Publication No. US20050070470A1
```

GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 9
; OTHER INFORMATION: Xaa = 4Pal
; NAME/KEY: MOD RES
; LOCATION: 12_17
; OTHER INFORMATION: Cys at positions 12 and 17 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-56

Query Match 68.8%; Score 55; DB 5; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSCFWKTCT 11
Db 10 YSCFWKTCT 18

RESULT 32
US-10-490-326-26
; Sequence 26, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-26

Query Match 68.8%; Score 55; DB 5; Length 19;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSCFWKTCT 11

Db 11 YSCFWKTCT 19

RESULT 33
US-10-490-326-58
; Sequence 58, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Abu
; NAME/KEY: MOD RES
; LOCATION: 13_18
; OTHER INFORMATION: Cys at positions 13 and 18 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-58

Query Match 68.8%; Score 55; DB 5; Length 19;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSCFWKTCT 11
Db 11 YSCFWKTCT 19

RESULT 34
US-10-490-326-40
; Sequence 40, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
US-10-490-326-40

```

; NAME/KEY: VARIANT
; LOCATION: 11
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 14, 19
; OTHER INFORMATION: Cys at positions 14 and 19 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-40

```

```

Query Match      68.8%; Score 55; DB 5; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

```

```

Qy 3 YYCFWKTKCT 11
   | | | | |
Db 12 YSCFWKTKCT 20

```

```

RESULT 35
US-10-490-326-29
; Sequence 29, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 12
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 15, 20
; OTHER INFORMATION: Cys at positions 15 and 20 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-29

```

```

Query Match      68.8%; Score 55; DB 5; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

```

```

Qy 3 YYCFWKTKCT 11
   | | | | |
Db 13 YSCFWKTKCT 21

```

```

RESULT 36
US-10-490-326-39
; Sequence 39, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or

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; TITLE OF INVENTION: Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 12
; OTHER INFORMATION: Xaa = Nle
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-39

```

```

Query Match      68.8%; Score 55; DB 5; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

```

```

Qy 3 YYCFWKTKCT 11
   | | | | |
Db 13 YSCFWKTKCT 21

```

```

RESULT 37
US-10-490-326-57
; Sequence 57, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 13
; OTHER INFORMATION: Xaa = Nva
; NAME/KEY: MOD RES
; LOCATION: 16, 21
; OTHER INFORMATION: Cys at positions 16 and 21 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-57

```

```

Query Match      68.8%; Score 55; DB 5; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

```

```

Qy 3 YYCFWKTKCT 11
   | | | | |
Db 14 YSCFWKTKCT 22

```

RESULT 38
US-09-781-980-5
; Sequence 5, Application US/09781980
; Publication No. US20010029035A1
; GENERAL INFORMATION:
; APPLICANT: EISENHUT, MICHAEL
; APPLICANT: MIER, WALTER
; APPLICANT: ERITJA, RAMON
; APPLICANT: HABERKORN, UWE
; TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
; FILE REFERENCE: 2502498.991110
; CURRENT APPLICATION NUMBER: US/09/781,980
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: DE 100 06 572
; PRIOR FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-781-980-5

Query Match 66.2%; Score 53; DB 3; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
Db 1 FCFWKTCCT 8

RESULT 39
US-10-818-246-1
; Sequence 1, Application US/10818246
; Publication No. US20040249121A1
; GENERAL INFORMATION:
; APPLICANT: Novetide, Ltd.
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF CYCLIC PEPTIDES
; FILE REFERENCE: 12647/46002
; CURRENT APPLICATION NUMBER: US/10/818,246
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: 60/461,222
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-818-246-1

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
Db 1 FCFWKTCCT 8

RESULT 40
US-10-473-721A-15
; Sequence 15, Application US/10473721A
; Publication No. US2005004000A1
; GENERAL INFORMATION:

; APPLICANT: SHECHTER, Yoram
; APPLICANT: GOLDWASER, Itzhak
; APPLICANT: LAVON, Iris
; APPLICANT: BRODIE, David
; APPLICANT: EYAL, Nurit
; APPLICANT: FASS, Stanley
; APPLICANT: FRIDKIN, Matityahu
; TITLE OF INVENTION: ORAL ABSORBED DRUGS
; FILE REFERENCE: SHECTERS
; CURRENT APPLICATION NUMBER: US/10/473,721A
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/IL02/00252
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: IL 142353
; PRIOR FILING DATE: 2001-04-01
; PRIOR APPLICATION NUMBER: IL 146383
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(8)
; OTHER INFORMATION: Cyclic eight-amino acid peptide. Phe (residue 1) is D-Phe. Trp (residue 4) is D-Trp. Thr (residue 8) is Thr-O-acetate.
; OTHER INFORMATION: (residue 4) is D-Trp. Thr (residue 8) is Thr-O-acetate.
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (2)-(7)
; OTHER INFORMATION: Disulfide bond between the two Cys amino acid residues.
US-10-473-721A-15

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
Db 1 FCFWKTCCT 8

RESULT 41
US-10-473-721A-16
; Sequence 16, Application US/10473721A
; Publication No. US2005004000A1
; GENERAL INFORMATION:
; APPLICANT: SHECHTER, Yoram
; APPLICANT: GOLDWASER, Itzhak
; APPLICANT: LAVON, Iris
; APPLICANT: BRODIE, David
; APPLICANT: EYAL, Nurit
; APPLICANT: FASS, Stanley
; APPLICANT: FRIDKIN, Matityahu
; TITLE OF INVENTION: ORAL ABSORBED DRUGS
; FILE REFERENCE: SHECTERS
; CURRENT APPLICATION NUMBER: US/10/473,721A
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/IL02/00252
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: IL 142353
; PRIOR FILING DATE: 2001-04-01
; PRIOR APPLICATION NUMBER: IL 146383
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial

```
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(8)
; OTHER INFORMATION: Cyclic eight-amino acid peptide. Phe (residue 1) is D-Phe. Trp
; OTHER INFORMATION: (residue 4) is D-Trp. Lys (residue 5) is N-Fmoc-Lys or N-Fms-Lys
; OTHER INFORMATION: Thr (residue 8) is Thr-O-acetate.
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; OTHER INFORMATION: Disulfide bond between the two Cys amino acid groups.
US-10-473-721A-16

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTKT 11
DB 1 FCFWKTKT 8

RESULT 42
US-10-916-522A-4
; Sequence 4, Application US/10916522A
; Publication No. US20050043226A1
; GENERAL INFORMATION:
; APPLICANT: Hornik, Vared
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOG
; FILE REFERENCE: 87534-3059
; CURRENT APPLICATION NUMBER: US/10/916,522A
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 09/734,593
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Phe residue is a D isomer
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: The Thr residue ends with CH2OH
; FEATURE:
; NAME/KEY: DISULFIDE BRIDGE
; LOCATION: (2)..(2)
; OTHER INFORMATION: A disulfide bridge is formed between Cys residues 2 and 7
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: The Trp residue is a D isomer
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-916-522A-4

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTKT 11
DB 1 FCFWKTKT 8

RESULT 43
US-10-505-239-12
; Sequence 12, Application US/10505239
```

```
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(8)
; OTHER INFORMATION: wherein the peptide is carboxylated at either the N-or C-
; OTHER INFORMATION: terminus
US-10-505-239-12

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTKT 11
DB 1 FCFWKTKT 8

RESULT 44
US-11-006-071-7
; Sequence 7, Application US/11006071
; Publication No. US2005029275A1
; GENERAL INFORMATION:
; APPLICANT: Koprowski, Hilary
; APPLICANT: Yusibov, Vidadi
; TITLE OF INVENTION: Production Of Biomedical Peptides And Proteins In
; TITLE OF INVENTION: Plants Using Plant Virus Vectors
; FILE REFERENCE: JEPF-KOP01.P0001
; CURRENT APPLICATION NUMBER: US/11/006,071
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US/09/673,174
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/118,867
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: PCT/US99/25566
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A peptide to
; OTHER INFORMATION: suppress the synthesis of human growth hormone
US-11-006-071-7

Query Match 66.2%; Score 53; DB 6; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy 4 YCFWKTKT 11
:|||||
Db 2 FCFWKTKT 9

RESULT 45
US-10-258-766A-1
; Sequence 1, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosynthema, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816.17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Arg (Pmc)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: Asp (OtBu)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Dtyr (OtBu)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Asp (beta-Oall)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: Lys (Mct)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Dphe
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Cys (Acm)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: Tyr (OtBu)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: DTrp (tBoc)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: Lys (tBoc)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (12)..(12)
; OTHER INFORMATION: Thr (OtBu)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: Cys (Acm)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (14)..(14)

; OTHER INFORMATION: Thr (OtBu) -O-RESIN
US-10-258-766A-1
Query Match 65.0%; Score 52; DB 4; Length 14;
Best Local Similarity 63.6%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYVCFWKTKT 11
:|||||
Db 4 YDKFCYWKTKT 14

RESULT 46
US-10-258-766A-6
; Sequence 6, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosynthema, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816.17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: DISULPID
; LOCATION: (8)..(13)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Amide bond between residues 1 and 5
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Dtyr
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Dphe
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: DTrp
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Thr-OH
US-10-258-766A-6
Query Match 65.0%; Score 52; DB 4; Length 14;
Best Local Similarity 63.6%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYVCFWKTKT 11
:|||||
Db 4 YDKFCYWKTKT 14

RESULT 47
US-10-258-766A-7
; Sequence 7, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosynthema, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816.17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25

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; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)..(13)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Amide bond between residues 1 and 5
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: DTyr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: NH-DTPA
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: DPhe
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: DTrp
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Thr-OH
US-10-258-766A-7
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```
Query Match 65.0%; Score 52; DB 4; Length 14;
Best Local Similarity 63.6%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 YCYFCFWKTCCT 11
| : : : :
Db 4 YDKFCYWKTCCT 14
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RESULT 48
US-10-258-766A-8
; Sequence 8, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosynthesma, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816.17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Arg (Pmc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: DTyr (OtBu)
; NAME/KEY: MOD_RES
```

```
; LOCATION: (5)..(5)
; OTHER INFORMATION: Asp (beta-Oall)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: Lys (Mtt)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: DPhe
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Cys (Acm)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: Tyr (OtBu)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: DTrp (tBoc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: Lys (tBoc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)..(12)
; OTHER INFORMATION: Thr (OtBu)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: Cys (Acm)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Thr (ol) (OtBu) -O-RESIN
US-10-258-766A-8
```

```
Query Match 65.0%; Score 52; DB 4; Length 14;
Best Local Similarity 63.6%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 YCYFCFWKTCCT 11
| : : : :
Db 4 YDKFCYWKTCCT 14
```

```
RESULT 49
US-10-258-766A-13
; Sequence 13, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosynthesma, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816.17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: DTyr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: DPhe
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November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications New databases older published applications make up the Published Applications Main database.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions **.rnpbm** (Published Applications NA Main) and **.rnpbn** (Published Applications NA New). Searches run against Amino Acid Published Applications produce two sets of results, with the extensions **.rapbm** (Published Applications AA Main) and **.rapbn** (Published Applications AA New).

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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:10:45 ; Search time 10 Seconds
(without alignments)
50.913 Million cell updates/sec

Title: US-10-796-158-5

Perfect score: 80

Sequence: 1 YCYCFWKCT 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA_New*

1: /SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /SIDSS5/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS5/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS5/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
7: /SIDSS5/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
8: /SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
10: /SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
11: /SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
12: /SIDSS5/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	68.8	12	9	US-10-506-223-16
2	55	68.8	12	9	US-10-506-223-17
3	55	68.8	12	9	US-10-506-223-39
4	55	68.8	12	9	US-10-506-223-40
5	55	68.8	13	9	US-10-506-223-21
6	55	68.8	13	9	US-10-506-223-22
7	55	68.8	14	9	US-10-506-223-23
8	55	68.8	15	9	US-10-506-223-24
9	55	68.8	16	9	US-10-506-223-25
10	55	68.8	17	9	US-10-506-223-26
11	55	68.8	18	9	US-10-506-223-27
12	55	68.8	19	9	US-10-506-223-28
13	55	68.8	20	9	US-10-506-223-29
14	55	68.8	21	9	US-10-506-223-30
15	55	68.8	22	9	US-10-506-223-31
16	55	68.8	23	9	US-10-506-223-32
17	55	68.8	24	9	US-10-506-223-33
18	55	68.8	25	9	US-10-506-223-34
19	55	68.8	26	9	US-10-506-223-35
20	55	68.8	27	9	US-10-506-223-36
21	53	66.2	8	9	US-10-626-719-158
					Sequence 16, Appl
					Sequence 17, Appl
					Sequence 39, Appl
					Sequence 40, Appl
					Sequence 21, Appl
					Sequence 22, Appl
					Sequence 23, Appl
					Sequence 24, Appl
					Sequence 25, Appl
					Sequence 26, Appl
					Sequence 27, Appl
					Sequence 28, Appl
					Sequence 29, Appl
					Sequence 30, Appl
					Sequence 31, Appl
					Sequence 32, Appl
					Sequence 33, Appl
					Sequence 34, Appl
					Sequence 35, Appl
					Sequence 36, Appl
					Sequence 158, Appl

22	50	62.5	8	9	US-10-626-719-159	Sequence 159, App
23	49	61.3	21	11	US-11-198-847-234	Sequence 234, App
24	49	61.3	40	11	US-11-198-847-231	Sequence 231, App
25	49	61.3	93	11	US-11-198-847-116	Sequence 116, App
26	48	60.0	8	9	US-10-626-719-156	Sequence 156, App
27	47	58.8	45	11	US-11-198-847-280	Sequence 280, App
28	47	58.8	95	11	US-11-198-847-89	Sequence 89, Appl
29	45	56.2	6	9	US-10-506-223-37	Sequence 37, Appl
30	45	56.2	6	9	US-10-506-223-38	Sequence 38, Appl
31	45	56.2	8	9	US-10-626-719-157	Sequence 157, App
32	44	55.0	10	11	US-11-198-847-322	Sequence 322, App
33	44	55.0	21	11	US-11-198-847-232	Sequence 232, App
34	44	55.0	21	11	US-11-198-847-233	Sequence 233, App
35	44	55.0	40	11	US-11-198-847-229	Sequence 229, App
36	44	55.0	40	11	US-11-198-847-230	Sequence 230, App
37	44	55.0	93	11	US-11-198-847-32	Sequence 32, Appl
38	44	55.0	93	11	US-11-198-847-41	Sequence 41, Appl
39	44	55.0	285	11	US-11-043-004-1161	Sequence 1161, Ap
40	43	53.8	479	11	US-11-087-099-6677	Sequence 6677, Ap
41	43	53.8	479	11	US-11-188-298-17131	Sequence 17131, A
42	42	52.5	362	11	US-11-079-463-7253	Sequence 7253, Ap
43	41	51.2	9	11	US-11-198-847-316	Sequence 316, App
44	41	51.2	11	11	US-11-198-847-313	Sequence 313, App
45	41	51.2	15	11	US-11-198-847-311	Sequence 311, App
46	41	51.2	64	11	US-11-096-568A-8330	Sequence 8330, Ap
47	41	51.2	68	11	US-11-096-568A-8329	Sequence 8329, Ap
48	41	51.2	81	11	US-11-079-463-6337	Sequence 6337, Ap
49	40	50.0	7	9	US-10-626-719-160	Sequence 160, App
50	40	50.0	21	11	US-11-198-847-290	Sequence 290, App
51	40	50.0	26	11	US-11-198-847-303	Sequence 303, App
52	40	50.0	30	11	US-11-198-847-285	Sequence 285, App
53	40	50.0	30	11	US-11-198-847-286	Sequence 286, App
54	40	50.0	71	11	US-11-198-847-29	Sequence 29, Appl
55	40	50.0	71	11	US-11-198-847-110	Sequence 110, App
56	40	50.0	81	11	US-11-198-847-92	Sequence 92, Appl
57	40	50.0	81	11	US-11-198-847-95	Sequence 95, Appl
58	40	50.0	275	11	US-11-264-096-1910	Sequence 1910, Ap
59	40	50.0	275	11	US-11-264-096-1911	Sequence 1911, Ap
60	40	50.0	445	9	US-10-063-703-32	Sequence 32, Appl
61	40	50.0	445	9	US-10-194-487-148	Sequence 148, App
62	40	50.0	445	9	US-10-195-883-148	Sequence 148, App
63	40	50.0	445	9	US-10-195-888-148	Sequence 148, App
64	40	50.0	445	9	US-10-195-889-148	Sequence 148, App
65	40	50.0	445	11	US-11-102-240-32	Sequence 32, Appl
66	40	50.0	445	11	US-11-103-195-32	Sequence 32, Appl
67	40	50.0	648	11	US-10-330-773-825	Sequence 825, App
68	40	50.0	706	11	US-11-188-298-11676	Sequence 11676, A
69	39.5	49.4	64	11	US-11-264-096-454	Sequence 454, App
70	39	48.8	603	11	US-11-024-959-484	Sequence 484, App
71	39	48.8	2048	11	US-11-285-818-12	Sequence 12, Appl
72	39	48.8	2057	11	US-11-285-818-10	Sequence 10, Appl
73	39	48.8	2058	11	US-11-072-175-188	Sequence 188, App
74	39	48.8	2058	11	US-11-285-818-17	Sequence 17, Appl
75	38	47.5	6	9	US-10-532-452-9	Sequence 9, Appl
76	38	47.5	8	9	US-10-532-452-7	Sequence 7, Appl
77	38	47.5	10	11	US-11-198-847-320	Sequence 320, App
78	38	47.5	11	9	US-10-532-452-1	Sequence 1, Appl
79	38	47.5	12	9	US-10-875-800-7	Sequence 7, Appl
80	38	47.5	12	9	US-10-532-452-2	Sequence 2, Appl
81	38	47.5	12	9	US-10-532-452-3	Sequence 3, Appl
82	38	47.5	12	9	US-10-532-452-4	Sequence 4, Appl
83	38	47.5	12	9	US-10-532-452-6	Sequence 6, Appl
84	38	47.5	14	9	US-10-532-452-5	Sequence 5, Appl
85	38	47.5	14	9	US-10-532-452-8	Sequence 8, Appl
86	38	47.5	66	11	US-11-079-463-9692	Sequence 9692, Ap
87	38	47.5	119	11	US-11-072-512-2041	Sequence 2041, Ap
88	38	47.5	124	9	US-10-242-586-26	Sequence 26, Appl
89	38	47.5	124	9	US-10-242-902-26	Sequence 26, Appl
90	38	47.5	124	9	US-10-243-116-26	Sequence 26, Appl
91	38	47.5	124	9	US-10-243-136-26	Sequence 26, Appl
92	38	47.5	124	9	US-10-243-189-26	Sequence 26, Appl
93	38	47.5	124	9	US-10-243-215-26	Sequence 26, Appl
94	38	47.5	124	9	US-10-243-236-26	Sequence 26, Appl

971 31 38.8 662 11 US-11-072-512-3398 Sequence 3398, Ap
972 31 38.8 668 11 US-11-087-099-5101 Sequence 5101, Ap
973 31 38.8 669 9 US-10-501-941-8 Sequence 8, Appli
974 31 38.8 669 11 US-11-198-886-6 Sequence 6, Appli
975 31 38.8 673 11 US-10-055-877-321 Sequence 321, Ap
976 31 38.8 673 11 US-11-188-298-1612 Sequence 1612, Ap
977 31 38.8 674 9 US-10-055-877-319 Sequence 319, App
978 31 38.8 675 9 US-10-055-877-117 Sequence 117, App
979 31 38.8 675 9 US-10-055-877-317 Sequence 317, App
980 31 38.8 675 9 US-10-055-877-318 Sequence 318, App
981 31 38.8 675 9 US-10-455-772-912 Sequence 912, App
982 31 38.8 675 9 US-10-455-772-918 Sequence 918, App
983 31 38.8 675 11 US-11-188-298-14160 Sequence 14160, A
984 31 38.8 678 11 US-11-096-568A-27775 Sequence 27775, A
985 31 38.8 686 9 US-10-194-487-524 Sequence 524, App
986 31 38.8 686 9 US-10-195-883-524 Sequence 524, App
987 31 38.8 686 9 US-10-195-888-524 Sequence 524, App
988 31 38.8 686 9 US-10-195-889-524 Sequence 524, App
989 31 38.8 688 11 US-11-106-674-1 Sequence 1, Appli
990 31 38.8 689 11 US-11-096-568A-27707 Sequence 27707, A
991 31 38.8 692 11 US-11-188-298-11563 Sequence 11563, A
992 31 38.8 698 11 US-11-188-298-20261 Sequence 20261, A
993 31 38.8 698 11 US-11-188-298-20369 Sequence 20369, A
994 31 38.8 699 11 US-11-188-298-12461 Sequence 12461, A
995 31 38.8 701 11 US-11-188-298-12461 Sequence 12461, A
996 31 38.8 702 11 US-11-188-298-12930 Sequence 12930, A
997 31 38.8 707 11 US-11-096-568A-27774 Sequence 27774, A
998 31 38.8 745 11 US-11-188-298-1275 Sequence 1275, Ap
999 31 38.8 745 11 US-11-188-298-13969 Sequence 13969, A
1000 31 38.8 747 11 US-11-096-568A-27773 Sequence 27773, A

ALIGNMENTS

RESULT 1
US-10-506-223-16
; Sequence 16, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa at position 3 is Nle
US-10-506-223-16
Query Match 68.8%; Score 55; DB 9; Length 12;
Best Local Similarity 88.9%; Pred.No. 0.077;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;
Qy 3 YSCFWKTCT 11
Db 4 YSCFWKTCT 12
US-10-506-223-39
; Sequence 39, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa at position 3 is Nle
US-10-506-223-39
Query Match 68.8%; Score 55; DB 9; Length 12;
Best Local Similarity 88.9%; Pred.No. 0.077;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;
Qy 3 YSCFWKTCT 11
Db 4 YSCFWKTCT 12

```
Query Match      68.8%; Score 55; DB 9; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.077;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
Db 4 YSCFWKTKCT 12

RESULT 4
US-10-506-223-40
; Sequence 40, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa at position 3 is Nle
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 6, 11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
US-10-506-223-40

Query Match      68.8%; Score 55; DB 9; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.077;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
Db 4 YSCFWKTKCT 12

RESULT 5
US-10-506-223-21
; Sequence 21, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 13

Query Match      68.8%; Score 55; DB 9; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.077;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
Db 4 YSCFWKTKCT 12

RESULT 6
US-10-506-223-22
; Sequence 22, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa at position 4 is Nle
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 7, 12
; OTHER INFORMATION: Cys at positions 7 and 12 are circularized
US-10-506-223-22

Query Match      68.8%; Score 55; DB 9; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.081;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
Db 5 YSCFWKTKCT 13

RESULT 7
US-10-506-223-23
; Sequence 23, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
```

```
, CURRENT FILING DATE: 2004-08-31
, PRIOR APPLICATION NUMBER: PCT/03/06657
, PRIOR FILING DATE: 2003-03-03
, PRIOR APPLICATION NUMBER: US 60/360,831
, PRIOR FILING DATE: 2002-03-01
, NUMBER OF SEQ ID NOS: 40
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 23
, LENGTH: 14
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Synthetic
, NAME/KEY: VARIANT
, LOCATION: 5
, OTHER INFORMATION: Xaa at position 5 is Nle
US-10-506-223-23
```

```
Query Match      68.8%; Score 55; DB 9; Length 14;
Best Local Similarity 88.9%; Pred. No. 0.086;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 YYCFWKTKCT 11
        | | | | |
Db      6 YSCFWKTKCT 14
```

```
RESULT 8
US-10-506-223-24
, Sequence 24, Application US/10506223
, Publication No. US20060009622A1
, GENERAL INFORMATION:
, APPLICANT: Fuselier, Joseph A.
, TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
, TITLE OF INVENTION: Agents and Biologically Active Peptides
, FILE REFERENCE: 07005/007002
, CURRENT APPLICATION NUMBER: US/10/506,223
, CURRENT FILING DATE: 2004-08-31
, PRIOR APPLICATION NUMBER: PCT/03/06657
, PRIOR FILING DATE: 2003-03-03
, PRIOR APPLICATION NUMBER: US 60/360,831
, PRIOR FILING DATE: 2002-03-01
, NUMBER OF SEQ ID NOS: 40
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 24
, LENGTH: 15
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Synthetic
, NAME/KEY: VARIANT
, LOCATION: 6
, OTHER INFORMATION: Xaa at position 6 is Nle
US-10-506-223-24
```

```
Query Match      68.8%; Score 55; DB 9; Length 15;
Best Local Similarity 88.9%; Pred. No. 0.09;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 YYCFWKTKCT 11
        | | | | |
Db      7 YSCFWKTKCT 15
```

```
RESULT 9
US-10-506-223-25
, Sequence 25, Application US/10506223
, Publication No. US20060009622A1
, GENERAL INFORMATION:
, APPLICANT: Fuselier, Joseph A.
```

```
, APPLICANT: Coy, David H.
, TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
, TITLE OF INVENTION: Agents and Biologically Active Peptides
, FILE REFERENCE: 07005/007002
, CURRENT APPLICATION NUMBER: US/10/506,223
, CURRENT FILING DATE: 2004-08-31
, PRIOR APPLICATION NUMBER: PCT/03/06657
, PRIOR FILING DATE: 2003-03-03
, PRIOR APPLICATION NUMBER: US 60/360,831
, PRIOR FILING DATE: 2002-03-01
, NUMBER OF SEQ ID NOS: 40
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 25
, LENGTH: 16
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Synthetic
, NAME/KEY: VARIANT
, LOCATION: 7
, OTHER INFORMATION: Xaa at position 7 is Nle
US-10-506-223-25
```

```
Query Match      68.8%; Score 55; DB 9; Length 16;
Best Local Similarity 88.9%; Pred. No. 0.094;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 YYCFWKTKCT 11
        | | | | |
Db      8 YSCFWKTKCT 16
```

```
RESULT 10
US-10-506-223-26
, Sequence 26, Application US/10506223
, Publication No. US20060009622A1
, GENERAL INFORMATION:
, APPLICANT: Fuselier, Joseph A.
, TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
, TITLE OF INVENTION: Agents and Biologically Active Peptides
, FILE REFERENCE: 07005/007002
, CURRENT APPLICATION NUMBER: US/10/506,223
, CURRENT FILING DATE: 2004-08-31
, PRIOR APPLICATION NUMBER: PCT/03/06657
, PRIOR FILING DATE: 2003-03-03
, PRIOR APPLICATION NUMBER: US 60/360,831
, PRIOR FILING DATE: 2002-03-01
, NUMBER OF SEQ ID NOS: 40
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 26
, LENGTH: 17
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Synthetic
, NAME/KEY: VARIANT
, LOCATION: 8
, OTHER INFORMATION: Xaa at position 8 is Nle
US-10-506-223-26
```

```
Query Match      68.8%; Score 55; DB 9; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 YYCFWKTKCT 11
        | | | | |
Db      9 YSCFWKTKCT 17
```

```
RESULT 11
```

US-10-506-223-27
; Sequence 27, Application US/10506223
; Publication No. US2006009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 9
; OTHER INFORMATION: Xaa at position 9 is Nle
US-10-506-223-27

Query Match 68.8%; Score 55; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YVCFWKTKCT 11
Db 10 YVCFWKTKCT 18

RESULT 12
US-10-506-223-28
; Sequence 28, Application US/10506223
; Publication No. US2006009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa at position 10 is Nle
US-10-506-223-28

Query Match 68.8%; Score 55; DB 9; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YVCFWKTKCT 11

Db 11 YVCFWKTKCT 19

RESULT 13
US-10-506-223-29
; Sequence 29, Application US/10506223
; Publication No. US2006009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 11
; OTHER INFORMATION: Xaa at position 11 is Nle
US-10-506-223-29

Query Match 68.8%; Score 55; DB 9; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YVCFWKTKCT 11
Db 12 YVCFWKTKCT 20

RESULT 14
US-10-506-223-30
; Sequence 30, Application US/10506223
; Publication No. US2006009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 12
; OTHER INFORMATION: Xaa at position 12 is Nle
US-10-506-223-30

```
Query Match      68.8%; Score 55; DB 9; Length 21;
Best Local Similarity 88.9%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 YYCFWKTKCT 11
DB      13 YSCFWKTKCT 21

RESULT 15
US-10-506-223-31
; Sequence 31, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 13
; OTHER INFORMATION: Xaa at position 13 is Nle
US-10-506-223-31

Query Match      68.8%; Score 55; DB 9; Length 22;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 YYCFWKTKCT 11
DB      14 YSCFWKTKCT 22

RESULT 16
US-10-506-223-32
; Sequence 32, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 14
; OTHER INFORMATION: Xaa at position 14 is Nle
US-10-506-223-32

Query Match      68.8%; Score 55; DB 9; Length 23;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 YYCFWKTKCT 11
DB      15 YSCFWKTKCT 23

RESULT 17
US-10-506-223-33
; Sequence 33, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 15
; OTHER INFORMATION: Xaa at position 15 is Nle
US-10-506-223-33

Query Match      68.8%; Score 55; DB 9; Length 24;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 YYCFWKTKCT 11
DB      16 YSCFWKTKCT 24

RESULT 18
US-10-506-223-34
; Sequence 34, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 25
```


; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 16
; OTHER INFORMATION: Xaa at position 16 is Nle
US-10-506-223-34

Query Match 68.8%; Score 55; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YCFWKTCT 11
| | | | |
Db 17 YSCFWKTCT 25

RESULT 19
US-10-506-223-35
; Sequence 35, Application US/10506223
; Publication No. US2006009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuesliet, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 17
; OTHER INFORMATION: Xaa at position 17 is Nle
US-10-506-223-35

Query Match 68.8%; Score 55; DB 9; Length 26;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YCFWKTCT 11
| | | | |
Db 18 YSCFWKTCT 26

RESULT 20
US-10-506-223-36
; Sequence 36, Application US/10506223
; Publication No. US2006009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuesliet, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831

; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 18
; OTHER INFORMATION: Xaa at position 18 is Nle
US-10-506-223-36

Query Match 68.8%; Score 55; DB 9; Length 27;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YCFWKTCT 11
| | | | |
Db 19 YSCFWKTCT 27

RESULT 21
US-10-626-719-158
; Sequence 158, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-626-719-158

Query Match 66.2%; Score 53; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCT 11
| | | | |
Db 1 FCFWKTCT 8

RESULT 22
US-10-626-719-159
; Sequence 159, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS

; APPLICANT: SEMMLER, WOLFHARD
 ; APPLICANT: WEIDENMANN, BERTRAM
 ; APPLICANT: HESSNIUS, CARSTEN
 ; APPLICANT: VOLKMER-ENGERT, RUDOLF
 ; APPLICANT: SCHNEIDER-MERGENER, JENS
 ; APPLICANT: BHARGAVA, SARAH
 ; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
 ; TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
 ; FILE REFERENCE: SCH-1731
 ; CURRENT APPLICATION NUMBER: US/10/626,719
 ; CURRENT FILING DATE: 2003-07-25
 ; PRIOR APPLICATION NUMBER: US/09/528,200
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: DE 199 17 713.9
 ; PRIOR FILING DATE: 1999-09-04
 ; NUMBER OF SEQ ID NOS: 196
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 159
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 US-10-626-719-159

Query Match 62.5%; Score 50; DB 9; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
 :|||||
 Db 1 PCFWKTKT 8

RESULT 23
 US-11-198-847-234
 ; Sequence 234, Application US/11198847
 ; Publication No. US20050271589A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Jones, Robert M.
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Olivera, Baldomero M.
 ; TITLE OF INVENTION: B-Superfamily Conotoxins
 ; FILE REFERENCE: 2314-296
 ; CURRENT APPLICATION NUMBER: US/11/198,847
 ; CURRENT FILING DATE: 2005-08-08
 ; PRIOR APPLICATION NUMBER: US 10/838,226
 ; PRIOR FILING DATE: 2004-05-05
 ; PRIOR APPLICATION NUMBER: US 10/058,053
 ; PRIOR FILING DATE: 2000-01-29
 ; PRIOR APPLICATION NUMBER: US 60/264323
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 340
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 234
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Conus geographus
 US-11-198-847-234

Query Match 61.3%; Score 49; DB 11; Length 21;
 Best Local Similarity 75.0%; Pred. No. 0.75;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
 :|||||
 Db 2 PCFWKTKT 9

RESULT 24
 US-11-198-847-231
 ; Sequence 231, Application US/11198847
 ; Publication No. US20050271589A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Jones, Robert M.
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Olivera, Baldomero M.
 ; TITLE OF INVENTION: B-Superfamily Conotoxins
 ; FILE REFERENCE: 2314-296
 ; CURRENT APPLICATION NUMBER: US/11/198,847
 ; CURRENT FILING DATE: 2005-08-08
 ; PRIOR APPLICATION NUMBER: US 10/838,226
 ; PRIOR FILING DATE: 2004-05-05
 ; PRIOR APPLICATION NUMBER: US 10/058,053
 ; PRIOR FILING DATE: 2000-01-29
 ; PRIOR APPLICATION NUMBER: US 60/264323
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 340
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 231
 ; LENGTH: 40
 ; TYPE: PRT
 ; ORGANISM: Conus geographus
 US-11-198-847-231

Query Match 61.3%; Score 49; DB 11; Length 40;
 Best Local Similarity 75.0%; Pred. No. 1.2;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
 :|||||
 Db 21 PCFWKTKT 28

RESULT 25
 US-11-198-847-116
 ; Sequence 116, Application US/11198847
 ; Publication No. US20050271589A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Jones, Robert M.
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Olivera, Baldomero M.
 ; TITLE OF INVENTION: B-Superfamily Conotoxins
 ; FILE REFERENCE: 2314-296
 ; CURRENT APPLICATION NUMBER: US/11/198,847
 ; CURRENT FILING DATE: 2005-08-08
 ; PRIOR APPLICATION NUMBER: US 10/838,226
 ; PRIOR FILING DATE: 2004-05-05
 ; PRIOR APPLICATION NUMBER: US 10/058,053
 ; PRIOR FILING DATE: 2000-01-29
 ; PRIOR APPLICATION NUMBER: US 60/264323
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 340
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 116
 ; LENGTH: 93
 ; TYPE: PRT
 ; ORGANISM: Conus geographus
 US-11-198-847-116

Query Match 61.3%; Score 49; DB 11; Length 93;
 Best Local Similarity 75.0%; Pred. No. 2.1;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
 :|||||

```
Db      71 FCFWKSCT 78

RESULT 26
US-10-626-719-156
; Sequence 156, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARTSEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-626-719-156

Query Match      60.0%; Score 48; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 YCFWKYCT 11
      : |||||
Db      1 FCFWKVCT 8

RESULT 27
US-11-198-847-280
; Sequence 280, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Conus cinereus
; OTHER INFORMATION:
US-11-198-847-280

Query Match      58.8%; Score 47; DB 11; Length 45;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 YYCFWKYCT 11
      : |||||
Db      10 FCFWKSCT 18

RESULT 28
US-11-198-847-89
; Sequence 89, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Conus cinereus
; OTHER INFORMATION:
US-11-198-847-89

Query Match      58.8%; Score 47; DB 11; Length 95;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 YYCFWKYCT 11
      : |||||
Db      60 FCFWKSCT 68

RESULT 29
US-10-506-223-37
; Sequence 37, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fusellier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-506-223-37
```

```
Query Match      56.2%; Score 45; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CFWKTC 10
Db 1 CFWKTC 6

RESULT 30
US-10-506-223-38
; Sequence 38, Application US/10506223
; Publication No. US2006009622A1
; GENERAL INFORMATION:
; APPLICANT: Fueslier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MOD RES
; LOCATION: 1, 6
; OTHER INFORMATION: Cys at positions 1 and 6 are circularized
US-10-506-223-38

Query Match      56.2%; Score 45; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CFWKTC 10
Db 1 CFWKTC 6

RESULT 31
US-10-626-719-157
; Sequence 157, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 157
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-626-719-157

Query Match      56.2%; Score 45; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.9e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YCFWKTC 11
Db 1 FCFWKVCT 8

RESULT 32
US-11-198-847-322
; Sequence 322, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 322
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-322

Query Match      55.0%; Score 44; DB 11; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.2;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTC 10
Db 1 FCFWKSC 7

RESULT 33
US-11-198-847-232
; Sequence 232, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
```

; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 232
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Conus tulipa
US-11-198-847-232

Query Match 55.0%; Score 44; DB 11; Length 21;
Best Local Similarity 71.4%; Pred. No. 3.7;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:
Db 2 FCFWKSC 8

RESULT 34

US-11-198-847-233
; Sequence 233, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 233
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-233

Query Match 55.0%; Score 44; DB 11; Length 21;
Best Local Similarity 71.4%; Pred. No. 3.7;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:
Db 2 FCFWKSC 8

RESULT 35

US-11-198-847-229
; Sequence 229, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847

; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 229
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus tulipa
US-11-198-847-229

Query Match 55.0%; Score 44; DB 11; Length 40;
Best Local Similarity 71.4%; Pred. No. 5.7;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:
Db 21 FCFWKSC 27

RESULT 36

US-11-198-847-230
; Sequence 230, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 230
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-230

Query Match 55.0%; Score 44; DB 11; Length 40;
Best Local Similarity 71.4%; Pred. No. 5.7;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:
Db 21 FCFWKSC 27

RESULT 37

US-11-198-847-32
; Sequence 32, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.

; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Conus tulipa
US-11-198-847-32

Query Match 55.0%; Score 44; DB 11; Length 93;
Best Local Similarity 71.4%; Pred. No. 10;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:
Db 71 FCFWKSC 77

RESULT 38

US-11-198-847-41
; Sequence 41, Application US/11/198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-41

Query Match 55.0%; Score 44; DB 11; Length 93;
Best Local Similarity 71.4%; Pred. No. 10;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:
Db 71 FCFWKSC 77

RESULT 39

US-11-045-004-1161
; Sequence 1161, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN
; APPLICANT: FRANGUL, LIONEL
; APPLICANT: COUVE, ELISABETH

; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHL, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARNIA
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394, 0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1161
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1161

Query Match 55.0%; Score 44; DB 11; Length 285;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YCYVCFWKT 9
:||||:
Db 61 YSIYCFWKS 69

RESULT 40

US-11-087-099-6677
; Sequence 6677, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6677
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Pseudomonas putida KT2440
US-11-087-099-6677

Query Match 53.8%; Score 43; DB 11; Length 479;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YCYCFWKT 10
DB 450 WCYLAWLTC 459

RESULT 41

US-11-188-298-17131
; Sequence 17131, Application US/11/188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 17131
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Pseudomonas putida KT2440
US-11-188-298-17131

Query Match 53.8%; Score 43; DB 11; Length 479;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YCYCFWKT 10
DB 450 WCYLAWLTC 459

RESULT 42

US-11-079-463-7253
; Sequence 7253, Application US/11/079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7253
; LENGTH: 362
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-7253

Query Match 52.5%; Score 42; DB 11; Length 362;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YCYCFWKT 9
DB 244 YGYDFWKT 252

RESULT 43

US-11-198-847-316
; Sequence 316, Application US/11/198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 316
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Conus magus
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(9)
; OTHER INFORMATION: Xaa may be Phe (D or L)
US-11-198-847-316

Query Match 51.2%; Score 41; DB 11; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 CFWKT 10
DB 3 CFWKT 8

RESULT 44

US-11-198-847-313
; Sequence 313, Application US/11/198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 313
; LENGTH: 11
; TYPE: PRT

```
; ORGANISM: Conus magus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(11)
; OTHER INFORMATION: Xaa may be Phe (D or L)
US-11-198-847-313

Query Match          51.2%; Score 41; DB 11; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 CFWKTC 10
      |||||.
Db      3 CFWKSC 8

RESULT 45
US-11-198-847-311
; Sequence 311, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 311
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Conus magus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Xaa may be Phe (D or L)
US-11-198-847-311

Query Match          51.2%; Score 41; DB 11; Length 15;
Best Local Similarity 83.3%; Pred. No. 7.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 CFWKTC 10
      |||||.
Db      3 CFWKSC 8

RESULT 46
US-11-096-568A-8330
; Sequence 8330, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8330
; LENGTH: 64
; TYPE: PRT
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```
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(64)
; OTHER INFORMATION: Ceres Seq. ID no. 15224829
US-11-096-568A-8330

Query Match          51.2%; Score 41; DB 11; Length 64;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CYICFW 7
      |||||
Db      5 CLYCFW 10

RESULT 47
US-11-096-568A-8329
; Sequence 8329, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8329
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(68)
; OTHER INFORMATION: Ceres Seq. ID no. 15224828
US-11-096-568A-8329

Query Match          51.2%; Score 41; DB 11; Length 68;
Best Local Similarity 83.3%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CYICFW 7
      |||||
Db      9 CLYCFW 14

RESULT 48
US-11-079-463-6337
; Sequence 6337, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRAGILIS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 6337
; LENGTH: 81
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-6337

Query Match          51.2%; Score 41; DB 11; Length 81;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```


Qy 1 YCYCP 6
| | | | |
Db 6 YCYFCP 11

RESULT 49

US-10-626-719-160
; Sequence 160, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHIA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGNER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 160
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: Abu
US-10-626-719-160

Query Match 50.0%; Score 40; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.9e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
| | | | |
Db 1 FCYWKXC 7

RESULT 50

US-11-198-847-290
; Sequence 290, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 290
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Conus tulipa
US-11-198-847-290

Query Match 50.0%; Score 40; DB 11; Length 21;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YCFCWKTC 10
| | | | |
Db 10 YICWKVC 17

Search completed: May 9, 2006, 12:16:20
Job time : 13 secs

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GenCore version 5.1.8
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 OM protein - protein search, using sw model
 Run on: May 9, 2006, 12:04:09 ; Search time 49.6667 Seconds
 (without alignments)
 97.312 Million cell updates/sec

Title: US-10-796-158-6

Perfect score: 80

Sequence: 1 CYRYCFWKCT 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: A_Geneseq_21.*

2: Geneseqp1980s.*

3: Geneseqp1990s.*

4: Geneseqp2000s.*

5: Geneseqp2001s.*

6: Geneseqp2002s.*

7: Geneseqp2003s.*

8: Geneseqp2003bs.*

9: Geneseqp2004s.*

10: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	11	8	ADS74378 Somatosta
2	71	88.8	11	2	AAW48645 Somatosta
3	71	88.8	11	8	ADM35520 Somatosta
4	71	88.8	11	9	ADM95422 Amino aci
5	64	80.0	9	2	AAW48642 Somatosta
6	64	80.0	10	7	ADII14934 Somatosta
7	64	80.0	10	8	ADU05247 Cyclic so
8	64	80.0	11	7	ADII14956 Somatosta
9	64	80.0	11	7	ADII14951 Somatosta
10	64	80.0	11	7	ADII14959 Somatosta
11	64	80.0	11	7	ADII14954 Somatosta
12	64	80.0	11	8	ADS74377 Somatosta
13	64	80.0	12	7	ADU05246 Cyclic so
14	64	80.0	13	7	ADII14894 Somatosta
15	64	80.0	13	7	ADII14957 Somatosta
16	64	80.0	13	7	ADII14895 Somatosta
17	64	80.0	14	7	ADII14952 Somatosta
18	64	80.0	15	6	ABR42184 Somatosta
19	64	80.0	15	7	ADII14935 Somatosta
20	64	80.0	15	7	ADII14898 Somatosta
21	64	80.0	20	6	ABR42192 Peptide a
22	64	80.0	20	6	ABR42198 Somatosta
23	64	80.0	20	7	ADII14936 Somatosta
24	64	80.0	20	7	ADII14897 Somatosta

25	64	80.0	22	6	ABR42181	AdBr42181 Somatosta
26	64	80.0	25	6	ABR42199	AdBr42199 Somatosta
27	64	80.0	30	6	ABR42197	AdBr42197 Somatosta
28	62	77.5	11	8	ADS74379	AdS74379 Somatosta
29	61	76.2	10	8	ADU05266	Cyclic so
30	61	76.2	11	8	ADU05270	Cyclic so
31	61	76.2	11	8	ADU05281	Cyclic so
32	59	73.8	10	7	ADII14944	Somatosta
33	59	73.8	11	7	ADII14943	Somatosta
34	59	73.8	15	7	ADII14945	Somatosta
35	57	71.2	8	6	AAO26828	Somatosta
36	57	71.2	8	6	AAO26832	Somatosta
37	57	71.2	8	6	AAO26830	Somatosta
38	57	71.2	8	6	AAO26825	Somatosta
39	57	71.2	8	6	AAO26827	Somatosta
40	57	71.2	8	6	AAO26826	Somatosta
41	57	71.2	8	6	AAO26829	Somatosta
42	57	71.2	8	6	AAO26831	Somatosta
43	57	71.2	14	8	ADU97615	Novel cyt
44	57	71.2	14	8	ADU97600	Novel cyt
45	57	71.2	14	8	ADU97630	Novel cyt
46	57	71.2	15	8	ADU97599	Novel cyt
47	57	71.2	15	8	ADU97629	Novel cyt
48	57	71.2	15	8	ADU97614	Novel cyt
49	57	71.2	16	8	ADU97616	Novel cyt
50	57	71.2	16	8	ADU97631	Novel cyt
51	57	71.2	16	8	ADU97601	Novel cyt
52	56	70.0	9	2	AAI14231	Somatosta
53	56	70.0	9	2	AAW48644	Somatosta
54	56	70.0	10	2	AAI14235	Somatosta
55	56	70.0	10	7	ADII14971	Somatosta
56	56	70.0	10	8	ADU05212	Cyclic so
57	56	70.0	10	8	ADU05243	Cyclic so
58	56	70.0	10	8	ADU05276	Cyclic so
59	56	70.0	10	8	ADU05235	Cyclic so
60	56	70.0	10	8	ADU05239	Cyclic so
61	56	70.0	10	8	ADU05271	Cyclic so
62	56	70.0	10	8	ADU95289	Novel cyt
63	56	70.0	10	8	ADU96133	Novel cyt
64	56	70.0	10	8	ADU96505	Novel cyt
65	56	70.0	10	8	ADU95827	Novel cyt
66	56	70.0	10	8	ADU95290	Novel cyt
67	56	70.0	10	8	ADU96194	Novel cyt
68	56	70.0	10	8	ADU97505	Novel cyt
69	56	70.0	10	8	ADU97103	Novel cyt
70	56	70.0	10	8	ADU95224	Novel cyt
71	56	70.0	10	8	ADU96455	Novel cyt
72	56	70.0	10	8	ADU95758	Novel cyt
73	56	70.0	10	8	ADU95848	Novel cyt
74	56	70.0	10	8	ADU96537	Novel cyt
75	56	70.0	10	8	ADU95335	Novel cyt
76	56	70.0	10	8	ADU97531	Novel cyt
77	56	70.0	10	8	ADU97068	Novel cyt
78	56	70.0	10	8	ADU97050	Novel cyt
79	56	70.0	10	8	ADU95318	Novel cyt
80	56	70.0	11	7	ADII14990	Somatosta
81	56	70.0	11	7	ADII14972	Somatosta
82	56	70.0	11	8	ADU05242	Cyclic so
83	56	70.0	11	8	ADU05238	Cyclic so
84	56	70.0	11	8	ADU05252	Cyclic so
85	56	70.0	11	8	ADU05234	Cyclic so
86	56	70.0	11	8	ADU05280	Cyclic so
87	56	70.0	11	8	ADU05275	Cyclic so
88	56	70.0	11	8	ADU95644	Novel cyt
89	56	70.0	11	8	ADU96193	Novel cyt
90	56	70.0	11	8	ADU97111	Novel cyt
91	56	70.0	11	8	ADU97483	Novel cyt
92	56	70.0	11	8	ADU95271	Novel cyt
93	56	70.0	11	8	ADU95847	Novel cyt
94	56	70.0	11	8	ADU96463	Novel cyt
95	56	70.0	11	8	ADU95297	Novel cyt
96	56	70.0	11	8	ADU96507	Novel cyt
97	56	70.0	11	8	ADU96594	Novel cyt

390	53	66.2	8	2	AA05177	Adh68893	Synthetic
391	53	66.2	8	2	AA05188	Abg99249	Somatosta
392	53	66.2	8	2	AA14236	Abg99248	Somatosta
393	53	66.2	8	2	AA14227	AA026852	Somatosta
394	53	66.2	8	2	AA10501	AA026824	Somatosta
395	53	66.2	8	2	AA11518	AA026818	Somatosta
396	53	66.2	8	2	AA126368	AA026822	Somatosta
397	53	66.2	8	2	AA226368	AA026851	Somatosta
398	53	66.2	8	2	AA228859	AA026819	Somatosta
399	53	66.2	8	2	AA233948	AA026820	Somatosta
400	53	66.2	8	2	AA23948	AA026821	Somatosta
401	53	66.2	8	2	AA41504	AA026823	Somatosta
402	53	66.2	8	2	AA41500	AA026823	Somatosta
403	53	66.2	8	2	AA39595	ABP55049	Octreotid
404	53	66.2	8	2	AA31512	ABP55050	Octreotid
405	53	66.2	8	2	AA37097	ADA1667	Cyclic te
406	53	66.2	8	2	AA42651	Adh88527	Somatosta
407	53	66.2	8	2	AA42655	Adf61742	Somatosta
408	53	66.2	8	2	AA56777	Adi14899	Somatosta
409	53	66.2	8	2	AA50278	AD116034	Octreotid
410	53	66.2	8	2	AA76206	Adh3166	Octreotid
411	53	66.2	8	2	AA76201	ADJ56707	Cyclic pe
412	53	66.2	8	2	AA85572	Adm35518	Somatosta
413	53	66.2	8	2	AA62014	Adr87508	Backbone
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415	53	66.2	8	2	AAW33184	Adi2361	Octreotid
416	53	66.2	8	2	AAW12315	ADU5219	Cyclic so
417	53	66.2	8	2	AAW19221	ADU5227	Novel cyc
418	53	66.2	8	2	AAW29371	ADU07144	Octreotid
419	53	66.2	8	2	AAW51854	Adw95415	Peptide #
420	53	66.2	8	2	AAW51861	Adw95416	Peptide #
421	53	66.2	8	2	AAW51666	Adw95412	Peptide #
422	53	66.2	8	2	AAW22040	ADW95413	Peptide #
423	53	66.2	8	2	AAW18225	ADW95411	Peptide #
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425	53	66.2	8	2	AAW45742	ADW95419	Peptide #
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427	53	66.2	8	2	AAW97187	ADW95417	Peptide #
428	53	66.2	8	2	AAW04039	ADW95420	Peptide #
429	53	66.2	8	2	AAW04041	ADY1780	Cyclic pe
430	53	66.2	8	2	AAW29832	Ady1780	Cyclic pe
431	53	66.2	8	2	AAW23161	Adz99635	Somatosta
432	53	66.2	8	2	ADH35402	Adz99636	Somatosta
433	53	66.2	8	2	ADH35403	Adp92299	Peptide s
434	53	66.2	8	2	ADH68004	Adp92299	Peptide s
435	53	66.2	8	2	ADH68003	Adp92299	Peptide s
436	53	66.2	8	2	AD124864	Adp92299	Peptide s
437	53	66.2	8	2	ADK11155	Adp92299	Peptide s
438	53	66.2	8	2	ADK11156	Adp92299	Peptide s
439	53	66.2	8	2	AAW82555	Adp92299	Peptide s
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441	53	66.2	8	2	AAW81017	Adp92299	Peptide s
442	53	66.2	8	2	AAW81016	Adp92299	Peptide s
443	53	66.2	8	2	AAW83802	Adp92299	Peptide s
444	53	66.2	8	2	AAW824186	Adp92299	Peptide s
445	53	66.2	8	2	AAW824182	Adp92299	Peptide s
446	53	66.2	8	2	AAW19026	Adp92299	Peptide s
447	53	66.2	8	2	ABW77167	Adp92299	Peptide s
448	53	66.2	8	2	AAU05146	Adp92299	Peptide s
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450	53	66.2	8	2	AAW51439	Adp92299	Peptide s
451	53	66.2	8	2	AAW51439	Adp92299	Peptide s
452	53	66.2	8	2	AAW51439	Adp92299	Peptide s
453	53	66.2	8	2	AAW51439	Adp92299	Peptide s
454	53	66.2	8	2	AAW51439	Adp92299	Peptide s
455	53	66.2	8	2	AAW51439	Adp92299	Peptide s
456	53	66.2	8	2	AAW51439	Adp92299	Peptide s
457	53	66.2	8	2	AAW51439	Adp92299	Peptide s
458	53	66.2	8	2	AAW51439	Adp92299	Peptide s
459	53	66.2	8	2	AAW51439	Adp92299	Peptide s
460	53	66.2	8	2	AAW51439	Adp92299	Peptide s
461	53	66.2	8	2	AAW51439	Adp92299	Peptide s
462	53	66.2	8	2	AAW51439	Adp92299	Peptide s

536	52	65.0	8	2	ADH35405	Human som	609	50	62.5	8	4	AAG67680	Amino aci
537	52	65.0	8	2	ADH68006	Somatosta	610	50	62.5	8	4	AAG67680	ADH68006
538	52	65.0	8	2	ADH68006	Somatosta	611	50	62.5	8	4	AAG67680	ADH68006
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540	52	65.0	8	3	ADH68006	Somatosta	613	50	62.5	8	4	AAG67680	ADH68006
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544	52	65.0	8	4	ADH68006	Somatosta	617	50	62.5	8	4	AAG67680	ADH68006
545	52	65.0	8	5	ADH68006	Somatosta	618	50	62.5	8	4	AAG67680	ADH68006
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549	52	65.0	8	9	ADH68006	Somatosta	622	50	62.5	8	5	ADH68006	ADH68006
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555	51	63.7	12	7	ADH68006	Somatosta	628	50	62.5	8	5	ADH68006	ADH68006
556	51	63.7	13	7	ADH68006	Somatosta	629	50	62.5	8	6	ADH68006	ADH68006
557	51	63.7	15	7	ADH68006	Somatosta	630	50	62.5	8	6	ADH68006	ADH68006
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560	50	62.5	7	8	ADH68006	Somatosta	633	50	62.5	8	6	ADH68006	ADH68006
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565	50	62.5	8	2	ADH68006	Somatosta	638	50	62.5	8	6	ADH68006	ADH68006
566	50	62.5	8	2	ADH68006	Somatosta	639	50	62.5	8	6	ADH68006	ADH68006
567	50	62.5	8	2	ADH68006	Somatosta	640	50	62.5	8	6	ADH68006	ADH68006
568	50	62.5	8	2	ADH68006	Somatosta	641	50	62.5	8	6	ADH68006	ADH68006
569	50	62.5	8	2	ADH68006	Somatosta	642	50	62.5	8	6	ADH68006	ADH68006
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699 50 62.5 9 2 ADK11179 Somatosta Adk11179 Somatosta 772 50 62.5 9 9 ADZ99659 Somatosta
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Aao26865 Somatosta
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Aao26861 Somatosta
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Adv99688 Cyclic Cy
Adz99644 Somatosta
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Adh35431 Human som
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Adh68030 Somatosta
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Adk11184 Somatosta
Aab06936 Somatosta
Aay81043 Somatosta
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Aau08855 Somatosta
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Abg99275 Somatosta
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Aao26878 Somatosta
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Adc33481 Peptide K
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Aaw48641 Somatosta
Abr42193 Somatosta
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Abp68795 Marine sn
Abr42196 Somatosta
Abp68792 Marine sn
Aap10588 GH, gastr
Aay15361 Somatosta
Aay04040 Heptapept
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Aap10589 GH, gastr
Aap20266 Peptide s
Aap40502 Sequence

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999 46 57.5 12 8 ADU95710 Novel cyt
1000 46 57.5 12 8 ADU95832 Novel cyt

ALIGNMENTS

RESULT 1
ID ADS74378 standard; peptide; 11 AA.
XX AC ADS74378;
XX DT 16-DEC-2004 (first entry)
XX DE Somatostatin analogue.
XX KW Somatostatin analogue; cytostatic; gene therapy.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 1.4 /note= "D-form residues"
FT Disulfide-bond 5.10
FT Misc-difference 7 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide or alcohol"
XX WO2004081031-A2.
XX PD 23-SEP-2004.
XX PF 10-MAR-2004; 2004WO-US007143.
XX PR 10-MAR-2003; 2003US-0452928P.
XX PA (BIOG-) BIOGEN IDEC INC.
XX PI Braslawsky GR, Chinn P;
XX DR WPI; 2004-668933/65.
XX A composition comprising a somatostatin analog useful for thiol-specific
PT drug attachment to somatostatin and other targeting peptides, or for
PT diagnosing or treating somatostatin receptor-associated disorders, e.g.
PT cancer.

XX Claim 4; SEQ ID NO 6; 43pp; English.
XX The present sequence is that of a synthetic somatostatin analogue. The
XX peptide can be used as component B in a claimed composition comprising a
XX somatostatin analogue of formula (A-B), where A is Cys, or a peptide
XX chain comprising one or more Cys residues, which is suitable for binding
XX to a drug or chelator via a thiol linkage, and B is a naturally occurring
XX or synthetic somatostatin peptide, or its fragment, that binds to the
XX somatostatin receptor (SSTR). The drug or chelator is bound to the Cys
XX residue(s) of component A by a thiol linkage. The drug is a therapeutic
XX drug such as a radioisotope, a cytotoxin, an immunostimulant, an
XX antiangiogenic agent, a therapeutic gene, or a chemotherapeutic agent.
XX The somatostatin analogue preferably binds to SSTR-positive cells,
XX especially human cancer cells. A claimed method for detecting SSTR-
XX positive cells comprises administering the somatostatin analogue in which
XX a detectable label is bound to the Cys residue(s) of component A, and
XX detecting the label. A claimed method for treating an SSTR-associated
XX disorder comprises administering a somatostatin analogue in which a
XX therapeutic agent is bound to the Cys residue(s) of component A. The SSTR
XX -associated disorder is especially cancer. Thiol-mediated drug attachment
XX can also be used with other targeting peptides.
XX SQ Sequence 11 AA;
Query Match 100.0%; Score 80; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CYYCFWKTCCT 11
Db 1 CYYCFWKTCCT 11
RESULT 2
AAW48645
ID AAW48645 standard; peptide; 11 AA.
XX AC AAW48645;
XX DT 04-AUG-1998 (first entry)
XX DE Somatostatin peptide analog WOC-4.
XX KW Somatostatin; acromegaly; radiolocalisation; blood-brain barrier; cancer;
XX halogen.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Disulfide-bond 5.10
FT Misc-difference 7 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
XX WO9639161-A1.
XX PD 12-DEC-1996.
XX PF 03-JUN-1996; 96WO-US008437.
XX PR 05-JUN-1995; 95US-00462223.
XX (TULA) TULANE EDUCATIONAL FUND.
XX (OHIS) UNIV OHIO STATE RES FOUND.
XX (LOU) UNIV LOUISIANA STATE MEDICAL CENT FOUND.
XX (CHIL-) CHILDRENS HOSPITAL INC.

XX Coy DH, Woltering EA, Odorisio MS, Odorisio TM, Murphy WA;
 XX WPI; 1997-042842/04.
 XX Multi-tyrosinated somatostatin analogues - useful for diagnosis and
 PT treatment of diseases related to altered somatostatin receptor
 PT expression.
 XX Claim 7; Page 60; 63pp; English.
 XX The invention provides for conventional somatostatin analogues (AAW48638-
 CC W48640 and AAW48644) and multi-tyrosinated analogues (AAW48641-W48645)
 CC such as the present one. The multi-tyrosinated somatostatin analogues
 CC bind to somatostatin receptors with practically the same affinity as
 CC native somatostatin. The somatostatin analogues are claimed to be useful
 CC for treating disease associated with increased production of factors
 CC which can be regulated by somatostatin, e.g. acromegaly. Also when
 CC radioactively labelled, the analogues are claimed to be useful for
 CC diagnosing cancer in vitro or in situ where aberrant expression of
 CC somatostatin receptors is involved. When halogenated, these analogues are
 CC found to bind somatostatin receptors with such high affinity that binding
 CC is nearly irreversible under physiological conditions. Therefore, by
 CC using radioactive halogenated analogues, the invention claims for
 CC improved sensitivity of radiolocalisation of the receptors. Multi-
 CC tyrosinated analogues have increased half-lives in vivo relative to
 CC conventional somatostatin analogues, are resistant to enzymatic
 CC degradation and have increased blood-brain barrier penetration
 XX
 XX Sequence 11 AA;
 SQ Query Match 88.8%; Score 71; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 YYICFWKTCT 11
 Db |||||
 2 YYICFWKTCT 11

RESULT 3
 ADM35520
 ID ADM35520 standard; peptide; 11 AA.
 XX
 AC ADM35520;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Somatostatin analogue, Woc-4D.
 XX
 KW retinopathy of prematurity; neonatal; somatostatin; Woc-4D; octreotide;
 KW lanreotide; vapreotide; Woc-2A; Woc-2B; Woc-3A; Woc-3B; Woc-4; Woc-4D;
 KW Woc-5; Woc-8; octreotide acetate; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1 /note= "D form residues"
 FT Misc-difference 2 /note= "D form residues"
 FT Disulfide-bond 5.10
 FT Misc-difference 7 /note= Forms a cyclic region of the peptide
 FT Misc-difference 7 /note= "D form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT
 XX US2003207811-A1.
 XX
 XX 06-NOV-2003.
 XX
 XX 03-MAY-2002; 2002US-00138554.
 XX
 XX 03-MAY-2002; 2002US-00138554.
 PR

XX (SCHR/) SCHRIER B K.
 PA (HIGG/) HIGGINS R D.
 XX
 PI Schrier BK, Higgins RD;
 XX
 XX WPI; 2004-069300/07.
 DR
 XX Treatment or prevention of retinopathy of prematurity in neonatal mammal,
 PT comprises administering somatostatin analog having composition that
 PT provides therapeutic benefit to mammal.
 XX Example; Page 5; 12pp; English.
 PS The invention relates to a method of treating retinopathy of prematurity
 XX in a neonatal mammal. The condition is treated or prevented by
 CC administering to the mammal a somatostatin analogue. Also described is a
 CC pharmaceutical composition Woc-4D and carrier for treating or preventing
 CC retinopathy of prematurity in neonatal mammal. The somatostatin analogue
 CC is octreotide, Woc4D, somatostatin analogue having serum half-life of
 CC octreotide, somatostatin analogue having serum half-life more than that
 CC of octreotide, or somatostatin analogue having serum half-life of Woc-4D.
 CC It is selected from octreotide, lanreotide, vapreotide, Woc-2A, Woc-2B,
 CC Woc-3A, Woc-3B, Woc-4, Woc-4D, Woc-5, or Woc-8. The invention provides a
 CC therapeutic benefit without affecting growth of the neonates. The present
 CC sequence represents somatostatin analogue, Woc-4D.
 XX
 XX Sequence 11 AA;
 SQ Query Match 88.8%; Score 71; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 YYICFWKTCT 11
 Db |||||
 2 YYICFWKTCT 11

RESULT 4
 ADW95422
 ID ADW95422 standard; peptide; 11 AA.
 XX
 AC ADW95422;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE Amino acid sequence of WOC4D.
 XX
 KW cytostatic; dispersed phase formulation; microsphere;
 KW sustained drug release; controlled drug release;
 KW testosterone dependent disorder; prostate disease; prostate cancer;
 KW octreotide drug; WOC4D.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1 /note= "D-form residue with H attached"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Disulfide-bond 5.10
 FT Misc-difference 7 /note= "D-form residue"
 FT Modified-site 11 /note= "NH2 attached"
 FT
 XX WO2005007122-A2.
 XX
 XX 27-JAN-2005.

XX 19-JUL-2004; 2004WO-US023324.
 XX
 XX 18-JUL-2003; 2003US-0498573P.
 XX
 XX (OAKW-) OAKWOOD LAB LLC.
 XX
 XX Thanoo BC, Murtagh J, Johns G;
 XX WPI, 2005-122673/13.
 XX
 XX Dispersed phase formulation useful for providing sustained release of
 XX drug suppressing gonadotropin releasing hormone comprises nucleophilic
 XX substance catalyzing ester bond cleavage and causing molecular weight
 XX reduction of polymer.
 XX
 XX Example; Page 63; 114pp; English.
 XX
 XX The specification describes a dispersed phase formulation which comprises
 XX a biocompatible and biodegradable polymer, at least one nucleophilic
 XX substance capable of catalyzing ester bond cleavage and causing molecular
 XX weight reduction of the polymer, and acid additive in an amount such that
 XX the polymer is less susceptible to molecular reduction as compared to the
 XX formulation without the acid additive. The formulation of the invention
 XX is useful for preparing microspheres providing a sustained or controlled
 XX release of drug. This is useful for suppressing gonadotropin releasing
 XX hormone in the treatment of testosterone dependent disorder, benign
 XX prostate hypertrophy or prostate cancer. The present sequence represents
 XX WO04D (a somatostatin analog), a peptide which was contained in
 XX microspheres of the invention.
 XX
 XX Sequence 11 AA;
 XX
 XX Query Match 88.8%; Score 71; DB 9; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 0.029;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 YYCFWKTCT 11
 XX | | | | | | | | | |
 XX Db 2 YYCFWKTCT 11
 XX
 XX RESULT 5
 XX AAW48642
 XX ID AAW48642 standard; peptide; 9 AA.
 XX AC AAW48642;
 XX DT 04-AUG-1998 (first entry)
 XX DE Somatostatin peptide analog WOC-2B.
 XX KW Somatostatin; acromegaly; radiolocalisation; blood-brain barrier; cancer;
 XX halogen.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX FH Misc-difference 2 /note= "D-form residue"
 XX FT Disulfide-bond 3. .8
 XX FT Misc-difference 5 /note= "D-form residue"
 XX FT Modified-site 9 /note= "C-terminal amide"
 XX
 XX PN WO9639161-A1.
 XX PD 12-DEC-1996.
 XX PF 03-JUN-1996; 96WO-US008437.
 XX

PR 05-JUN-1995; 95US-00462223.
 XX (TULA) TULANE EDUCATIONAL FUND.
 PA (OHIS) UNIV OHIO STATE RES FOUND.
 PA (LOUU) UNIV LOUISIANA STATE MEDICAL CENT FOUND.
 PA (CHIL-) CHILDRENS HOSPITAL INC.
 XX
 XX Coy DH, Woltering EA, Odorizio MS, Odorizio TM, Murphy WA;
 XX WPI, 1997-042842/04.
 XX
 XX Multi-tyrosinated somatostatin analogues - useful for diagnosis and
 XX treatment of diseases related to altered somatostatin receptor
 XX expression.
 XX
 XX Claim 7; Page 60; 63pp; English.
 XX
 XX The invention provides for conventional somatostatin analogues (AAW48638-
 XX W48640 and AAW48664) and multi-tyrosinated analogues (AAW48641-W48645)
 XX such as the present one. The multi-tyrosinated somatostatin analogues
 XX bind to somatostatin receptors with practically the same affinity as
 XX native somatostatin. The somatostatin analogues are claimed to be useful
 XX for treating disease associated with increased production of factors
 XX which can be regulated by somatostatin, e.g. acromegaly. Also when
 XX radioactively labelled, the analogues are claimed to be useful for
 XX diagnosing cancer in vitro or in situ where aberrant expression of
 XX somatostatin receptors is involved. When halogenated, these analogues are
 XX found to bind somatostatin receptors with such high affinity that binding
 XX is nearly irreversible under physiological conditions. Therefore, by
 XX using radioactive halogenated analogues, the invention claims for
 XX improved sensitivity of radiolocalisation of the receptors. Multi-
 XX tyrosinated analogues have increased half-lives in vivo relative to
 XX conventional somatostatin analogues, are resistant to enzymatic
 XX degradation and have increased blood-brain barrier penetration
 XX
 XX Sequence 9 AA;
 XX
 XX Query Match 80.0%; Score 64; DB 2; Length 9;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 3 YYCFWKTCT 11
 XX | | | | | | | | | |
 XX Db 1 YYCFWKTCT 9
 XX
 XX RESULT 6
 XX ADI14934
 XX ID ADI14934 standard; peptide; 10 AA.
 XX AC ADI14934;
 XX DT 22-APR-2004 (first entry)
 XX DE Somatostatin-dopamine chimeric analogue-related peptide 45.
 XX KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 XX vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 XX anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 XX tranquiliser; antilipaeimic; nephrotropic; antitumor; antiarthritic;
 XX hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 XX somatostatin receptor agonist; lung cancer; glioma; anorexia;
 XX hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 XX acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 XX pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 XX gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 XX AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 XX irritable bowel syndrome; pancreatitis; small bowel obstruction;
 XX gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 XX gonadotropinoma; hyperparathyroidism; Graves disease;
 XX diabetic neuropathy; Paget's disease; polycystic ovary disease;
 XX thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 XX orthostatic; hypotension; postprandial hypotension; panic attack;
 XX

KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiotomy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreatocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 XX Synthetic.
 OS Unidentified.
 XX

PH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Optionally bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methylsulfonyl-acetic acid. Optionally bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methyl-carbamoyl acid. Optionally bound to carbonic acid
 FT mono-(7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fg]quinolin-9-yl-methyl) ester. Optionally bound to 4-((7-
 FT propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fg]quinolin-9-yl-methyl) carbonyl) butyric acid.
 FT Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carboxylic acid.
 FT Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
 FT ethylureidopropyl)-Gly-"
 FT Misc-difference 2. 3
 FT /note= "D-form residue"
 FT Modified-site 4
 FT /note= "Residue forms a bond to residue 9 to form a
 FT cyclic peptide"
 FT Misc-difference 6
 FT /note= "D-form residue"
 FT Modified-site 9
 FT /note= "Residue forms a bond to residue 4 to form a
 FT cyclic peptide"
 FT Modified-site 10
 FT /note= "C-terminal OL"
 XX WO2002100888-A1.
 XX 19-DEC-2002.
 XX 07-JUN-2002; 2002WO-US017859.
 XX 08-JUN-2001; 2001US-0297059P.
 XX (SCRC) SCRAS SOC CONSELLS RECH & APPL SCI.
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 XX WPI; 2003-239103/23.
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 XX e.g. lung cancer.
 XX Claim 3; Page 133; 85pp; English.
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 XX or their salts. The invention may be useful for the development of
 XX compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 XX antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 XX antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeamic,
 XX nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or
 XX antiaddictive activity through action as a dopamine receptor agonist and
 XX somatostatin receptor agonist. The invention may be useful for the
 XX treatment of lung cancer, glioma, anorexia, hypothyroidism,
 XX hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 XX restenosis, Crohn's disease, systemic sclerosis, external and internal

CC pancreatic pseudocysts and ascites, VIPoma, mesodiblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreatocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX

XX Sequence 10 AA;
 SQ

Query Match 80.0%; Score 64; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCT 11
 |||||
 Db 2 YYCFWKTCT 10

RESULT 7
 ADU05247
 ID ADU05247 standard; peptide; 10 AA.
 XX
 AC ADU05247;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Cyclic somatostatin-dopamine chimeric peptide analogue #37.
 XX
 KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective tissue disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytotatic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antiulcer;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipaeamic; analgesic;
 KW antiantral; anorectic; immunomodulator; cardiac; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX Synthetic.
 OS

PH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "An N-terminal dopamine derivative (Dop1 to Dop6
 FT inclusive) is attached to a Lys(dopamine derivative)
 FT modified residue, where this second dopamine derivative
 FT must match the type occurring at the N-terminus, e.g.
 FT Dop1-Lys(Dop1), Dop2-Lys(Dop2) etc."
 FT Misc-difference 2
 FT /note= "D-form residue"
 FT Misc-difference 3
 FT /note= "D-form residue"
 FT Disulfide-bond 4. 9
 FT /note = This disulphide bond cyclises the peptide
 FT Misc-difference 6
 FT /note= "D-form residue"

FT Modified-site 10
 FT /note= "C-terminal alcohol"
 XX WO2004091490-A2.
 PN 28-OCT-2004.
 XX 08-APR-2004; 2004WO-US010891.
 XX 11-APR-2003; 2003US-0462374P.
 XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX Dong ZX, Dewitt Culler M, Shen Y;
 XX WPI; 2004-784484/77.
 DR New chimeric analog comprising at least one moiety which binds to one or
 XX more somatostatin and dopamine receptor(s) useful to treat e.g.
 FT neuroendocrine tumor, vascular diseases, connective tissue disease,
 PT immune disease and cachexia.
 FT
 XX Claim 12; Page 103; 138pp; English.
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC that comprise at least one moiety that binds to one or more somatostatin
 CC receptors and at least one moiety that binds to one or more dopamine
 CC receptors, or a salt derived thereof. Specifically, it refers to
 CC analogues that may be used in vitro or in vivo for research, diagnostic
 CC and therapeutic agents to enhance the activity of somatostatin and
 CC dopamine i.e. working as receptor agonists. The present invention
 CC describes analogues with specificity for different types of somatostatin
 CC receptor subtypes that are accordingly associated with the treatment of
 CC particular diseases or conditions. As such, these analogues may be used
 CC to treat neoplasia and acromegaly as well as various neuroendocrine
 CC tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
 CC scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
 CC tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
 CC hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
 CC disorder or an opioid overdose. Accordingly, they exhibit activities that
 CC include cytostatic, osteoplastic, antithyroid, vasotropic, antiangiogenic,
 CC ophthalmological, antidiabetic, dermatological, immunosuppressive,
 CC antiarthritic, antirheumatic, antiinflammatory, antiulcer,
 CC antiarthritic, nephrotropic, hepatotropic, antilipase, analgesic,
 CC antiangiinal, anorectic, immunomodulator, cardiant, tranquilizer and
 CC antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
 CC analogue of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 80.0%; Score 64; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 YYCFWKTCCT 11
 DQ 2 YYCFWKTCCT 10
 RESULT 8
 ADI14956
 ID ADI14956 standard; peptide; 11 AA.
 AC ADI14956;
 XX 22-APR-2004 (first entry)
 DT Somatostatin-dopamine chimeric analogue-related peptide 66.
 XX Somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiabetic; anti-HIV; dermatological;
 KW anti-diabetic; osteoplastic; antibacterial; immunomodulator; hypertensive;
 KW tranquilizer; antilipase; nephrotropic; antiulcer; antiarthritic;

KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreatocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 XX Modified-site 1
 FT /note= "Amino acid is Doc. Bound to 1-(7-allyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-
 FT carbonyl)-3-ethylureidomethylsulfanyl acetic acid"
 FT Misc-difference 3..4
 FT /note= "D-form residue"
 FT Modified-site 5
 FT /note= "Residue forms a bond to residue 10 to form a
 FT cyclic peptide"
 FT Misc-difference 7
 FT /note= "D-form residue"
 FT Modified-site 10
 FT /note= "Residue forms a bond to residue 5 to form a
 FT cyclic peptide"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX
 PN WO2002100888-A1.
 XX 19-DEC-2002.
 XX 07-JUN-2002; 2002WO-US017859.
 XX 08-JUN-2001; 2001US-0297059P.
 XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 XX WPI; 2003-239103/23.
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 FT e.g. lung cancer.
 XX Claim 3; Page 144; 85pp; English.
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiabetic, anti-HIV, dermatological, anti-diabetic, osteoplastic,
 CC antibacterial, immunomodulator, hypertensive, tranquilizer, antilipase,
 CC nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or
 CC antiaddictive activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,

CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiotensin, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 11 AA;

Query Match 80.0%; Score 64; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.21; Length 11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
 |||||
 Db 3 YYCFWKTCCT 11

RESULT 9
 ADI14951
 ID ADI14951 standard; peptide; 11 AA.
 XX
 AC ADI14951;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Somatostatin-dopamine chimeric analogue-related peptide 61.
 XX
 KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antileptemic; nephrotropic; antiulcer; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidoblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW GH secreting adenoma; postprandial hypotension; panic attack;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiotensin;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.

XX
 OS Synthetic.
 OS Unidentified.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1 /note= "Amino acid is Doc. Bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo(4,3-fg)quinolin-9-yl-
 FT methylsulfonyl-acetic acid"
 FT Misc-difference 3..4
 FT /note= "D-form residue"
 FT Modified-site 5
 FT /note= "Residue forms a bond to residue 10 to form a
 FT cyclic peptide"
 FT Misc-difference 7
 FT /note= "D-form residue"
 FT Modified-site 10
 FT /note= "Residue forms a bond to residue 5 to form a
 FT cyclic peptide"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX
 PN W02002100888-A1.
 XX
 PD 19-DEC-2002.
 XX
 XX 07-JUN-2002; 2002WO-US017859.
 XX
 XX 08-JUN-2001; 2001US-0297059P.
 XX
 PA (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 XX
 PI Culler WD, Dong ZX, Kim SH, Moreau J;
 XX
 XX WPI; 2003-239103/23.
 DR
 XX
 PT New somatostatin-dopamine chimeric analogs useful for the treatment of
 PT e.g. lung cancer.
 XX
 XX Claim 3; Page 144; 85pp; English.
 PS
 CC
 CC This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antileptemic,
 CC nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or
 CC antiaddictive activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiotensin, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to

CC produce the somatostatin-dopamine chimeric analogues of the invention.

XX

SQ Sequence 11 AA;

Query Match 80.0%; Score 64; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 |||||

Db 3 YYCFWKTCCT 11

RESULT 10

AD114959

ID AD114959 standard; peptide; 11 AA.

XX AC

XX AD114959;

XX 22-APR-2004 (first entry)

XX Somatostatin-dopamine chimeric analogue-related peptide 69.

XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 tranquiliser; antilipaeamic; nephrotropic; antilucer; antiarthritic;
 hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 somatostatin receptor agonist; lung cancer; glioma; anorexia;
 hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 gastrinoma; Zollinger-Elison Syndrome; diarrhoea;
 AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 irritable bowel syndrome; pancreatitis; small bowel obstruction;
 gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 gonadotropinoma; hyperparathyroidism; Graves disease;
 diabetic neuropathy; Paget's disease; polycystic ovary disease;
 thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 orthostatic; hypotension; postprandial hypotension; panic attack;
 GH secreting adenoma; acromegally; TSH secreting adenoma;
 prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 proliferative retinopathy; dawn phenomenon; nephropathy;
 gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 pancreaticocutaneous fistula; dumping syndrome;
 watery diarrhoea syndrome; pancreatitis;
 gastrointestinal hormone secreting tumour; angio genesis; arthritis;
 allograft rejection; graft vessel bleeding; portal hypertension;
 gastrointestinal bleeding; obesity; opioid overdose.

XX Synthetic.

OS Unidentified.

XX

Key Location/Qualifiers

FT Modified-site 1

FT /note= "4-(2-aminoethyl)-1-carboxymethyl-piperazine.
 Bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-
 octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
 ethylureidomethylsulfonyl acetic acid"

FT Misc-difference 3..4

FT /note= "D-form residue"

FT Modified-site 5

FT /note= "Residue forms a bond to residue 10 to form a
 cyclic peptide"

FT Misc-difference 7

FT /note= "D-form residue"

FT Modified-site 10

FT /note= "Residue forms a bond to residue 5 to form a
 cyclic peptide"

FT Modified-site 11

FT /note= "C-terminal amide"

XX

PN WO2002100888-A1.

XX 19-DEC-2002.

XX 07-JUN-2002; 2002WO-US017859.

XX 08-JUN-2001; 2001US-0297059P.

XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.

XX Culler MD, Dong ZX, Kim SH, Moreau J;

XX WPI; 2003-239103/23.

XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 e.g. lung cancer.

XX Claim 3; Page 145; 85pp; English.

XX This invention relates to novel somatostatin-dopamine chimeric analogues
 or their salts. The invention may be useful for the development of
 compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeamic,
 nephrotropic, antilucer, antiarthritic, hypotensive, anorectic or
 antiaddictive activity through action as a dopamine receptor agonist and
 somatostatin receptor agonist. The invention may be useful for the
 treatment of lung cancer, glioma, anorexia, hypothyroidism,
 hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 restenosis, Crohn's disease, systemic sclerosis, external and internal
 pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis,
 hyperinsulinism, gastrinoma, Zollinger-Elison Syndrome, diarrhoea, AIDS
 related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 secreting adenomas, prolactin secreting adenomas, insulinoma,
 glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 portal hypertension, gastrointestinal bleeding, obesity and opioid
 overdose. The compounds simultaneously elicit dopamine receptor agonist
 and somatostatin receptor agonist effects in vivo with enhanced
 biological activity over the native somatostatin and dopamine analogues
 alone. The present sequence is that of a peptide which was used to
 produce the somatostatin-dopamine chimeric analogues of the invention.

XX

SQ Sequence 11 AA;

Query Match 80.0%; Score 64; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 |||||

Db 3 YYCFWKTCCT 11

RESULT 11

AD114954

ID AD114954 standard; peptide; 11 AA.

XX AC

XX AD114954;

XX 22-APR-2004 (first entry)

XX Somatostatin-dopamine chimeric analogue-related peptide 64.

XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilepaemic; nephrotropic; antitumor; antidiarrhetic;
 KW hypotensive; anorectic; antidiabetic; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW somatostatin receptor agonist; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiotropathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 XX Synthetic.
 OS Unidentified.

XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "4-(2-aminoethyl)-1-carboxymethyl-piperazine.
 FT Bound to 7-propyl-4,6,6,7,8,9,10,10a-octahydroindolo[4,3
 FT -f]quinolin-9-yl-methylsulfonyl-acetic acid"
 FT Misc-difference 3. .4
 FT /note= "D-form residue"
 FT Modified-site 5
 FT /note= "Residue forms a bond to residue 10 to form a
 FT cyclic peptide"
 FT Misc-difference 7
 FT /note= "D-form residue"
 FT Modified-site 10
 FT /note= "Residue forms a bond to residue 5 to form a
 FT cyclic peptide"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX WO2002100888-A1.
 XX 19-DEC-2002.
 XX 07-JUN-2002; 2002WO-US017859.
 XX 08-JUN-2001; 2001US-0297059P.
 XX (SCRC) SCRAS SOC CONSIGLS RECH & APPL SCI.
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 XX WPI; 2003-239103/23.
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 FT e.g. lung cancer.
 XX Claim 3; Page 144; 85pp; English.
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,

CC antibacterial, immunomodulator, hypertensive, tranquiliser, antilepaemic,
 CC nephrotropic, antitumor, antidiarrhetic, antidiarrhetic, anorectic or
 CC antidiabetic activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC secreting adenomas, prolactin secreting adenomas, acromegaly, TSH
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiotropathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX Sequence 11 AA;
 SQ

Query Match 80.0%; Score 64; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 |||||
 Db 3 YYCFWKTCCT 11

RESULT 12
 ADS74377
 ID ADS74377 standard; peptide; 11 AA.
 AC ADS74377;
 XX 16-DEC-2004 (first entry)
 XX Somatostatin analogue.
 XX Somatostatin analogue; cytostatic; gene therapy.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 1. .4
 FT /note= "D-form residues"
 FT Disulfide-bond 5. .10
 FT Misc-difference 7
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /note= "C-terminal amide or alcohol"
 XX WO2004081031-A2.
 XX 23-SEP-2004.
 XX 10-MAR-2004; 2004WO-US007143.
 XX 10-MAR-2003; 2003US-0452928P.
 XX (BIOG-) BIOGEN IDEC INC.

XX Braslavsky GR, Chinn P;
 XX WPI; 2004-668933/65.
 XX A composition comprising a somatostatin analog useful for thiol-specific
 PT drug attachment to somatostatin and other targeting peptides, or for
 PT diagnosing or treating somatostatin receptor-associated disorders, e.g.
 PT cancer.
 XX Claim 4; SEQ ID NO 5; 43pp; English.
 XX
 CC The present sequence is that of a synthetic somatostatin analogue. The
 CC peptide can be used as component B in a claimed composition comprising a
 CC somatostatin analogue of formula (A-B), where A is Cys, or a peptide
 CC chain comprising one or more Cys residues, which is suitable for binding
 CC to a drug or chelator via a thiol linkage, and B is a naturally occurring
 CC or synthetic somatostatin peptide, or its fragment, that binds to the
 CC somatostatin receptor (sstr). The drug or chelator is bound to the Cys
 CC residue(s) of component A by a thiol linkage. The drug is a therapeutic
 CC drug such as a radioisotope, a cytotoxin, an immunostimulant, an
 CC antiangiogenic agent, a therapeutic gene, or a chemotherapeutic agent.
 CC The somatostatin analogue preferably binds to SSTR-positive cells,
 CC especially human cancer cells. A claimed method for detecting SSTR-
 CC positive cells comprises administering the somatostatin analogue in which
 CC a detectable label is bound to the Cys residue(s) of component A, and
 CC detecting the label. A claimed method for treating an SSTR-associated
 CC disorder comprises administering a somatostatin analogue in which a
 CC therapeutic agent is bound to the Cys residue(s) of component A. The SSTR
 CC -associated disorder is especially cancer. Thiol-mediated drug attachment
 CC can also be used with other targeting peptides.
 XX
 SQ Sequence 11 AA;
 Query Match 80.0%; Score 64; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 YYCFWKTCCT 11
 Db 3 YYCFWKTCCT 11
 RESULT 13
 ADU05246
 ID ADU05246 standard; peptide; 11 AA.
 XX
 AC ADU05246;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Cyclic somatostatin-dopamine chimeric peptide analogue #36.
 XX
 KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective tissue disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cystostatic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antitumor;
 KW antiarrhythmic; nephrotropic; hepatotropic; antilipemic; analgesic;
 KW antianginal; anorectic; immunomodulator; cardiant; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "An N-terminal dopamine derivative (Dop1 to Dop6
 FT inclusive) is attached to a Lys(dopamine derivative)
 FT modified residue, where this second dopamine derivative
 FT must match the type occurring at the N-terminus, e.g.
 FT

FT Misc-difference 3 Dop1-Lys (Dop1), Dop2-Lys (Dop2) etc. "
 FT /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Disulfide-bond 5.10 /note= "D-form residue"
 FT Misc-difference 7 /note= This disulphide bond cyclises the peptide
 FT /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal alcohol"
 XX
 PN WO2004091490-A2.
 XX
 PD 28-OCT-2004.
 XX
 PF 08-APR-2004; 2004WO-US010891.
 XX
 PR 11-APR-2003; 2003US-0462374P.
 XX
 PA (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX
 PI Dong ZX, Dewitt Culler M, Shen Y;
 XX WPI; 2004-784484/77.
 XX
 CC New chimeric analog comprising at least one moiety which binds to one or
 PT more somatostatin and dopamine receptor(s) useful to treat e.g.
 PT neuroendocrine tumor, vascular diseases, connective tissue disease,
 PT immune disease and cachexia.
 XX
 PS Claim 12; Page 103; 138pp; English.
 XX
 CC This invention relates to novel somatostatin-dopamine chimeric analogues
 CC that comprise at least one moiety that binds to one or more somatostatin
 CC receptors and at least one moiety that binds to one or more dopamine
 CC receptors, or a salt derived thereof. Specifically, it refers to
 CC analogues that may be used in vitro or in vivo for research, diagnostic
 CC and therapeutic agents to enhance the activity of somatostatin and
 CC dopamine i.e. working as receptor agonists. The present invention
 CC describes analogues with specificity for different types of somatostatin
 CC receptor subtypes that are accordingly associated with the treatment of
 CC particular diseases or conditions. As such, these analogues may be used
 CC to treat neoplasia and acromegaly as well as various neuroendocrine
 CC tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
 CC scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
 CC tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
 CC hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
 CC disorder or an opioid overdose. Accordingly, they exhibit activities that
 CC include cytostatic, osteopathic, antithyroid, vasotropic, antiangiogenic,
 CC ophthalmological, antidiabetic, dermatological, immunosuppressive,
 CC antiarthritic, antirheumatic, antiinflammatory, antitumor, antilipemic,
 CC antiarrhythmic, nephrotropic, hepatotropic, antilipemic, analgesic,
 CC antianginal, anorectic, immunomodulator, cardiant, tranquilizer and
 CC antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
 CC analogue of the invention.
 XX
 SQ Sequence 11 AA;
 Query Match 80.0%; Score 64; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 YYCFWKTCCT 11
 Db 3 YYCFWKTCCT 11
 RESULT 14
 ADI14894
 ID ADI14894 standard; peptide; 12 AA.
 XX
 AC ADI14894;

22-APR-2004 (first entry)
Somatostatin-dopamine chimeric analogue-related peptide 7.

1
somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
anti-diabetic; osteopathic; antidiarrhoeic; immunomodulator; hypertensive;
tranquilliser; antilipemic; nephrotropic; antiulcer; antiarthritic;
hypotensive; anorectic; antidiabetic; dopamine receptor agonist;
somatostatin receptor agonist; lung cancer; glioma; anorexia;
hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
acromegaly; restenosis; Crohn's disease; systemic sclerosis;
pancreatic pseudocyst; ascites; VIPoma; nesidioblastosis; hyperinsulinism;
gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
irritable bowel syndrome; pancreatitis; small bowel obstruction;
gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
gonadotropinoma; hyperparathyroidism; Graves disease;
diabetic neuropathy; Paget's disease; polycystic ovary disease;
thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
orthostatic; hypotension; postprandial hypotension; panic attack;
GH secreting adenoma; acromegaly; TSH secreting adenoma;
prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
hyperlipidaemia; insulin insensitivity; Syndrome X; angiopathy;
proliferative retinopathy; dawn phenomenon; nephropathy;
gastric acid secretion; peptic ulcer; enterocutaneous fistula;
pancreaticoduodenal fistula; dumping syndrome;
watery diarrhoea syndrome; pancreatitis;
gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
allograft rejection; graft vessel bleeding; portal hypertension;
gastrointestinal bleeding; obesity; opioid overdose; cyclic; circular.

2
Synthetic.
Unidentified.

3
Key Location/Qualifiers

4
Modified-site 1
/note= "Amino acid is Doc. Optionally bound to 7-propyl-
methylethylsulfonyl-acetic acid. Optionally bound to 7-propyl-
4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
methyl-carbamate acid. Optionally bound to carbonic acid
mono-(7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
fg]quinolin-9-yl-methyl) ester. Optionally bound to 4-((7-
propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
fg]quinolin-9-yl-methyl) carbonyl) butyric acid.
Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-
octahydroindolo[4,3-fg]quinolin-9-carboxylic acid.
Optionally bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-
octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
ethylureidomethylsulfonyl acetic acid. Optionally bound
to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
fg]quinolin-9-carbonyl)-3-ethylureidopropyl)carbamate
acid. Optionally bound to carbonic acid mono-(3-(1-(7-
allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-
9-carbonyl)-3-ethylureido)propyl)carbamate acid.
Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-
octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
ethylureidopropyl)-Gly-. Optionally bound to 4-(3-(1-(7-
allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-
9-carbonyl)-3-ethylureido)propyl)carbamate acid"

5
Modified-site 2
/note= "Amino acid is Doc"

6
Misc-difference 4. .5
/note= "D-form residue"

7
Modified-site 6
/note= "Residue forms a bond to residue 11 to form a
cyclic peptide"

8
Misc-difference 8
/note= "D-form residue"

9
Modified-site 11
/note= "Residue forms a bond to residue 6 to form a
cyclic peptide"

10
Query Match 80.0%; Score 64; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

11
Query 3 YTCFWKTCT 11
Db 4 YTCFWKTCT 12
RESULT 15
ADI14957
ID ADI14957 standard; peptide; 13 AA.
AC ADI14957;

XX DT 22-APR-2004 (first entry)

XX DE Somatostatin-dopamine chimeric analogue-related peptide 67.

XX KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipemic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiotropathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.

XX OS Synthetic.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "Amino acid is Doc. Bound to 1-(7-allyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-
 FT carbonyl)-3-ethylureidomethylsulfanyl acetic acid"

FT Modified-site 2..3 /note= "Amino acid is Doc"

FT Misc-difference 5..6 /note= "D-form residue"

FT Modified-site 7 /note= "Residue forms a bond to residue 12 to form a
 FT cyclic peptide"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 12 /note= "Residue forms a bond to residue 7 to form a
 FT cyclic peptide"

FT Modified-site 13 /note= "C-terminal amide"

XX WO2002100888-A1.

XX 19-DEC-2002.

XX 07-JUN-2002; 2002WO-US017859.

XX 08-JUN-2001; 2001US-0297059P.

XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.

XX Culler MD, Dong ZX, Kim SH, Moreau J;

XX WPI; 2003-239103/23.

XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 FT e.g. lung cancer.

PS Claim 3; Page 145; 85pp; English.

XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antilipemic,
 CC nephrotropic, antitumor, antiarthritic, hypotensive, anorectic or
 CC antiaddictive activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiotropathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.

XX SQ Sequence 13 AA;

Query Match 80.0%; Score 64; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 Y Y C F W K T C T 1 1
 | | | | | | | | | |
 Db 5 Y Y C F W K T C T 1 3

RESULT 16

AD114895

ID AD114895 standard; peptide; 13 AA.

XX AC AD114895;

XX 22-APR-2004 (first entry)

DE Somatostatin-dopamine chimeric analogue-related peptide 8.

XX KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipemic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;

orthostatic; hypotension; postprandial hypotension; panic attack;
 GH secreting adenoma; acromegaly; TSH secreting adenoma;
 prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 proliferative retinopathy; dawn phenomenon; nephropathy;
 gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 pancreaticocutaneous fistula; dumping syndrome;
 watery diarrhoea syndrome; pancreatitis;
 gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 allograft rejection; graft vessel bleeding; portal hypertension;
 gastrointestinal bleeding; obesity; opioid overdose; cyclic; circular.

OS Synthetic.
 OS Unidentified.

XX Key Location/Qualifiers
 XX Modified-site 1
 FT /note= "Amino acid is Doc. Optionally bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methylsulfonyl-acetic acid. Optionally bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methyl-carbamoyl acid. Optionally bound to carbonyl acid
 FT mono-(7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fg]quinolin-9-yl-methyl) ester. Optionally bound to 4-((7-
 FT propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fg]quinolin-9-yl-methyl) carbonyl) butyric acid.
 FT Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carboxylic acid.
 FT Optionally bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
 FT ethylureidoethylsulfonyl acetic acid. Optionally bound
 FT to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fg]quinolin-9-carbonyl)-3-ethylureidopropyl)carbamoyl
 FT acid. Optionally bound to carbonyl acid mono-(3-(1-(7-
 FT allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin
 FT 9-carbonyl)-3-ethylureido)propyl)carbamoyl acid.
 FT Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
 FT ethylureidopropyl)-Gly-. Optionally bound to 4-(3-(1-(7-
 FT allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin
 FT 9-carbonyl)-3-ethylureido)propyl)carbamoyl)butyric acid"

FT 2. . 3 "Amino acid is Doc"
 FT /note= "Amino acid is Doc"
 FT Misc-difference 5. . 6
 FT /note= "D-form residue"
 FT Modified-site 7
 FT /note= "Residue forms a bond to residue 12 to form a
 FT cyclic peptide"
 FT Misc-difference 9
 FT /note= "D-form residue"
 FT Modified-site 12
 FT /note= "Residue forms a bond to residue 7 to form a
 FT cyclic peptide"
 FT Modified-site 13
 FT /note= "C-terminal amide"

XX WO2002100888-A1.
 XX
 XX 19-DEC-2002.
 XX
 XX 07-JUN-2002; 2002WO-US017859.
 XX
 XX 08-JUN-2001; 2001US-0297059P.
 XX
 XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 XX
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 XX WPI; 2003-239103/23.
 XX
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 XX e.g. lung cancer.

PS Claim 3; Page 103; 85pp; English.

XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antipalpaemic,
 CC nephrotropic, antitumor, antiarthritic, hypotensive, anorectic or
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, mesodiblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.

XX SQ Sequence 13 AA;
 Query Match 80.0%; Score 64; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
 |||||
 Db 5 YYCFWKTKCT 13

RESULT 17
 ADI14952
 ID ADI14952 standard; peptide; 14 AA.
 XX
 XX AC ADI14952;
 XX
 XX DT 22-APR-2004 (first entry)
 XX
 XX DE
 XX Somatostatin-dopamine chimeric analogue-related peptide 62.
 XX
 XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 XX vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 XX anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 XX tranquiliser; antipalpaemic; nephrotropic; antitumor; antiarthritic;
 XX hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 XX somatostatin receptor agonist; lung cancer; glioma; anorexia;
 XX hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 XX acromegaly; restenosis; Crohn's disease; systemic sclerosis; hyperinsulinism;
 XX pancreatic pseudocyst; ascite; VIPoma; mesodiblastosis; diarrhoea;
 XX gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 XX AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 XX irritable bowel syndrome; pancreatitis; small bowel obstruction;
 XX gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 XX gonadotropinoma; hyperparathyroidism; Graves disease;
 XX diabetic neuropathy; Paget's disease; polycystic ovary disease;
 XX thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;

orthostatic; hypotension; postprandial hypotension; panic attack;
 GH secreting adenoma; acromegaly; TSH secreting adenoma;
 prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 hyperlipidaemia; insulin insensitivity; Syndrome X; angiotensin;
 proliferative retinopathy; dawn phenomenon; nephropathy;
 gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 pancreaticocutaneous fistula; dumping syndrome;
 watery diarrhoea syndrome; pancreatitis;
 gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 allograft rejection; graft vessel bleeding; portal hypertension;
 gastrointestinal bleeding; obesity; opioid overdose.
 Synthetic.
 Unidentified.

Key Location/Qualifiers
 Modified-site 1
 /note= "Amino acid is Doc. Bound to 7-propyl-
 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 methylsulfonyl-acetic acid"
 Modified-site 2..4
 /note= "Amino acid is Doc"
 Misc-difference 6..7
 /note= "D-form residue"
 Modified-site 8
 /note= "Residue forms a bond to residue 13 to form a
 cyclic peptide"
 Misc-difference 10
 /note= "D-form residue"
 Modified-site 13
 /note= "Residue forms a bond to residue 8 to form a
 cyclic peptide"
 Modified-site 14
 /note= "C-terminal amide"

WO2002100888-A1.
 19-DEC-2002.
 07-JUN-2002; 2002WO-US017859.
 08-JUN-2001; 2001US-0297059P.
 (SCRC) SCRAS SOC CONSRILS RECH & APPL SCI.
 Culler MD, Dong ZX, Kim SH, Moreau J;
 WPI; 2003-239103/23.
 New somatostatin-dopamine chimeric analogs useful for the treatment of
 e.g. lung cancer.
 Claim 3; Page 144; 85pp; English.

This invention relates to novel somatostatin-dopamine chimeric analogues
 or their salts. The invention may be useful for the development of
 compounds with a cytostatic, antitumor, vasotropic, anti-inflammatory,
 antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 antibacterial, immunomodulator, hypertensive, tranquiliser, antilipemic,
 nephrotropic, antitumor, antirheumatic, hypotensive, anorectic or
 antiaddictive activity through action as a dopamine receptor agonist and
 somatostatin receptor agonist. The invention may be useful for the
 treatment of lung cancer, glioma, anorexia, hypothyroidism,
 hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 restenosis, Crohn's disease, systemic sclerosis, external and internal
 pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,
 hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 meningioma, cancer cachexia, orthostatic, hypotension, postprandial

CC hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiotensin, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 14 AA;
 Query Match 80.0%; Score 64; DB 7; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 YYCFWKTCT 11
 Db 6 YYCFWKTCT 14
 RESULT 18
 ABR42184
 ID ABR42184 standard; peptide; 15 AA.
 XX AC ABR42184;
 XX DT 28-JUL-2003 (first entry)
 XX DE Somatostatin analogue peptide JF-08-87A.
 XX KW Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 XX KW antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 Modified-site 1
 /note= "Optional methotrexate-acetyl moiety or 2-bromo-
 acetyl-D-tert-butyl or D-tert butyl modification, D-form
 residue"
 Misc-difference 2
 /note= "D-form residue, optional tert-butyl modification"
 Misc-difference 3
 /note= "D-form residue, optional tert-butyl modification"
 Misc-difference 4
 /note= "D-form residue, optional tert-butyl modification"
 Misc-difference 5
 /note= "D-form residue, optional tert-butyl modification"
 Modified-site 6
 /note= "Optional epsilon-tert-butyloxycarbonyl
 modification"
 Misc-difference 7
 /note= "D-form residue, optional tert-butyl modification"
 Modified-site 8
 /note= "Optional tert-butyl modification"
 Disulfide-bond 9..14
 /note= "Optional Cys circularization"
 Modified-site 9
 /note= "Optional S-trityl modification"
 Misc-difference 11
 /note= "D-form residue"
 Modified-site 12
 /note= "Optional epsilon-tert-butyloxycarbonyl
 modification"
 Modified-site 13
 /note= "Optional tert-butyl modification"
 Modified-site 14

FT /note= "optional epsilon-tert-butyl-oxycarbonyl
FT modification"
FT 15
FT /note= "C-terminal amide, optional tert-butyl
FT modification"
FT 15
XX WO2003028527-A2.
XX
XX 10-APR-2003.
XX
XX 20-SEP-2002; 2002WO-US030143.
XX
XX 21-SEP-2001; 2001US-0323851P.
XX
XX (TULA) TULANE EDUCATIONAL FUND.
XX
XX Coy DH, Fuselier JA, Murphy WA, Sun L;
XX WPI; 2003-441067/41.
XX
XX Biologically active peptides such as somatostatin or bombesin conjugated
FT to chemical compounds through linkers, useful for treating tumors of the
FT lung and breast, carcinoid syndrome, and tumors of angiogenic blood
FT vessels.
XX
XX Disclosure; Page 16; 86pp; English.
XX
XX The present sequence is that of somatostatin analogue peptide JP-08-87A.
CC It is an example of peptide agents of the invention that comprise a
CC biologically active peptide, such as somatostatin or bombesin, conjugated
CC to a chemical compound through a linker that maintains the peptide's
CC biological activity. The peptide agents may also include a cytostatic or
CC therapeutic agent, label or chelating group and a peptide that increases
CC the hydrophilic biolubricity of the agent. They are useful for
CC treating tumors of the lung, breast, brain, eye, prostate, or colon,
CC tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
CC angiogenic blood vessels (claimed). Other diseases that can also be
CC treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
CC arthritis, neoplastic cells or aberrantly proliferating cells, and
CC acromegaly. Peptide JP-08-87A has the ability to inhibit growth hormone
CC release from primary cultures of rat pituitary cells, having an IC50 of
CC 0.16 nM (compared with 0.15 nM for somatostatin-14). Note: The present
CC sequence is identified as SEQ ID 2 in the disclosure (page 16), but it is
CC not the same as the sequence given as SEQ ID 2 in the sequence listing
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 80.0%; Score 64; DB 6; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 0.27;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 YYCFWKTKCT 11
XX |||||
XX 7 YYCFWKTKCT 15
XX
XX RESULT 19
XX ADI14935
XX ID ADI14935 standard; peptide; 15 AA.
XX
XX AC ADI14935;
XX
XX 22-APR-2004 (first entry)
XX
XX Somatostatin-dopamine chimeric analogue-related peptide 46.
XX
XX somatostatin-dopamine chimeric analogue; cytostatic; antihypertensive;
XX vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
XX anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
XX tranquilliser; antilipase; nephrotoxic; antiulcer; antiarthritic;
XX hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
XX somatostatin receptor agonist; lung cancer; glioma; anorexia;
XX hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;

XX acromegaly; restenosis; Crohn's disease; systemic sclerosis;
KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
KW gonadotropinoma; hyperparathyroidism; Graves disease;
KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
KW orthostatic; hypotension; postprandial hypotension; panic attack;
KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiopathy;
KW proliferative retinopathy; dawn phenomenon; nephropathy;
KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
KW pancreatocutaneous fistula; dumping syndrome;
KW watery diarrhoea syndrome; pancreatitis;
KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
KW allograft rejection; graft vessel bleeding; portal hypertension;
KW gastrointestinal bleeding; obesity; opioid overdose.
XX
XX Synthetic.
OS Unidentified.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note= "D-form residue. Optionally bound to 7-propyl-
FT 4, 6, 6a, 7, 8, 9, 10, 10a-octahydroindolo[4,3-fg]quinolin-9-yl-
FT methylsulfonyl-acetic acid. Optionally bound to 7-propyl-
FT 4, 6, 6a, 7, 8, 9, 10, 10a-octahydroindolo[4,3-fg]quinolin-9-yl-
FT methyl-carbamate acid. Optionally bound to carbonic acid
FT mono-(7-propyl-4, 6, 6a, 7, 8, 9, 10, 10a-octahydroindolo[4,3-
FT fg]quinolin-9-yl-methyl) ester. Optionally bound to 4-(7-
FT propyl-4, 6, 6a, 7, 8, 9, 10, 10a-octahydroindolo[4,3-
FT fg]quinolin-9-yl-methyl) carbonyl) butyric acid.
FT Optionally bound to 7-propyl-4, 6, 6a, 7, 8, 9, 10, 10a-
FT octahydroindolo[4,3-fg]quinolin-9-carboxylic acid.
FT Optionally bound to 3-(1-(7-allyl-4, 6, 6a, 7, 8, 9, 10, 10a-
FT octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
FT ethylureidopropyl)-gly-"
FT Misc-difference 2. .5
FT /note= "D-form residue"
FT Misc-difference 7. .8
FT /note= "D-form residue"
FT Modified-site 9
FT /note= "Residue forms a bond to residue 14 to form a
FT cyclic peptide"
FT Misc-difference 11
FT /note= "D-form residue"
FT Modified-site 14
FT /note= "Residue forms a bond to residue 9 to form a
FT cyclic peptide"
FT Modified-site 15
FT /note= "C-terminal OL"
XX
XX WO2002100888-A1.
XX
XX 19-DEC-2002.
XX
XX 07-JUN-2002; 2002WO-US017859.
XX
XX 08-JUN-2001; 2001US-0297059P.
XX
XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
XX
XX Culler MD, Dong ZX, Kim SH, Moreau J;
XX WPI; 2003-239103/23.
XX
XX New somatostatin-dopamine chimeric analogs useful for the treatment of
XX e.g. lung cancer.
XX
XX Claim 3; Page 133; 85pp; English.
PS

XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antilipæmic,
 CC nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or
 CC antiaddictive activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX

SQ Sequence 15 AA;

Query Match 80.0%; Score 64; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTCT 11
 DQ 7 YYCFWKTCT 15
 |||||

RESULT 20
 ADI14898
 ID ADI14898 standard; peptide; 15 AA.
 XX
 AC ADI14898;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Somatostatin-dopamine chimeric analogue-related peptide 11.
 XX
 KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipæmic; nephrotropic; antiulcer; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;

KW GH secreting adenoma; acromegally; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose; cyclic; circular.
 XX Synthetic.
 OS Unidentified.

Key Location/Qualifiers
 Modified-site 1
 FT /note= "D-form residue. Optionally bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methylsulfonyl-acetic acid. Optionally bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methyl-carbanic acid. Optionally bound to carbonic acid
 FT mono-(7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]
 FT fglquinolin-9-yl-methyl) ester. Optionally bound to 4-(7-
 FT fglquinolin-9-yl-methyl) carboxylic acid.
 FT fglquinolin-9-yl-methyl) carboxylic acid.
 FT Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carboxylic acid.
 FT Optionally bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carboxyl)-3-
 FT ethylureidomethylsulfonyl acetic acid. Optionally bound
 FT to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fglquinolin-9-carboxyl)-3-ethylureidopropyl)carbanic
 FT acid. Optionally bound to carbonic acid mono-(3-(1-(7-
 FT allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin
 FT -9-carboxyl)-3-ethylureido)propyl)carbanic acid.
 FT Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-
 FT ethylureidopropyl)-gly-
 FT fglquinolin-9-carboxyl)-3-
 FT ethylureidopropyl)-gly-
 FT allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin
 FT -9-carboxyl)-3-ethylureido)propyl)carbanic acid".
 FT
 FT Misc-difference 2. .5 /note= "D-form residue"
 FT Misc-difference 7. .8 /note= "D-form residue"
 FT
 FT Modified-site 9 /note= "Residue forms a bond to residue 14 to form a
 FT cyclic peptide"
 FT
 FT Misc-difference 11 /note= "D-form residue"
 FT
 FT Modified-site 14 /note= "Residue forms a bond to residue 9 to form a
 FT cyclic peptide"
 FT
 FT Modified-site 15 /note= "C-terminal amide"
 FT
 XX WO2002100888-A1.
 XX
 XX 19-DEC-2002.
 PD
 XX 07-JUN-2002; 2002WO-US017859.
 XX
 XX 08-JUN-2001; 2001US-0297059P.
 PR
 XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 FA
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 PI
 XX MPI; 2003-239103/23.
 DR
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 FT e.g. lung cancer.
 XX
 PS Claim 3; Page 103; 85pp; English.

XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antilipemic,
 CC nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreatocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 XX Sequence 15 AA;
 SQ

Query Match 80.0%; Score 64; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
 Db 7 YYCFWKTCCT 15

RESULT 21
 ABR42192
 ID ABR42192 standard; peptide; 20 AA.
 XX
 AC ABR42192;
 XX
 DT 28-JUL-2003 (first entry)
 XX
 DE Peptide analogue conjugate.
 XX
 KW Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 KW antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "DOTA moiety or optional DOTA-O-benzyl or O-benzyl
 FT modification, D-form residue"
 FT Misc-difference 2 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 3 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 4 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT

FT Misc-difference 5 residue"
 FT /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 6 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 7 /note= "optionally modified D-with O-benzyl, D-form
 FT residue"
 FT Misc-difference 8 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 9 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 10 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Modified-site 11 /note= "optionally modified with N-epsilon- (2-
 FT chlorobenzylloxycarbonyl)"
 FT Modified-site 12 /note= "optionally modified with O-2,6- dichlorobenzyl"
 FT Modified-site 13 /note= "optionally modified with O-2,6- dichlorobenzyl"
 FT Disulfide-bond 14..19 /note= "Optional Cys circularization"
 FT Modified-site 14 /note= "optionally modified with S-4-methylbenzyl"
 FT Misc-difference 16 /note= "D-form residue"
 FT Modified-site 17 /note= "optionally modified with N-epsilon-(2-
 FT (chlorobenzylloxycarbonyl)"
 FT Modified-site 19 /note= "optionally modified with S-4-methylbenzyl"
 FT Misc-difference 20 /note= "optionally modified with O-benzyl, C-terminal
 FT amide, Rink-amide resin or MBHA resin"
 XX
 XX WO2003028527-A2.
 XX 10-APR-2003.
 XX 20-SEP-2002; 2002WO-US030143.
 XX 21-SEP-2001; 2001US-0323851P.
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX Coy DH, Fueslier JA, Murphy WA, Sun L;
 XX WPI; 2003-441067/41.
 XX
 XX Biologically active peptides such as somatostatin or bombesin conjugated
 XX to chemical compounds through linkers, useful for treating tumors of the
 XX lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 XX vessels.
 XX
 XX Example 15; Page 45; 86pp; English.
 XX
 XX The present sequence is that of a peptide analogue conjugate that is an
 XX example of peptide agents of the invention that comprise a biologically
 XX active peptide, such as somatostatin or bombesin, conjugated to a
 XX chemical compound through a linker that maintains the peptide's
 XX biological activity. The peptide agents may also include a cytostatic or
 XX therapeutic agent, label or chelating group and a peptide that increases
 XX the hydrophilic biodistribution of the agent. They are useful for
 XX treating tumors of the lung, breast, brain, eye, prostate, or colon,
 XX tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
 XX angiogenic blood vessels (claimed). Other diseases that can also be
 XX treated are inflammatory bowel disease, autoimmune disorders, rheumatoid

CC arthritis, neoplastic cells or aberrantly proliferating cells, and
 CC acromegaly
 XX
 SQ Sequence 20 AA;

Query Match 80.0%; Score 64; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTCT 11
 |||||
 Db 12 YYCFWKTCT 20

RESULT 22
 ABR42198
 ID ABR42198 standard; peptide; 20 AA.
 XX
 AC ABR42198;
 XX
 DT 28-JUL-2003 (first entry)
 XX
 DE Somatostatin analogue peptide.
 XX
 KW Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 KW antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FH Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Misc-difference 6 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 8 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 10 /note= "D-form residue"
 FT Misc-difference 12 /note= "D-form residue"
 FT Misc-difference 13 /note= "D-form residue"
 FT Disulfide-bond 14. .19
 FT Misc-difference 16 /note= "D-form residue"
 FT Modified-site 20 /note= "C-terminal amide"
 FT
 XX WO2003028527-A2.
 PN
 XX
 PD 10-APR-2003.
 XX
 XX 20-SEP-2002; 2002WO-US030143.
 PF
 XX
 PR 21-SEP-2001; 2001US-0323851P.
 XX
 XX (TULA) TULANE EDUCATIONAL FUND.
 FA
 XX Coy DH, Fuselier JA, Murphy WA, Sun L;
 FI
 XX WPI; 2003-441067/41.
 DR

XX
 PT Biologically active peptides such as somatostatin or bombesin conjugated
 PT to chemical compounds through linkers, useful for treating tumors of the
 PT lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 PT vessels.
 XX
 PS Example 26; Page 55; 86pp; English.
 XX
 CC The present sequence is that of a somatostatin analogue peptide. It is an
 CC example of peptide agents of the invention that comprise a biologically
 CC active peptide, such as somatostatin or bombesin, conjugated to a
 CC chemical compound through a linker that maintains the peptide's
 CC biological activity. The peptide agents may also include a cytostatic or
 CC therapeutic agent, label or chelating group and a peptide that increases
 CC the hydrophilic biodistribution of the agent. They are useful for
 CC treating tumors of the lung, breast, brain, eye, prostate, or colon,
 CC tumours of neuroendocrine origin (for e.g. carcinoid syndrome), and
 CC angiogenic blood vessels (claimed). Other diseases that can also be
 CC treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
 CC arthritis, neoplastic cells or aberrantly proliferating cells, and
 CC acromegaly. The present peptide has the ability to inhibit growth hormone
 CC release from primary cultures of rat pituitary cells, having an IC50 of
 CC 0.24 nM (compared with 0.15 nM for somatostatin-14)
 XX
 SQ Sequence 20 AA;
 XX

Query Match 80.0%; Score 64; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTCT 11
 |||||
 Db 12 YYCFWKTCT 20

RESULT 23
 ADI14936
 ID ADI14936 standard; peptide; 20 AA.
 XX
 AC ADI14936;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Somatostatin-dopamine chimeric analogue-related peptide 47.
 XX
 KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrheic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antileptemic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothalamic; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 XX

4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methyl carbonyl) butyric acid. Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carboxylic acid. Optionally bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidomethylsulfanyl acetic acid. Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidopropyl)carbamate acid. Optionally bound to carbonic acid mono-(3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureido)propyl)carbamate acid. Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureido)propyl)carbamate acid. Optionally bound to 4-(3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureido)propyl)carbamoyl)butyric acid".

Misc-difference 2. 10 /note= "D-form residue"

Misc-difference 12. 13 /note= "D-form residue"

Modified-site 14 /note= "Residue forms a bond to residue 19 to form a cyclic peptide"

Misc-difference 16 /note= "D-form residue"

Modified-site 19 /note= "Residue forms a bond to residue 14 to form a cyclic peptide"

Modified-site 20 /note= "C-terminal amide"

WO2002100888-A1.

19-DEC-2002.

07-JUN-2002; 2002WO-US017859.

08-JUN-2001; 2001US-0297059P.

(SCRC) SCRAS SOC CONSRILS RECH & APPL SCI.

Culler MD, Dong ZX, Kim SH, Moreau J;

WPT; 2003-239103/23.

New somatostatin-dopamine chimeric analogs useful for the treatment of e.g. lung cancer.

Claim 3; Page 103; 85pp; English.

This invention relates to novel somatostatin-dopamine chimeric analogues or their salts. The invention may be useful for the development of compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory, antidiarrhoeal, anti-HIV, dermatological, anti-diabetic, osteopathic, antibacterial, immunomodulator, hypertensive, tranquiliser, antipalpaemic, nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or antiaddictive activity through action as a dopamine receptor agonist and somatostatin receptor agonist. The invention may be useful for the treatment of lung cancer, glioma, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and internal pancreatic pseudocysts and ascites, VIPoma, neuroblastosis, hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia, meningioma, cancer cachexia, orthostatic, hypotension, postprandial hypotension, panic attacks, GH secreting adenomas, acromegally, TSH secreting adenomas, prolactin secreting adenomas, insulinoma, glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,

CC Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon, CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour, CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding, CC portal hypertension, gastrointestinal bleeding, obesity and opioid overdose. The compounds simultaneously elicit dopamine receptor agonist CC and somatostatin receptor agonist effects in vivo with enhanced CC biological activity over the native somatostatin and dopamine analogues CC alone. The present sequence is that of a peptide which was used to CC produce the somatostatin-dopamine chimeric analogues of the invention.

XX SQ Sequence 20 AA;

Query Match 80.0%; Score 64; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.34;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11

Db 12 YYCFWKTKCT 20

RESULT 25

ABR42181

ID ABR42181 standard; peptide; 22 AA.

AC ABR42181;

XX 28-JUL-2003 (first entry)

XX Somatostatin analogue peptide JF-08-73.

XX Somatostatin; peptide conjugate; cytostatic; antiangiogenic;

XX antiinflammatory; antiarthritic; antirheumatic; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "125I-Succinoyl-Aspartic acid, D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 3 /note= "D-form residue"

FT Misc-difference 4 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

FT Misc-difference 6 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 8 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Misc-difference 10 /note= "D-form residue"

FT Misc-difference 11 /note= "D-form residue"

FT Misc-difference 12 /note= "D-form residue"

FT Misc-difference 13 /note= "D-form residue"

FT Misc-difference 14 /note= "D-form residue"

FT Misc-difference 15 /note= "D-form residue"

FT Disulfide-bond 16. 21

FT Misc-difference 18 /note= "D-form residue"

FT Modified-site 22

```

FT XX /note= "C-terminal amide"
XX PN WO2003028527-A2.
XX PD 10-APR-2003.
XX XX
XX PF 20-SEP-2002; 2002WO-US030143.
XX XX
XX PR 21-SEP-2001; 2001US-0323851P.
XX XX
XX PA (TULA ) TULANE EDUCATIONAL FUND.
XX PI Coy DH, Fuesel JA, Murphy WA, Sun L;
XX DR WPI; 2003-441067/41.
XX XX
XX PT Biologically active peptides such as somatostatin or bombesin conjugated
XX PT to chemical compounds through linkers, useful for treating tumors of the
XX PT lung and breast, carcinoid syndrome, and tumors of angiogenic blood
XX PT vessels.
XX XX
XX PS Example 19; Page 47; 86pp; English.
XX XX
XX CC The present sequence is that of somatostatin analogue peptide JP-08-73.
XX CC It is an example of peptide agents of the invention that comprise a
XX CC biologically active peptide, such as somatostatin or bombesin, conjugated
XX CC to a chemical compound through a linker that maintains the peptide's
XX CC biological activity. The peptide agents may also include a cytostatic or
XX CC therapeutic agent, label or chelating group and a peptide that increases
XX CC the hydrophilic biodistribution of the agent. They are useful for
XX CC treating tumors of the lung, breast, brain, eye, prostate, or colon,
XX CC tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
XX CC angiogenic blood vessels (claimed). Other diseases that can also be
XX CC treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
XX CC arthritis, neoplastic cells or aberrantly proliferating cells, and
XX CC acromegaly. Peptide JP-08-73 was used in an examination of the
XX CC biodistribution of hydrophilic peptide agents. A lack of accumulation of
XX CC radioactivity was noted in normal tissue including liver, but rapid and
XX CC high efficiency elimination of the peptide agent in urine and faeces.
XX CC Note: The present sequence is identified as SEQ ID 11 in the disclosure
XX CC (page 14), but it is not the same as the sequence given as SEQ ID 11 in
XX CC the sequence listing
XX SQ Sequence 22 AA;

Query Match 80.0%; Score 64; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTKT 11
Db 14 YYCFWKTKT 22

RESULT 26
ABR42199
ID ABR42199 standard; peptide; 25 AA.
XX AC ABR42199;
XX XX
XX DT 28-JUL-2003 (first entry)
XX XX
XX DE Somatostatin analogue peptide.
XX XX
XX KW Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
XX KW antiinflammatory; antiarthritic; antirheumatic; cyclic.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal 3-N,N-dimethylaminobenzoic acid
FT moiety, D-form residue"

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FT FT Misc-difference 2 /note= "D-form residue"
FT FT Misc-difference 3 /note= "D-form residue"
FT FT Misc-difference 4 /note= "D-form residue"
FT FT Misc-difference 5 /note= "D-form residue"
FT FT Misc-difference 6 /note= "D-form residue"
FT FT Misc-difference 7 /note= "D-form residue"
FT FT Misc-difference 8 /note= "D-form residue"
FT FT Misc-difference 9 /note= "D-form residue"
FT FT Misc-difference 10 /note= "D-form residue"
FT FT Misc-difference 11 /note= "D-form residue"
FT FT Misc-difference 12 /note= "D-form residue"
FT FT Misc-difference 13 /note= "D-form residue"
FT FT Misc-difference 14 /note= "D-form residue"
FT FT Misc-difference 15 /note= "D-form residue"
FT FT Misc-difference 17 /note= "D-form residue"
FT FT Misc-difference 18 /note= "D-form residue"
FT FT Disulfide-bond 19.24
FT FT Misc-difference 21 /note= "D-form residue"
FT FT Modified-site 25 /note= "C-terminal amide"
FT XX WO2003028527-A2.
XX PD 10-APR-2003.
XX XX
XX PF 20-SEP-2002; 2002WO-US030143.
XX PR 21-SEP-2001; 2001US-0323851P.
XX PA (TULA ) TULANE EDUCATIONAL FUND.
XX PI Coy DH, Fuesel JA, Murphy WA, Sun L;
XX DR WPI; 2003-441067/41.
XX XX
XX PT Biologically active peptides such as somatostatin or bombesin conjugated
XX PT to chemical compounds through linkers, useful for treating tumors of the
XX PT lung and breast, carcinoid syndrome, and tumors of angiogenic blood
XX PT vessels.
XX XX
XX PS Example 26; Page 55; 86pp; English.
XX XX
XX CC The present sequence is that of a somatostatin analogue peptide. It is an
XX CC example of peptide agents of the invention that comprise a biologically
XX CC active peptide, such as somatostatin or bombesin, conjugated to a
XX CC chemical compound through a linker that maintains the peptide's
XX CC biological activity. The peptide agents may also include a cytostatic or
XX CC therapeutic agent, label or chelating group and a peptide that increases
XX CC the hydrophilic biodistribution of the agent. They are useful for
XX CC treating tumors of the lung, breast, brain, eye, prostate, or colon,
XX CC tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
XX CC angiogenic blood vessels (claimed). Other diseases that can also be
XX CC treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
XX CC arthritis, neoplastic cells or aberrantly proliferating cells, and
XX CC acromegaly. The present peptide has the ability to inhibit growth hormone
XX CC release from primary cultures of rat pituitary cells, having an IC50 of

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CC 0.27 nM (compared with 0.15 nM for somatostatin-14)
XX
SQ Sequence 25 AA;

Query Match      80.0%; Score 64; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
Db 17 YYCFWKTKCT 25

RESULT 27
ABR42197
ID ABR42197 standard; peptide; 30 AA.
XX AC ABR42197;
XX
XX 28-JUL-2003 (first entry)
XX
XX Somatostatin analogue peptide.
XX
XX Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
XX antiinflammatory; antiarthritic; antirheumatic; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH FT Misc-difference 1 /note= "D-form residue"
FT FT Misc-difference 2 /note= "D-form residue"
FT FT Misc-difference 3 /note= "D-form residue"
FT FT Misc-difference 4 /note= "D-form residue"
FT FT Misc-difference 5 /note= "D-form residue"
FT FT Misc-difference 6 /note= "D-form residue"
FT FT Misc-difference 7 /note= "D-form residue"
FT FT Misc-difference 8 /note= "D-form residue"
FT FT Misc-difference 9 /note= "D-form residue"
FT FT Misc-difference 10 /note= "D-form residue"
FT FT Misc-difference 11 /note= "D-form residue"
FT FT Misc-difference 12 /note= "D-form residue"
FT FT Misc-difference 13 /note= "D-form residue"
FT FT Misc-difference 14 /note= "D-form residue"
FT FT Misc-difference 15 /note= "D-form residue"
FT FT Misc-difference 16 /note= "D-form residue"
FT FT Misc-difference 17 /note= "D-form residue"
FT FT Misc-difference 18 /note= "D-form residue"
FT FT Misc-difference 19 /note= "D-form residue"
FT FT Misc-difference 20 /note= "D-form residue"
FT FT Misc-difference 22 /note= "D-form residue"
FT FT Misc-difference 23 /note= "D-form residue"
FT FT Misc-difference 24 /note= "D-form residue"

Disulfide-bond 24..29
Misc-difference 26 /note= "D-form residue"
Modified-site 30 /note= "C-terminal amide"
XX
XX WO2003028527-A2.
XX
XX 10-APR-2003.
XX
XX 20-SEP-2002; 2002WO-US030143.
XX
XX 21-SEP-2001; 2001US-0323851P.
XX
XX (TULA ) TULANE EDUCATIONAL FUND.
XX
XX Coy DH, Fusellier JA, Murphy WA, Sun L;
XX WPI; 2003-441067/41.
XX
XX Biologically active peptides such as somatostatin or bombesin conjugated
XX to chemical compounds through linkers, useful for treating tumors of the
XX lung and breast, carcinoid syndrome, and tumors of angiogenic blood
XX vessels.
XX
XX Example 26; Page 55; 86pp; English.
XX
XX The present sequence is that of a somatostatin analogue peptide. It is an
XX example of peptide agents of the invention that comprise a biologically
XX active peptide, such as somatostatin or bombesin, conjugated to a
XX chemical compound through a linker that maintains the peptide's
XX biological activity. The peptide agents may also include a cytostatic or
XX therapeutic agent, label or chelating group and a peptide that increases
XX the hydrophilic biotransformation of the agent. They are useful for
XX treating tumors of the lung, breast, brain, eye, prostate, or colon,
XX tumours of neuroendocrine origin (for e.g. carcinoid syndrome), and
XX angiogenic blood vessels (claimed). Other diseases that can also be
XX treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
XX arthritis, neoplastic cells or aberrantly proliferating cells, and
XX acromegaly
XX
XX SQ Sequence 30 AA;
XX
XX Query Match      80.0%; Score 64; DB 6; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 0.47;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
Db 22 YYCFWKTKCT 30

RESULT 28
ADS74379
ID ADS74379 standard; peptide; 11 AA.
XX
XX ADS74379;
XX
XX 16-DEC-2004 (first entry)
XX
XX Somatostatin analogue.
XX
XX Somatostatin analogue; cytostatic; gene therapy.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH FT Misc-difference 1..4 /note= "D-form residues"
FT FT Disulfide-bond 5..10
FT FT Misc-difference 7 /note= "D-form residue"
FT FT Modified-site 11

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PT /note= "C-terminal amide or alcohol"
 XX WO2004081031-A2.
 XX
 XX 23-SEP-2004.
 XX
 XX 10-MAR-2004; 2004WO-US007143.
 XX
 XX 10-MAR-2003; 2003US-0452928P.
 XX (BIOG-) BIOGEN IDEC INC.
 XX
 XX Braslawsky GR, Chinn P;
 XX
 XX WPI; 2004-668933/65.
 XX
 XX A composition comprising a somatostatin analog useful for thiol-specific
 PT drug attachment to somatostatin and other targeting peptides, or for
 PT diagnosing or treating somatostatin receptor-associated disorders, e.g.
 PT cancer.
 XX
 XX Claim 4; SEQ ID NO 7; 43pp; English.
 XX
 XX The present sequence is that of a synthetic somatostatin analogue. The
 CC peptide can be used as component B in a claimed composition comprising a
 CC somatostatin analogue of formula (A-B), where A is Cys, or a peptide
 CC chain comprising one or more Cys residues, which is suitable for binding
 CC to a drug or chelator via a thiol linkage, and B is a naturally occurring
 CC or synthetic somatostatin peptide, or its fragment, that binds to the
 CC somatostatin receptor (SSTR). The drug or chelator is bound to the Cys
 CC residue(s) of component A by a thiol linkage. The drug is a therapeutic
 CC drug such as a radioisotope, a cytotoxin, an immunostimulant, an
 CC antiangiogenic agent, a therapeutic gene, or a chemotherapeutic agent.
 CC The somatostatin analogue preferably binds to SSTR-positive cells,
 CC especially human cancer cells. A claimed method for detecting SSTR-
 CC positive cells comprises administering the somatostatin analogue in which
 CC a detectable label is bound to the Cys residue(s) of component A, and
 CC detecting the label. A claimed method for treating an SSTR-associated
 CC disorder comprises administering a somatostatin analogue in which a
 CC therapeutic agent is bound to the Cys residue(s) of component A. The SSTR
 CC -associated disorder is especially cancer. Thiol-mediated drug attachment
 CC can also be used with other targeting peptides.
 XX
 XX Sequence 11 AA;
 SQ

Query Match 77.5%; Score 62; DB 8; Length 11;
 Best Local Similarity 90.0%; Pred. No. 0.37;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 YYCFWKTCT 11
 Db 2 YCYCFWKTCT 11

RESULT 29
 ADU05266
 ID ADU05266 standard; peptide; 10 AA.
 XX
 XX AC ADU05266;
 XX
 XX 13-JAN-2005 (first entry)
 XX
 XX Cyclic somatostatin-dopamine chimeric peptide analogue #56.
 XX
 XX somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective tissue disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytosatic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antiulcer;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipaemic; analgesic;

XX antiangiinal; anorectic; immunomodulator; cardiant; tranquillizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Modified-site 1 /note= "An N-terminal dopamine derivative (Dop1, Dop2 or
 FT Dop5) is attached to a Lys(dopamine derivative) modified
 FT residue, where this second dopamine derivative must match
 FT the type occurring at the N-terminus, e.g. Dop1-
 FT Lys(Dop1), Dop2-Lys(Dop2) etc. Optionally Lys can be a D-
 FT form residue."
 FT
 FT Misc-difference 2 /note= "D-form residue"
 FT
 FT Misc-difference 3 /note= "D-form residue"
 FT
 FT Disulfide-bond 4..9 /note= "This disulphide bond cyclises the peptide
 FT
 FT Modified-site 5 /label= 3-iodo tyrosine
 FT
 FT Misc-difference 6 /note= "D-form residue"
 FT
 FT Modified-site 10 /note= "C-terminal amide"
 FT
 FT WO2004091490-A2.
 XX
 XX 28-OCT-2004.
 XX
 XX 08-APR-2004; 2004WO-US010891.
 XX
 XX 11-APR-2003; 2003US-0462374P.
 XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX
 XX Dong ZX, Dewitt Culler M, Shen Y;
 XX WPI; 2004-784484/77.
 XX
 XX New chimeric analog comprising at least one moiety which binds to one or
 PT more somatostatin and dopamine receptor(s) useful to treat e.g.
 PT neuroendocrine tumor, vascular diseases, connective tissue disease,
 PT immune disease and cachexia.
 XX
 XX Claim 12; Page 115; 138pp; English.
 PS
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC that comprise at least one moiety that binds to one or more somatostatin
 CC receptors and at least one moiety that binds to one or more dopamine
 CC receptors, or a salt derived thereof. Specifically, it refers to
 CC analogues that may be used in vitro or in vivo for research, diagnostic
 CC and therapeutic agents to enhance the activity of somatostatin and
 CC dopamine i.e. working as receptor agonists. The present invention
 CC describes analogues with specificity for different types of somatostatin
 CC receptor subtypes that are accordingly associated with the treatment of
 CC particular diseases or conditions. As such, these analogues may be used
 CC to treat neoplasia and acromegaly as well as various neuroendocrine
 CC tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
 CC scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
 CC tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
 CC hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
 CC disorder or an opioid overdose. Accordingly, they exhibit activities that
 CC include cytostatic, osteopathic, antithyroid, vasotropic, antiangiogenic,
 CC ophthalmological, antidiabetic, dermatological, immunosuppressive,
 CC antiarthritic, antirheumatic, antiinflammatory, antiulcer,
 CC antidiarrhoeic, hepatotropic, antilipaemic, analgesic,
 CC antiangiinal, anorectic, immunomodulator, cardiant, tranquillizer and
 CC antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
 CC analogue of the invention.
 XX
 XX Sequence 10 AA;
 SQ

Query Match 76.2%; Score 61; DB 8; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.45;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
 Db 2 YYCYWKTKCT 10

RESULT 30
 ADU05270
 ID ADU05270 standard; peptide; 11 AA.
 AC ADU05270;
 DT 13-JAN-2005 (first entry)
 DE Cyclic somatostatin-dopamine chimeric peptide analogue #60.
 KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytosatic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antiulcer;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipaseic; analgesic;
 KW antianginal; anorectic; immunomodulator; cardiant; tranquillizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 OS Synthetic.

Key Location/Qualifiers
 Modified-site 1 /note= "An N-terminal dopamine derivative (Dop1, Dop2 or Dop3) is attached to a Lys(dopamine derivative) modified residue, where this second dopamine derivative must match the type occurring at the N-terminus, e.g. Dop1-Lys (Dop1), Dop2-Lys (Dop2) etc. Optionally Lys can be a D-form residue."
 Misc-difference 3 /note= "D-form residue"
 Misc-difference 4 /note= "D-form residue"
 Disulfide-bond 5..10 /note= "This disulphide bond cyclises the peptide"
 Modified-site 6 /label= 3-iodo tyrosine
 Misc-difference 7 /note= "D-form residue"
 Modified-site 11 /note= "C-terminal amide"

WO2004091490-A2.
 28-OCT-2004.
 08-APR-2004; 2004WO-US010891.
 11-APR-2003; 2003US-0462374P.
 (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 Dong ZX, Dewitt Culler M, Shen Y;
 WPI, 2004-784484/77.
 New chimeric analog comprising at least one moiety which binds to one or more somatostatin and dopamine receptor(s) useful to treat e.g. neuroendocrine tumor, vascular diseases, connective tissue disease, immune disease and cachexia.

PS Claim 12; Page 115; 138pp; English.
 XX This invention relates to novel somatostatin-dopamine chimeric analogues that comprise at least one moiety that binds to one or more somatostatin receptors and at least one moiety that binds to one or more dopamine analogues, or a salt derived thereof. Specifically, it refers to analogues that may be used in vitro or in vivo for research, diagnostic and therapeutic agents to enhance the activity of somatostatin and dopamine i.e. working as receptor agonists. The present invention describes analogues with specificity for different types of somatostatin receptor subtypes that are accordingly associated with the treatment of particular diseases or conditions. As such, these analogues may be used to treat neoplasia and acromegaly as well as various neuroendocrine tumours, vascular diseases e.g. angiogenesis, connective diseases e.g. scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g. hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic disorder or an opioid overdose. Accordingly, they exhibit activities that include cytostatic, osteopathic, antithyroid, vasotropic, antiangiogenic, ophthalmological, antidiabetic, dermatological, immunosuppressive, antiarthritic, antirheumatic, antiinflammatory, antiulcer, antidiarrhoeic, nephrotropic, hepatotropic, antilipaseic, analgesic, antianginal, anorectic, immunomodulator, cardiant, tranquillizer and antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric analogue of the invention.
 SQ Sequence 11 AA;
 Query Match 76.2%; Score 61; DB 8; Length 11;
 Best Local Similarity 88.9%; Pred. No. 0.48;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
 Db 3 YYCYWKTKCT 11

RESULT 31
 ADU05281
 ID ADU05281 standard; peptide; 11 AA.
 AC ADU05281;
 DT 13-JAN-2005 (first entry)
 DE Cyclic somatostatin-dopamine chimeric peptide analogue #71.
 KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytosatic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antiulcer;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipaseic; analgesic;
 KW antianginal; anorectic; immunomodulator; cardiant; tranquillizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 OS Synthetic.

Key Location/Qualifiers
 Modified-site 1 /note= "An N-terminal dopamine derivative (Dop2) is attached to a Lys(dopamine derivative) modified residue, where this second dopamine derivative must match the type occurring at the N-terminus, i.e. Dop2-Lys (Dop2). Optionally Lys can be a D-form residue."
 Modified-site 2 /label= OTHER
 Misc-difference 3 /note= "OTHER= Aepa, 4-(2-aminoethyl)-1-carboxy methyl-piperazine"

FT Misc-difference 4 /note= "D-form residue"
 FT /note= "D-form residue"
 FT Disulfide-bond 5 .10
 FT /note= This disulphide bond cyclises the peptide
 FT Modified-site 6
 FT /note= "3-iodo tyrosine"
 FT Misc-difference 7
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX WO2004091490-A2.
 XX 28-OCT-2004.
 XX 08-APR-2004; 2004WO-US010891.
 XX 11-APR-2003; 2003US-0462374P.
 XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX Dong ZX, Dewitt Culler M, Shen Y;
 XX WPI; 2004-784484/77.
 XX New chimeric analog comprising at least one moiety which binds to one or
 FT more somatostatin and dopamine receptor(s) useful to treat e.g.
 FT neuroendocrine tumor, vascular diseases, connective tissue disease,
 FT immune disease and cachexia.
 XX Claim 12; Page 116; 138pp; English.
 XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC that comprise at least one moiety that binds to one or more somatostatin
 CC receptors and at least one moiety that binds to one or more dopamine
 CC receptors, or a salt derived thereof. Specifically, it refers to
 CC analogues that may be used in vitro or in vivo for research, diagnostic
 CC and therapeutic agents to enhance the activity of somatostatin and
 CC dopamine i.e. working as receptor agonists. The present invention
 CC describes analogues with specificity for different types of somatostatin
 CC receptor subtypes that are accordingly associated with the treatment of
 CC particular diseases or conditions. As such, these analogues may be used
 CC to treat neoplasia and acromegaly as well as various neuroendocrine
 CC tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
 CC scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
 CC tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
 CC hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
 CC disorder or an opioid overdose. Accordingly, they exhibit activities that
 CC include cytostatic, osteopathic, antidiabetic, antithyroid, vasotropic, antiangiogenic,
 CC ophthalmological, antidiabetic, dermatological, immunosuppressive,
 CC antiarthritic, antirheumatic, antiinflammatory, antitumor,
 CC antidiarrhoeic, nephrotropic, hepatotropic, antilipemic, analgesic,
 CC antianginal, anorectic, immunomodulator, cardiac, tranquilizer and
 CC antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
 CC analogue of the invention.
 XX SQ Sequence 11 AA;
 SQ Query Match 76.2%; Score 61; DB 8; Length 11;
 Best Local Similarity 88.9%; Pred. No. 0.48;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 Y Y C F W K T C T 11
 Db 3 Y Y C F W K T C T 11
 RESULT 32
 ADI14944
 ID ADI14944 standard; peptide; 10 AA.
 XX AC ADI14944;
 22-APR-2004 (first entry)
 Somatostatin-dopamine chimeric analogue-related peptide 55.
 somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 tranquiliser; antilipemic; nephrotropic; antitumor; antiarthritic;
 hypotensive; anorectic; antidiabetic; dopamine receptor agonist;
 somatostatin receptor agonist; lung cancer; glioma; anorexia;
 hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 pancreatic pseudocyst; ascite; VIPoma; neuroblastoma; hyperinsulinism;
 gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 irritable bowel syndrome; pancreatitis; small bowel obstruction;
 gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 gonadotropinoma; hyperparathyroidism; Graves disease;
 diabetic neuropathy; Paget's disease; polycystic ovary disease;
 thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 orthostatic; hypotension; postprandial hypotension; panic attack;
 GH secreting adenoma; acromegaly; TSH secreting adenoma;
 prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 hyperlipidaemia; insulin insensitivity; Syndrome X; angiopathy;
 proliferative retinopathy; dawn phenomenon; nephropathy;
 gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 pancreaticocutaneous fistula; dumping syndrome;
 watery diarrhoea syndrome; pancreatitis;
 gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 allograft rejection; graft vessel bleeding; portal hypertension;
 gastrointestinal bleeding; obesity; opioid overdose.
 OS Synthetic.
 OS Unidentified.
 XX Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "D-form residue. Optionally bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methylsulfanyl-acetic acid. Optionally bound to 3-(1-(7-
 FT allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-
 FT -9-carbonyl)-3-ethylureidopropyl)-Gly-"
 FT Misc-difference 2 .3
 FT /note= "D-form residue"
 FT Modified-site 4
 FT /note= "Residue forms a bond to residue 9 to form a
 FT cyclic peptide"
 FT Misc-difference 6
 FT /note= "D-form residue"
 FT Modified-site 9
 FT /note= "Residue forms a bond to residue 4 to form a
 FT cyclic peptide"
 FT Modified-site 10
 FT /note= "C-terminal amide"
 XX WO2002100888-A1.
 XX 19-DEC-2002.
 XX 07-JUN-2002; 2002WO-US017859.
 XX 08-JUN-2001; 2001US-0297059P.
 XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 XX WPI; 2003-239103/23.
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 FT e.g. lung cancer.
 XX

CC hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 11 AA;

Query Match 73.8%; Score 59; DB 7; Length 11;
 Best Local Similarity 88.9%; Pred. No. 0.85;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTC 11
 |||||
 Db 3 YYCFWKTC 11

RESULT 34
 ADI14945
 ID ADI14945 standard; peptide; 15 AA.

AC ADI14945;

XX 22-APR-2004 (first entry)

XX Somatostatin-dopamine chimeric analogue-related peptide 56.

XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipaeic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antidiabetic; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascites; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.

OS Synthetic.
 OS Unidentified.

XX Key Location/Qualifiers
 FH Modified-site 1

FT /note= ". Optionally bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methylsulfanyl-acetic acid. Optionally bound to 3-(1-(7-
 FT allyl)-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin

FT -9-carbonyl)-3-ethylureidopropyl)-Gly-"
 FT Misc-difference 2. .5
 FT /note= "D-form residue"
 FT Misc-difference 7. .8
 FT /note= "D-form residue"
 FT Modified-site 9
 FT /note= "Residue forms a bond to residue 14 to form a
 FT cyclic peptide"
 FT Misc-difference 11
 FT /note= "D-form residue"
 FT Modified-site 14
 FT /note= "Residue forms a bond to residue 9 to form a
 FT cyclic peptide"
 FT Modified-site 15
 FT /note= "C-terminal amide"

XX WO2002100888-A1.

XX 19-DEC-2002.

XX 07-JUN-2002; 2002WO-US017859.

XX 08-JUN-2001; 2001US-0297059P.

XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.

XX Culler MD, Dong ZX, Kim SH, Moreau J;

XX WPI; 2003-239103/23.

XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 XX e.g. lung cancer.

XX Claim 3; Page 140; 85pp; English.

XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeic,
 CC nephrotropic, antitumor, antiarthritic, hypotensive, anorectic or
 CC antidiabetic activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC pancreatitis, pseudocysts and ascites, VIPoma, nesidioblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.

XX Sequence 15 AA;

Query Match 73.8%; Score 59; DB 7; Length 15;
 Best Local Similarity 88.9%; Pred. No. 1.1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YCFWKTKCT 11
 Db 7 YCFWKVKCT 15
 ||||| ||

RESULT 35
 AAO26828
 ID AAO26828 standard; peptide; 8 AA.
 XX AC AAO26828;
 XX
 DT 27-AUG-2003 (first entry)
 DE Somatostatin agonist compound #11.
 XX
 XX Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipaseic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 PH Modified-site 4
 FT Modified-site 8 /note= "Modified by N-Methyl. D-form residue"
 FT Modified-site 8 /note= "C-terminal amide"
 XX
 XX WO200281499-A2.
 XX
 PD 17-OCT-2002.
 XX
 XX 08-APR-2002; 2002WO-US010882.
 XX
 XX 09-APR-2001; 2001US-0282526P.
 XX
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX
 XX Coy DH, Rajeswaran WG;
 XX WPI; 2003-247842/24.
 XX
 XX Claim 19; Page 31; 43pp; English.
 XX
 XX The invention relates to novel somatostatin agonists, typically
 CC characterised by alkylation of the amide nitrogen, or its
 CC pharmaceutically acceptable salt. The novel somatostatin agonists are
 CC useful for binding one or more of human somatostatin subtype receptors -
 CC 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
 CC administering a somatostatin agonist or a pharmaceutically acceptable
 CC salt of it to a recipient in need of it. The somatostatin agonists are
 CC useful for treating a disease or condition in a human or other animal,
 CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
 CC Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
 CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
 CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
 CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
 CC cancer, peoriasis, hypotension, panic attacks, scleroderma, small bowel
 CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
 CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
 CC pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
 CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 CC inhibiting the accelerated growth of a solid tumour and decreasing body
 CC weight, treating insulin resistance, Syndrome X, prolonging the survival
 CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
 CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide

CC of a somatostatin agonist compound of the invention

XX Sequence 8 AA;
 SQ

Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTKCT 11
 Db 1 YCFWKTKCT 8
 ||||| ||

RESULT 36

AAO26832
 ID AAO26832 standard; peptide; 8 AA.
 XX

XX AAO26832;
 AC

XX 27-AUG-2003 (first entry)
 DT

XX Somatostatin agonist compound #15.
 DE

XX Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipaseic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.
 XX

OS Unidentified.
 XX

XX Key Location/Qualifiers
 PH

FT Misc-difference 4 /note= "D-form residue"
 FT

FT Modified-site 8
 FT

FT Modified-site 8 /note= "Modified by N-Methyl. C-terminal amide"
 XX

XX WO200281499-A2.
 PN

XX 17-OCT-2002.
 PD

XX 08-APR-2002; 2002WO-US010882.
 XX

XX 09-APR-2001; 2001US-0282526P.
 XX

XX (TULA) TULANE EDUCATIONAL FUND.
 PA

XX Coy DH, Rajeswaran WG;
 XX

XX WPI; 2003-247842/24.
 XX

XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
 FT hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
 FT Zollinger-Ellison syndrome, characterized by alkylation of amide
 FT nitrogen.
 XX

XX Claim 23; Page 32; 43pp; English.
 PS

XX The invention relates to novel somatostatin agonists, typically
 CC characterised by alkylation of the amide nitrogen, or its
 CC pharmaceutically acceptable salt. The novel somatostatin agonists are
 CC useful for binding one or more of human somatostatin subtype receptors -
 CC 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
 CC administering a somatostatin agonist or a pharmaceutically acceptable
 CC salt of it to a recipient in need of it. The somatostatin agonists are
 CC useful for treating a disease or condition in a human or other animal,
 CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
 CC Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
 CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
 CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
 CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
 CC cancer, peoriasis, hypotension, panic attacks, scleroderma, small bowel
 CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
 CC disease, polycystic ovary disease, upper gastrointestinal bleeding,

CC pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
 CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 CC inhibiting the accelerated growth of a solid tumour and decreasing body
 CC weight, treating insulin resistance, Syndrome X, prolonging the survival
 CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylianaemia,
 CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
 CC of a somatostatin agonist compound of the invention
 XX
 SQ Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
 |||||
 Db 1 YCFWKTKCT 8

RESULT 37
 AAO26830
 ID AAO26830 standard; peptide; 8 AA.

AC AAO26830;

XX 27-AUG-2003 (first entry)

DT Somatostatin agonist compound #13.

DE Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipaeic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.

XX Unidentified.

PH Key Location/Qualifiers

FT Misc-difference 4 /note= "D-form residue"

FT Modified-site 6 /note= "Modified by N-Methyl"

FT Modified-site 8 /note= "C-terminal amide"

XX WO200281499-A2.

XX 17-OCT-2002.

XX 08-APR-2002; 2002WO-US010882.

XX 09-APR-2001; 2001US-0282526P.

XX (TULA) TULANE EDUCATIONAL FUND.

XX Coy DH, Rajeswaran WG;

XX WPI; 2003-247842/24.

XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
 PT hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
 PT Zollinger-Ellison syndrome, characterized by alkylation of amide
 PT nitrogen.

XX Claim 21; Page 32; 43pp; English.

XX The invention relates to novel somatostatin agonists, typically
 CC characterised by alkylation of the amide nitrogen, or its
 CC pharmaceutically acceptable salt. The novel somatostatin agonists are
 CC useful for binding one or more of human somatostatin subtype receptors -
 CC 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
 CC administering a somatostatin agonist or a pharmaceutically acceptable
 CC salt of it to a recipient in need of it. The somatostatin agonists are
 CC useful for treating a disease or condition in a human or other animal,

CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
 CC Paget's disease, Vipoma, nesidioblastosis, hyperinsulinism, gastrinoma,
 CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
 CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
 CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
 CC cancer, psoriasis, hypotension, panic attacks, scleroderma, small bowel
 CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
 CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
 CC pancreatic pseudocysts, pancreatitis, ascites, leukaemia, meningioma, cancer
 CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 CC inhibiting the accelerated growth of a solid tumour and decreasing body
 CC weight, treating insulin resistance, Syndrome X, prolonging the survival
 CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylianaemia,
 CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
 CC of a somatostatin agonist compound of the invention
 XX
 SQ Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
 |||||
 Db 1 YCFWKTKCT 8

RESULT 38

AAO26825
 ID AAO26825 standard; peptide; 8 AA.

XX AAO26825;

XX 27-AUG-2003 (first entry)

DE Somatostatin agonist compound #8.

XX Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipaeic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Modified by N-Methyl"

FT Misc-difference 4 /note= "D-form residue"

FT Modified-site 8 /note= "C-terminal amide"

XX WO200281499-A2.

XX 17-OCT-2002.

XX 08-APR-2002; 2002WO-US010882.

XX 09-APR-2001; 2001US-0282526P.

XX (TULA) TULANE EDUCATIONAL FUND.

XX Coy DH, Rajeswaran WG;

XX WPI; 2003-247842/24.

XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
 PT hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
 PT Zollinger-Ellison syndrome, characterized by alkylation of amide
 PT nitrogen.

XX Claim 16; Page 31; 43pp; English.

CC The invention relates to novel somatostatin agonists, typically
CC characterised by alkylation of the amide nitrogen, or its
CC pharmaceutically acceptable salt. The novel somatostatin agonists are
CC useful for binding one or more of human somatostatin subtype receptors -
CC 1.-2.-3.-4 and -5, and for eliciting a somatostatin agonist effect, by
CC administering a somatostatin agonist or a pharmaceutically acceptable
CC salt of it to a recipient in need of it. The somatostatin agonists are
CC useful for treating a disease or condition in a human or other animal,
CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
CC Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
CC cancer, peoriasis, hypotension, panic attacks, scleroderma, small bowel
CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
CC pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
CC inhibiting the accelerated growth of a solid tumour and decreasing body
CC weight, treating insulin resistance, Syndrome X, prolonging the survival
CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
CC of a somatostatin agonist compound of the invention
XX
SQ Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 YCFWKTCT 11
DB 1 YCFWKTCT 8

RESULT 39
AAO26827
ID AAO26827 standard; peptide; 8 AA.
XX
AC AAO26827;
XX
DT 27-AUG-2003 (first entry)
DE Somatostatin agonist compound #10.
XX
XX Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
KW antilipaeamic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
KW hyperparathyroidism; cancer.
XX
OS Unidentified.

Key Location/Qualifiers
FH Modified-site 3 /note= "Modified by N-Methyl"
FT Misc-difference 4 /note= "D-form residue"
FT Modified-site 8 /note= "C-terminal amide"
FT
FN WO200281499-A2.
XX
PD 17-OCT-2002.
XX
XX 08-APR-2002; 2002WO-US010882.
XX
PR 09-APR-2001; 2001US-0282526P.
XX
XX (TULA) TULANE EDUCATIONAL FUND.
XX
XX Coy DH, Rajeswaran WG;
XX
XX MPI, 2003-247842/24.

XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
PT hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
PT Zollinger-Ellison syndrome, characterized by alkylation of amide
XX nitrogen.
PS Claim 18; Page 31; 43pp; English.
XX
CC The invention relates to novel somatostatin agonists, typically
CC characterised by alkylation of the amide nitrogen, or its
CC pharmaceutically acceptable salt. The novel somatostatin agonists are
CC useful for binding one or more of human somatostatin subtype receptors -
CC 1.-2.-3.-4 and -5, and for eliciting a somatostatin agonist effect, by
CC administering a somatostatin agonist or a pharmaceutically acceptable
CC salt of it to a recipient in need of it. The somatostatin agonists are
CC useful for treating a disease or condition in a human or other animal,
CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
CC Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
CC cancer, peoriasis, hypotension, panic attacks, scleroderma, small bowel
CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
CC inhibiting the accelerated growth of a solid tumour and decreasing body
CC weight, treating insulin resistance, Syndrome X, prolonging the survival
CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
CC of a somatostatin agonist compound of the invention
XX
SQ Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 YCFWKTCT 11
DB 1 YCFWKTCT 8

RESULT 40
AAO26826
ID AAO26826 standard; peptide; 8 AA.
XX
AC AAO26826;
XX
DT 27-AUG-2003 (first entry)
DE Somatostatin agonist compound #9.
XX
XX Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
KW antilipaeamic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
KW hyperparathyroidism; cancer.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 2 /note= "Modified by N-Methyl"
FT Misc-difference 4 /note= "D-form residue"
FT Modified-site 8 /note= "C-terminal amide"
FT
FN WO200281499-A2.
XX
XX 17-OCT-2002.
XX
XX 08-APR-2002; 2002WO-US010882.

XX 09-APR-2001; 2001US-0282526P.
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX Coy DH, Rajeswaran WG;
 XX WPI; 2003-247842/24.
 XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
 XX hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
 XX Zollinger-Ellison syndrome, characterized by alkylation of amide
 XX nitrogen.
 XX Claim 17; Page 31; 43pp; English.
 XX The invention relates to novel somatostatin agonists, typically
 XX characterised by alkylation of the amide nitrogen, or its
 XX pharmaceutically acceptable salt. The novel somatostatin agonists are
 XX useful for binding one or more of human somatostatin subtype receptors -
 XX 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
 XX administering a somatostatin agonist or a pharmaceutically acceptable
 XX salt of it to a recipient in need of it. The somatostatin agonists are
 XX useful for treating a disease or condition in a human or other animal,
 XX including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
 XX Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
 XX Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
 XX immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
 XX syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
 XX cancer, peptosis, hypotension, panic attacks, scleroderma, small bowel
 XX obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
 XX disease, polycystic ovary disease, upper gastrointestinal bleeding,
 XX pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
 XX cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 XX inhibiting the accelerated growth of a solid tumour and decreasing body
 XX weight, treating insulin resistance, Syndrome X, prolonging the survival
 XX of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylianaemia,
 XX hyperprolactinaemia and prolactinomas. This sequence represents a peptide
 XX of a somatostatin agonist compound of the invention
 XX Sequence 8 AA;
 SQ Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YCFWKTCT 11
 Db 1 YCFWKTCT 8
 RESULT 41
 AAO26829
 ID AAO26829 standard; peptide; 8 AA.
 XX AAO26829;
 AC AAO26829;
 XX 27-AUG-2003 (first entry)
 DT 27-AUG-2003 (first entry)
 DE Somatostatin agonist compound #12.
 XX Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipaeamic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 4
 FT /note= "D-form residue"
 FT Modified-site 5
 FT /note= "Modified by N-Methyl"

FT Modified-site 8 /note= "C-terminal amide"
 XX WO200281499-A2.
 XX 17-OCT-2002.
 PD 08-APR-2002; 2002WO-US010882.
 XX 09-APR-2001; 2001US-0282526P.
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX Coy DH, Rajeswaran WG;
 XX WPI; 2003-247842/24.
 XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
 XX hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
 XX Zollinger-Ellison syndrome, characterized by alkylation of amide
 XX nitrogen.
 XX Claim 20; Page 31; 43pp; English.
 XX The invention relates to novel somatostatin agonists, typically
 XX characterised by alkylation of the amide nitrogen, or its
 XX pharmaceutically acceptable salt. The novel somatostatin agonists are
 XX useful for binding one or more of human somatostatin subtype receptors -
 XX 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
 XX administering a somatostatin agonist or a pharmaceutically acceptable
 XX salt of it to a recipient in need of it. The somatostatin agonists are
 XX useful for treating a disease or condition in a human or other animal,
 XX including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
 XX Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
 XX Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
 XX immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
 XX syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
 XX cancer, peptosis, hypotension, panic attacks, scleroderma, small bowel
 XX obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
 XX disease, polycystic ovary disease, upper gastrointestinal bleeding,
 XX pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
 XX cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 XX inhibiting the accelerated growth of a solid tumour and decreasing body
 XX weight, treating insulin resistance, Syndrome X, prolonging the survival
 XX of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylianaemia,
 XX hyperprolactinaemia and prolactinomas. This sequence represents a peptide
 XX of a somatostatin agonist compound of the invention
 XX Sequence 8 AA;
 SQ Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YCFWKTCT 11
 Db 1 YCFWKTCT 8
 RESULT 42
 AAO26831
 ID AAO26831 standard; peptide; 8 AA.
 XX AAO26831;
 AC AAO26831;
 XX 27-AUG-2003 (first entry)
 DT 27-AUG-2003 (first entry)
 DE Somatostatin agonist compound #14.
 XX Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipaeamic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.

XX OS Unidentified.

XX PH Key Location/Qualifiers

XX FT Misc-difference 4 /note= "D-form residue"

XX FT Modified-site 7 /note= "Modified by N-Methyl"

XX FT Modified-site 8 /note= "C-terminal amide"

XX FT WO200281499-A2.

XX PN 17-OCT-2002.

XX PD 08-APR-2002; 2002WO-US010882.

XX PF 09-APR-2001; 2001US-0282526P.

XX PR (TULA) TULANE EDUCATIONAL FUND.

XX PA Coy DH, Rajeswaran WG;

XX PI WPI; 2003-247842/24.

XX DR Novel somatostatin agonist, useful for treating Cushing's syndrome, hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and Zollinger-Ellison syndrome, characterized by alkylation of amide nitrogen.

XX P8 Claim 22; Page 32; 43pp; English.

XX CC The invention relates to novel somatostatin agonists, typically characterised by alkylation of the amide nitrogen, or its pharmaceutically acceptable salt. The novel somatostatin agonists are useful for binding one or more of human somatostatin subtype receptors - 1-2-3-4 and -5, and for eliciting a somatostatin agonist effect, by administering a somatostatin agonist or a pharmaceutically acceptable salt of it to a recipient in need of it. The somatostatin agonists are useful for treating a disease or condition in a human or other animal, including Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma, Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired immunodeficiency syndrome (AIDS) and other conditions, irritable bowel syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid cancer, psoriasis, hypotension, panic attacks, scleroderma, small bowel obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's disease, polycystic ovary disease, upper gastrointestinal bleeding, pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma, inhibiting the accelerated growth of a solid tumour and decreasing body weight, treating insulin resistance, Syndrome X, prolonging the survival of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia, hyperprolactinaemia and prolactinomas. This sequence represents a peptide of a somatostatin agonist compound of the invention

XX SQ Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
|||||

Db 1 YCFWKTKCT 8

RESULT 43

ADU97615

ID ADU97615 standard; peptide; 14 AA.

XX AC ADU97615;

XX

DT 27-JAN-2005 (first entry)

XX Novel cytotoxic compound-related peptide #2396.

XX KW cytotoxic; cytostatic; antiarteriosclerotic; antiinflammatory; vasotropic; fibrosis; prostate hyperplasia; atherosclerosis; restenosis; cancer.

XX OS Unidentified.

XX OS Synthetic.

XX PH Key Location/Qualifiers

XX FT Modified-site 1. .4 /note= "8-amino-3, 6-dioxo-octanoic acid residues"

XX FT Misc-difference 6. .7 /note= "D-form residues"

XX FT Disulfide-bond 8. .13

XX FT Modified-site 9 /note= "3-iodo tyrosine"

XX FT Misc-difference 10 /note= "D-form residue"

XX FT Modified-site 14 /note= "C-terminal amide"

XX PN WO2004093807-A2.

XX PD 04-NOV-2004.

XX PF 21-APR-2004; 2004WO-US012200.

XX PR 22-APR-2003; 2003US-0464528P.

XX SC (SCRC) SAS SOC CONSEILS RECH & APPL SCI.

XX PH Dong ZX, Shen Y, Comatock JM, Kim SH;

XX WPI; 2004-813763/80.

XX PT New targeted cytotoxic compounds useful for treating e.g. fibrosis, benign prostatic hyperplasia and atherosclerosis, comprises a cytotoxic moiety bound to a targeting moiety.

XX PS Claim 19; Page 324; 327pp; English.

XX CC This invention relates to novel targeted cytotoxic compounds which comprise a cytotoxic moiety bound to a targeting moiety. The invention may be useful for the production of compounds with a cytostatic, antiarteriosclerotic, antiinflammatory or vasotropic activity acting as somatostatin receptor radioligand binders. The invention may be useful for the treatment of disease, for example fibrosis, benign prostatic hyperplasia, atherosclerosis, restenosis, cancer (such as breast, colon, pancreas, prostate, lung, small cell lung, ovarian, hematopoietic and epidermal cancer) and disease associated with undesired proliferation of cells that express at least one somatostatin-type, bombesin-type and LHRH -type receptors. The compounds have improved properties such as targeting specificity, systemic toxicity and pharmacokinetics. The present sequence is that of a peptide which may be used during the production of a compound of the invention.

XX SQ Sequence 14 AA;

Query Match 71.2%; Score 57; DB 8; Length 14;

Best Local Similarity 88.9%; Pred. No. 1.8;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
|||||

Db 6 YYCFWKTKCT 14

RESULT 44

ADU97600

ID ADU97600 standard; peptide; 14 AA.

XX AC ADU97600;
XX ADU97630
XX DT 27-JAN-2005 (first entry)
XX DE Novel cytotoxic compound-related peptide #2381.
XX KW cytotoxic; cytostatic; antiarteriosclerotic; antiinflammatory;
XX KW vasotrophic; fibrosis; prostate hyperplasia; atherosclerosis; restenosis;
XX KW cancer.
XX OS Unidentified.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Modified-site 1. .4
XX FT /note= "8-amino-3, 6-dioxaoctanoic acid residues"
XX FT Misc-difference 6. .7
XX FT /note= "D-form residues"
XX FT Disulfide-bond 8. .13
XX FT Modified-site 9
XX FT /note= "3-iodo tyrosine"
XX FT Misc-difference 10
XX FT /note= "D-form residue"
XX FT Modified-site 14
XX FT /note= "C-terminal amide"
XX FT WO2004093807-A2.
XX PN 04-NOV-2004.
XX PD
XX PF 21-APR-2004; 2004WO-US012200.
XX PR 22-APR-2003; 2003US-0464528P.
XX PA (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
XX PI Dong ZX, Shen Y, Comstock JM, Kim SH;
XX DR WPI; 2004-813763/80.
XX DR
XX PT New targeted cytotoxic compounds useful for treating e.g. fibrosis,
XX PT benign prostatic hyperplasia and atherosclerosis, comprises a cytotoxic
XX PT moiety bound to a targeting moiety.
XX PS Claim 19; Page 323; 327pp; English.
XX CC This invention relates to novel targeted cytotoxic compounds which
XX CC comprise a cytotoxic moiety bound to a targeting moiety. The invention
XX CC may be useful for the production of compounds with a cytostatic,
XX CC antiarteriosclerotic, antiinflammatory or vasotropic activity acting as
XX CC somatostatin receptor radioligand binders. The invention may be useful
XX CC for the treatment of disease, for example fibrosis, benign prostatic
XX CC hyperplasia, atherosclerosis, restenosis, cancer (such as breast, colon,
XX CC pancreas, prostate, lung, small cell lung, ovarian, hematopoietic and
XX CC epidermal cancer) and disease associated with undesired proliferation of
XX CC cells that express at least one somatostatin-type, bombesin-type and LHRH
XX CC -type receptors. The compounds have improved properties such as targeting
XX CC specificity, systemic toxicity and pharmacokinetics. The present sequence
XX CC is that of a peptide which may be used during the production of a
XX CC compound of the invention.
XX SQ Sequence 14 AA;

Query Match 71.2%; Score 57; DB 8; Length 14;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 YYCFWKTKCT 11
Db 6 YYCXWKTKCT 14

RESULT 45
ADU97630
ID ADU97630 standard; peptide; 14 AA.
XX AC ADU97630;
XX DT 27-JAN-2005 (first entry)
XX DE Novel cytotoxic compound-related peptide #2411.
XX KW cytotoxic; cytostatic; antiarteriosclerotic; antiinflammatory;
XX KW vasotrophic; fibrosis; prostate hyperplasia; atherosclerosis; restenosis;
XX KW cancer.
XX OS Unidentified.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "Succinyl residue"
XX FT Modified-site 2. .4
XX FT /note= "8-amino-3, 6-dioxaoctanoic acid residues"
XX FT Misc-difference 6. .7
XX FT /note= "D-form residues"
XX FT Disulfide-bond 8. .13
XX FT Modified-site 9
XX FT /note= "3-iodo tyrosine"
XX FT Misc-difference 10
XX FT /note= "D-form residue"
XX FT Modified-site 14
XX FT /note= "C-terminal amide"
XX FT WO2004093807-A2.
XX PN 04-NOV-2004.
XX PD
XX PF 21-APR-2004; 2004WO-US012200.
XX PR 22-APR-2003; 2003US-0464528P.
XX PA (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
XX PI Dong ZX, Shen Y, Comstock JM, Kim SH;
XX DR WPI; 2004-813763/80.
XX DR
XX PT New targeted cytotoxic compounds useful for treating e.g. fibrosis,
XX PT benign prostatic hyperplasia and atherosclerosis, comprises a cytotoxic
XX PT moiety bound to a targeting moiety.
XX PS Claim 19; Page 325; 327pp; English.
XX CC This invention relates to novel targeted cytotoxic compounds which
XX CC comprise a cytotoxic moiety bound to a targeting moiety. The invention
XX CC may be useful for the production of compounds with a cytostatic,
XX CC antiarteriosclerotic, antiinflammatory or vasotropic activity acting as
XX CC somatostatin receptor radioligand binders. The invention may be useful
XX CC for the treatment of disease, for example fibrosis, benign prostatic
XX CC hyperplasia, atherosclerosis, restenosis, cancer (such as breast, colon,
XX CC pancreas, prostate, lung, small cell lung, ovarian, hematopoietic and
XX CC epidermal cancer) and disease associated with undesired proliferation of
XX CC cells that express at least one somatostatin-type, bombesin-type and LHRH
XX CC -type receptors. The compounds have improved properties such as targeting
XX CC specificity, systemic toxicity and pharmacokinetics. The present sequence
XX CC is that of a peptide which may be used during the production of a
XX CC compound of the invention.
XX SQ Sequence 14 AA;

Query Match 71.2%; Score 57; DB 8; Length 14;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      3 YYCFWKTKT 11
      ||| |||||
Db      6 YYCXWKTKT 14

RESULT 46
ID      ADU97599
XX      ADU97599 standard; peptide; 15 AA.
AC      ADU97599;
XX
DT      27-JAN-2005 (first entry)
XX
DE      Novel cytotoxic compound-related peptide #2380.
XX
KW      cytotoxic; cytostatic; antiarteriosclerotic; antiinflammatory;
KW      vasotrophic; fibrosis; prostate hyperplasia; atherosclerosis; restenosis;
KW      cancer.
XX
OS      Unidentified.
OS      Synthetic.
FH      Key      Location/Qualifiers
FT      Modified-site 1. .4
FT      /note= "8-amino-3, 6-dioxaoctanoic acid residues"
FT      Modified-site 5
FT      /note= "Aepa"
FT      Misc-difference 7. .8
FT      /note= "D-form residues"
FT      Disulfide-bond 9. .14
FT      Modified-site 10
FT      /note= "3-iodo tyrosine"
FT      Misc-difference 11
FT      /note= "D-form residue"
FT      Modified-site 15
FT      /note= "C-terminal amide"
XX      WO2004093807-A2.
XX
PD      04-NOV-2004.
XX
PF      21-APR-2004; 2004WO-US012200.
XX
PR      22-APR-2003; 2003US-0464528P.
XX      (SCRC ) SAS SOC CONSEILS RECH & APPL SCI.
XX
PI      Dong ZX, Shen Y, Comstock JM, Kim SH;
XX      WPI; 2004-813763/80.
XX
PS      Claim 19; Page 323; 327pp; English.
XX
CC      This invention relates to novel targeted cytotoxic compounds which
CC      comprise a cytotoxic moiety bound to a targeting moiety. The invention
CC      may be useful for the production of compounds with a cytostatic,
CC      antiarteriosclerotic, antiinflammatory or vasotropic activity acting as
CC      somatostatin receptor radioligand binders. The invention may be useful
CC      for the treatment of disease, for example fibrosis, benign prostatic
CC      hyperplasia, atherosclerosis, restenosis, cancer (such as breast, colon,
CC      pancreas, prostate, lung, small cell lung, ovarian, hematopoietic and
CC      epidermal cancer) and disease associated with undesired proliferation of
CC      cells that express at least one somatostatin-type, bombesin-type and LHRH
CC      -type receptors. The compounds have improved properties such as targeting
CC      specificity, systemic toxicity and pharmacokinetics. The present sequence
CC      is that of a peptide which may be used during the production of a
CC      compound of the invention.
XX      Sequence 15 AA;

Query Match      71.2%; Score 57; DB 8; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 YYCFWKTKT 11
      ||| |||||
Db      7 YYCXWKTKT 15

RESULT 47
ID      ADU97629 standard; peptide; 15 AA.
XX
AC      ADU97629;
XX
DT      27-JAN-2005 (first entry)
XX
DE      Novel cytotoxic compound-related peptide #2410.
XX
KW      cytotoxic; cytostatic; antiarteriosclerotic; antiinflammatory;
KW      vasotrophic; fibrosis; prostate hyperplasia; atherosclerosis; restenosis;
KW      cancer.
XX
OS      Unidentified.
OS      Synthetic.
FH      Key      Location/Qualifiers
FT      Modified-site 1
FT      /note= "Succinyl residue"
FT      Modified-site 2. .4
FT      /note= "8-amino-3, 6-dioxaoctanoic acid residues"
FT      Modified-site 5
FT      /note= "Aepa"
FT      Misc-difference 7. .8
FT      /note= "D-form residues"
FT      Disulfide-bond 9. .14
FT      Modified-site 10
FT      /note= "3-iodo tyrosine"
FT      Misc-difference 11
FT      /note= "D-form residue"
FT      Modified-site 15
FT      /note= "C-terminal amide"
XX      WO2004093807-A2.
XX
PD      04-NOV-2004.
XX
PF      21-APR-2004; 2004WO-US012200.
XX
PR      22-APR-2003; 2003US-0464528P.
XX      (SCRC ) SAS SOC CONSEILS RECH & APPL SCI.
XX
PI      Dong ZX, Shen Y, Comstock JM, Kim SH;
XX      WPI; 2004-813763/80.
XX
PS      Claim 19; Page 325; 327pp; English.
XX
CC      This invention relates to novel targeted cytotoxic compounds which
CC      comprise a cytotoxic moiety bound to a targeting moiety. The invention
CC      may be useful for the production of compounds with a cytostatic,
CC      antiarteriosclerotic, antiinflammatory or vasotropic activity acting as
CC      somatostatin receptor radioligand binders. The invention may be useful
CC      for the treatment of disease, for example fibrosis, benign prostatic
CC      hyperplasia, atherosclerosis, restenosis, cancer (such as breast, colon,
CC      pancreas, prostate, lung, small cell lung, ovarian, hematopoietic and
CC      epidermal cancer) and disease associated with undesired proliferation of
CC      cells that express at least one somatostatin-type, bombesin-type and LHRH
CC      -type receptors. The compounds have improved properties such as targeting
CC      specificity, systemic toxicity and pharmacokinetics. The present sequence
CC      is that of a peptide which may be used during the production of a
CC      compound of the invention.
XX      Sequence 15 AA;

```

CC cells that express at least one somatostatin-type, bombesin-type and LHRH
 CC -type receptors. The compounds have improved properties such as targeting
 CC specificity, systemic toxicity and pharmacokinetics. The present sequence
 CC is that of a peptide which may be used during the production of a
 CC compound of the invention.

XX Sequence 15 AA;

Query Match 71.2%; Score 57; DB 8; Length 15;
 Best Local Similarity 88.9%; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
 ||| |||||
 Db 7 YYCXWKTKCT 15

RESULT 48
 ADU97614
 ID ADU97614 standard; peptide; 15 AA.

XX AC ADU97614;

XX DT 27-JAN-2005 (first entry)

XX Novel cytotoxic compound-related peptide #2395.

DE cytostatic; antiarteriosclerotic; antiinflammatory;
 KW vasotropic; fibrosis; prostate hyperplasia; atherosclerosis; restenosis;
 KW cancer.

XX Unidentified.
 OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1. .4 /note= "8-amino-3, 6-dioxaoctanoic acid residues"

FT Modified-site 5 /note= "Aapa"

FT Misc-difference 7. .8 /note= "D-form residues"

FT Disulfide-bond 9. .14

FT Modified-site 10

FT Misc-difference 11 /note= "3-iodo tyrosine"

FT Misc-difference 15 /note= "D-form residue"

FT Modified-site 15 /note= "C-terminal amide"

XX WO2004093807-A2.

XX 04-NOV-2004.

XX 21-APR-2004; 2004WO-US012200.

XX 22-APR-2003; 2003US-0464528P.

XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.

XX Dong ZX, Shen Y, Comstock JM, Kim SH;

XX WPI; 2004-813763/80.

XX New targeted cytotoxic compounds useful for treating e.g. fibrosis,
 PT benign prostatic hyperplasia and atherosclerosis, comprises a cytotoxic
 FT moiety bound to a targeting moiety.
 XX Claim 19; Page 324; 327pp; English.

XX This invention relates to novel targeted cytotoxic compounds which
 CC comprise a cytotoxic moiety bound to a targeting moiety. The invention
 CC may be useful for the production of compounds with a cytostatic,
 CC antiarteriosclerotic, antiinflammatory or vasotropic activity acting as

CC somatostatin receptor radioligand binders. The invention may be useful
 CC for the treatment of disease, for example fibrosis, benign prostatic
 CC hyperplasia, atherosclerosis, restenosis, cancer (such as breast, colon,
 CC pancreas, prostate, lung, small cell lung, ovarian, hematopoietic and
 CC epidermal cancer) and disease associated with undesired proliferation of
 CC cells that express at least one somatostatin-type, bombesin-type and LHRH
 CC -type receptors. The compounds have improved properties such as targeting
 CC specificity, systemic toxicity and pharmacokinetics. The present sequence
 CC is that of a peptide which may be used during the production of a
 CC compound of the invention.

XX Sequence 15 AA;

Query Match 71.2%; Score 57; DB 8; Length 15;
 Best Local Similarity 88.9%; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
 ||| |||||
 Db 7 YYCXWKTKCT 15

RESULT 49
 ADU97616
 ID ADU97616 standard; peptide; 16 AA.

XX AC ADU97616;

XX DT 27-JAN-2005 (first entry)

XX Novel cytotoxic compound-related peptide #2397.

DE cytostatic; antiarteriosclerotic; antiinflammatory;
 KW vasotropic; fibrosis; prostate hyperplasia; atherosclerosis; restenosis;
 KW cancer.

XX Unidentified.
 OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1. .6 /note= "8-amino-3, 6-dioxaoctanoic acid residues"

FT Misc-difference 8. .9 /note= "D-form residues"

FT Disulfide-bond 10. .15

FT Modified-site 11 /note= "3-iodo tyrosine"

FT Misc-difference 12 /note= "D-form residue"

FT Modified-site 16 /note= "C-terminal amide"

XX WO2004093807-A2.

XX 04-NOV-2004.

XX 21-APR-2004; 2004WO-US012200.

XX 22-APR-2003; 2003US-0464528P.

XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.

XX Dong ZX, Shen Y, Comstock JM, Kim SH;

XX WPI; 2004-813763/80.

XX New targeted cytotoxic compounds useful for treating e.g. fibrosis,
 PT benign prostatic hyperplasia and atherosclerosis, comprises a cytotoxic
 FT moiety bound to a targeting moiety.
 XX Claim 19; Page 324; 327pp; English.

XX This invention relates to novel targeted cytotoxic compounds which

CC comprise a cytotoxic moiety bound to a targeting moiety. The invention
 CC may be useful for the production of compounds with a cytostatic,
 CC antiarteriosclerotic, antiinflammatory or vasotropic activity acting as
 CC somatostatin receptor radioligand binders. The invention may be useful
 CC for the treatment of disease, for example fibrosis, benign prostatic
 CC hyperplasia, atherosclerosis, restenosis, cancer (such as breast, colon,
 CC pancreas, prostate, lung, small cell lung, ovarian, hematopoietic and
 CC epidermal cancer) and disease associated with undesired proliferation of
 CC cells that express at least one somatostatin-type, bombesin-type and LHRH
 CC -type receptors. The compounds have improved properties such as targeting
 CC specificity, systemic toxicity and pharmacokinetics. The present sequence
 CC is that of a peptide which may be used during the production of a
 CC compound of the invention.

XX Sequence 16 AA;

Query Match 71.2%; Score 57; DB 8; Length 16;
 Best Local Similarity 88.9%; Pred. No. 2;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
 ||| |||||
 Db 8 YYCAWKTKCT 16

RESULT 50

ADU97631
 ID ADU97631 standard; peptide; 16 AA.

XX AC

XX ADU97631;

XX 27-JAN-2005 (first entry)

DE Novel cytotoxic compound-related peptide #2412.

XX cytotoxic; cytostatic; antiarteriosclerotic; antiinflammatory;
 KW vasotropic; fibrosis; prostate hyperplasia; atherosclerosis; restenosis;
 KW cancer.

OS Unidentified.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 1

FT /note= "Succinyl residue"

FT Modified-site 2..6

FT /note= "8-amino-3, 6-dioxaoctanoic acid residues"

FT Misc-difference 8..9

FT /note= "D-form residues"

FT Disulfide-bond 10..15

FT Modified-site 11

FT /note= "3-iodo tyrosine"

FT Misc-difference 12

FT /note= "D-form residue"

FT Modified-site 16

FT /note= "C-terminal amide"

XX WO2004093807-A2.

XX 04-NOV-2004.

XX 21-APR-2004; 2004WO-US012200.

XX 22-APR-2003; 2003US-0464528P.

XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.

XX Dong ZX, Shen Y, Comstock JM, Kim SH;

XX WPI; 2004-813763/80.

XX New targeted cytotoxic compounds useful for treating e.g. fibrosis,

XX benign prostatic hyperplasia and atherosclerosis, comprises a cytotoxic

PT moiety bound to a targeting moiety.

XX Claim 19; Page 325; 327pp; English.

XX This invention relates to novel targeted cytotoxic compounds which

CC comprise a cytotoxic moiety bound to a targeting moiety. The invention

CC may be useful for the production of compounds with a cytostatic,
 CC antiarteriosclerotic, antiinflammatory or vasotropic activity acting as

CC somatostatin receptor radioligand binders. The invention may be useful
 CC for the treatment of disease, for example fibrosis, benign prostatic

CC hyperplasia, atherosclerosis, restenosis, cancer (such as breast, colon,
 CC pancreas, prostate, lung, small cell lung, ovarian, hematopoietic and

CC epidermal cancer) and disease associated with undesired proliferation of
 CC cells that express at least one somatostatin-type, bombesin-type and LHRH

CC -type receptors. The compounds have improved properties such as targeting
 CC specificity, systemic toxicity and pharmacokinetics. The present sequence
 CC is that of a peptide which may be used during the production of a
 CC compound of the invention.

XX Sequence 16 AA;

Query Match 71.2%; Score 57; DB 8; Length 16;
 Best Local Similarity 88.9%; Pred. No. 2;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11

Db 8 YYCAWKTKCT 16

Search completed: May 9, 2006, 12:08:20

Job time : 50.6667 secs

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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:05:35 ; Search time 19.3333 Seconds
(without alignments)
54.744 Million cell updates/sec

Title: US-10-796-158-6
Perfect score: 80
Sequence: 1 CYYCFWKTCT 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	62.5	1910	2 H88124	protein T12C9.3 [i
2	46.5	58.1	682	1 JH0550	cyclic nucleotide-
3	44	55.0	245	2 T28166	hypothetical prote
4	43	53.8	237	2 JN0302	hypothetical 237 p
5	42	52.5	144	2 S35716	glycine-rich prote
6	42	52.5	144	2 S04069	glycine-rich prote
7	42	52.5	670	2 H96707	probable receptor
8	42	52.5	998	2 A36368	transcription fact
9	41	51.2	214	2 A35349	H ₂ -transporting At
10	41	51.2	215	2 A49677	endoplasmic reticu
11	41	51.2	399	2 T21586	hypothetical prote
12	41	51.2	521	2 G96816	hypothetical prote
13	41	51.2	635	2 T00602	hypothetical prote
14	41	51.2	1513	2 A54895	mucin 2, intestina
15	40	50.0	157	2 S58014	probable olfactory
16	40	50.0	478	2 JQ1301	hemorrhagic protei
17	40	50.0	495	1 Q1AD52	early E1B 55K prot
18	40	50.0	496	1 Q1AD55	early E1B 55K prot
19	40	50.0	512	2 T30924	hypothetical prote
20	40	50.0	528	2 JN0620	UNP-glucuronosyltr
21	40	50.0	529	2 A35366	glucuronosyltransf
22	39	48.8	104	2 S19430	probable membrane
23	39	48.8	123	2 S70222	hypothetical prote
24	39	48.8	212	2 C87595	hypothetical prote
25	39	48.8	285	2 AG1214	methylases homolog
26	39	48.8	367	1 A46355	site-specific DNA-
27	39	48.8	367	2 T18185	probable site-spec
28	39	48.8	390	2 T38012	longevity-assuranc
29	39	48.8	407	2 T37888	hypothetical prote

30	39	48.8	698	2 T10541	cyclic nucleotide
31	39	48.8	706	2 F86143	hypothetical prote
32	39	48.8	716	2 T51354	cyclic nucleotide-
33	39	48.8	718	2 G84902	hypothetical prote
34	39	48.8	859	1 S65938	nitrate reductase
35	39	48.8	894	2 S52857	nitrate reductase
36	39	48.8	1291	2 T21267	hypothetical prote
37	38.5	48.1	810	2 T00368	hypothetical prote
38	38	47.5	12	1 UOGM2	urotensin II - lon
39	38	47.5	12	2 JS0423	urotensin II-A pep
40	38	47.5	12	2 S42765	urotensin II - tel
41	38	47.5	12	2 JS0424	urotensin II-B pep
42	38	47.5	13	2 PQ0445	urotensin II - lau
43	38	47.5	65	1 NTSR1C	urotensin II - bar
44	38	47.5	83	2 SI0706	neurotoxin 1 - bar
45	38	47.5	125	2 I50499	urotensin II-gamma
46	38	47.5	125	2 I50498	urotensin II-alpha
47	38	47.5	210	2 T16744	hypothetical protei
48	38	47.5	245	2 I51323	proteolipid protei
49	38	47.5	285	2 S76841	hypothetical prote
50	38	47.5	295	2 T00399	probable AP2 domai
51	38	47.5	325	2 T10669	hypothetical prote
52	38	47.5	368	2 T15096	hypothetical prote
53	38	47.5	387	2 D84424	hypothetical prote
54	38	47.5	461	2 D95083	ABC transporter, A
55	38	47.5	461	2 H97950	hypothetical prote
56	38	47.5	493	2 JC5486	membrane glycoprot
57	38	47.5	511	2 S58399	cellulagin I svtV
58	38	47.5	656	1 S59631	endo-1,4-beta-xyla
59	38	47.5	661	1 S59633	endo-1,4-beta-xyla
60	38	47.5	809	2 T32945	hypothetical prote
61	38	47.5	839	1 GNNYS2	genome polyprotein
62	38	47.5	844	1 T05179	S-receptor kinase
63	38	47.5	852	1 GNNYHA	genome polyprotein
64	38	47.5	859	2 S70584	nitrate reductase
65	38	47.5	867	1 JQ1525	nitrate reductase
66	38	47.5	868	1 JC4283	nitrate reductase
67	38	47.5	982	1 S16292	nitrate reductase
68	38	47.5	997	2 JC6067	CCNAAT-binding fac
69	38	47.5	998	2 S31735	NAD ADP-ribosyltra
70	38	47.5	1011	1 JH0581	NAD ADP-ribosyltra
71	38	47.5	1358	2 A03905	genome polyprotein
72	38	47.5	1381	1 Q0B545	major capsid prote
73	38	47.5	2105	1 A44059	genome polyprotein
74	38	47.5	2227	1 GNNYHB	genome polyprotein
75	38	47.5	2227	1 GNNYHM	genome polyprotein
76	38	47.5	2227	1 GNNYHR	genome polyprotein
77	38	47.5	2227	1 GNNYMK	genome polyprotein
78	38	47.5	2230	1 GNNYSA	genome polyprotein
79	37.5	46.9	1134	2 D65032	hypothetical prote
80	37.5	46.9	1551	1 A43364	M polyprotein prec
81	37	46.2	27	2 S64717	formin binding pro
82	37	46.2	60	1 H3NU3B	cytotoxin 3 - coBr
83	37	46.2	66	2 A55869	crustacean-specifi
84	37	46.2	87	2 JN0670	Na+-channel-blocki
85	37	46.2	100	2 A12472	hypothetical prote
86	37	46.2	105	2 B30010	hypothetical ORF-5
87	37	46.2	120	2 S36306	T-cell receptor de
88	37	46.2	129	1 FTRGB	follicotropin beta c
89	37	46.2	130	2 G71042	hypothetical prote
90	37	46.2	137	2 H71163	hypothetical prote
91	37	46.2	142	2 S36310	T-cell receptor de
92	37	46.2	142	2 S36316	T-cell receptor de
93	37	46.2	149	2 T11066	NADH2 dehydrogenas
94	37	46.2	216	2 E84450	hypothetical prote
95	37	46.2	221	1 S57469	endo-1,4-beta-xyla
96	37	46.2	221	2 JC7307	endo-1,4-beta-xyla
97	37	46.2	225	1 S57477	endo-1,4-beta-xyla
98	37	46.2	232	2 JC7577	endo-1,4-beta-xyla
99	37	46.2	241	2 S71473	endo-1,4-beta-xyla
100	37	46.2	277	2 T16020	hypothetical prote
101	37	46.2	332	2 T26308	hypothetical prote
102	37	46.2	332	2 E71916	probable lipopolys

103	37	46.2	333	1	J80590	endo-1,4-beta-xyla	176	36	45.0	659	2	D84633	probable multispan
104	37	46.2	335	2	T50601	endo-1,4-beta-xyla	177	36	45.0	729	2	T46328	probable adenosine
105	37	46.2	335	2	T50601	hypothetical prote	178	36	45.0	845	1	B71255	ribonucleoside-dip
106	37	46.2	336	2	T01306	hypothetical prote	179	36	45.0	859	2	S62441	chitin synthase (E
107	37	46.2	337	2	E96543	probable RAV-like	180	36	45.0	1007	2	T13693	hypothetical prote
108	37	46.2	340	2	H82942	ferrichrome ABC tr	181	36	45.0	1149	2	T18515	adenosinetriphosph
109	37	46.2	352	1	S27357	complement C5a ana	182	36	45.0	1149	2	T30869	probable adenosine
110	37	46.2	397	2	G84461	hypothetical prote	183	36	45.0	1227	2	AG2504	hypothetical prote
111	37	46.2	397	2	T46710	multidrug resistan	184	36	45.0	1323	2	A24534	regulatory protein
112	37	46.2	397	2	A81613	multidrug-efflux t	185	36	45.0	1484	2	T29275	hypothetical prote
113	37	46.2	397	2	A11250	multidrug-efflux t	186	36	45.0	1499	2	AC2555	hypothetical prote
114	37	46.2	461	1	S18994	protein C (activat	187	36	45.0	1888	2	T14273	zinc finger protei
115	37	46.2	617	2	T23092	hypothetical prote	188	35.5	44.4	245	2	T30127	hypothetical prote
116	37	46.2	654	2	AH2445	hypothetical prote	189	35	43.8	45	2	S33414	NUMA protein - hum
117	37	46.2	678	2	G84682	hypothetical prote	190	35	43.8	54	2	E64007	hypothetical prote
118	37	46.2	700	2	T05841	spliceosome-associ	191	35	43.8	54	2	D97847	hypothetical prote
119	37	46.2	705	2	T06682	hypothetical prote	192	35	43.8	82	2	B69506	probable 2-oxoisov
120	37	46.2	726	2	A85355	hypothetical prote	193	35	43.8	96	2	S35715	glycine-rich prote
121	37	46.2	756	2	G86308	Similar to disease	194	35	43.8	99	2	B25439	Beejin protein - s
122	37	46.2	873	1	S53828	cytochrome-c oxida	195	35	43.8	106	1	TNLJ52	trans-activating t
123	37	46.2	896	2	C85438	hypothetical prote	196	35	43.8	121	2	T04536	hypothetical prote
124	37	46.2	940	2	T01834	hypothetical prote	197	35	43.8	124	1	QQVZEL	Fli protein - vacc
125	37	46.2	1013	2	T46422	hypothetical prote	198	35	43.8	129	1	TNLJG3	trans-activating t
126	37	46.2	1680	2	A43434	furin (EC 3.4.21.7	199	35	43.8	131	2	T11557	tat protein - simi
127	37	46.2	1748	1	J01555	genome polypotein	200	35	43.8	132	2	T11564	tat protein - simi
128	37	46.2	2155	2	T30197	alpha tectorin - m	201	35	43.8	133	2	H42513	J5L 15.2K protein
129	36.5	45.6	81	2	S43288	MURF4 protein - He	202	35	43.8	133	2	T28520	hypothetical prote
130	36.5	45.6	279	2	C48826	high choriolytic h	203	35	43.8	133	2	H72160	MSL protein - vari
131	36.5	45.6	300	2	T24547	hypothetical prote	204	35	43.8	133	2	S33096	J5L protein - vari
132	36.5	45.6	581	2	B90539	hypothetical prote	205	35	43.8	134	2	T30680	hypothetical prote
133	36.5	45.6	2049	2	T43161	sodium channel pro	206	35	43.8	138	2	T18816	hypothetical prote
134	36	45.0	60	1	H3NJ7B	cytotoxin 1 - cobr	207	35	43.8	139	2	E72856	AcOrf-53 protein -
135	36	45.0	60	1	H3NJ1M	cytotoxin 1 - Moza	208	35	43.8	139	2	T41797	ACMPV orf53 - Bom
136	36	45.0	60	1	H3NJ2C	cytotoxin 2 - Cape	209	35	43.8	150	2	S43955	probable NADH2 deh
137	36	45.0	60	1	H3NJ2C	cytotoxin 2 - cobr	210	35	43.8	169	2	S51910	cryptogene protein
138	36	45.0	60	1	H3NJ2M	cytotoxin 2 - Moza	211	35	43.8	183	2	A84728	probable alanine a
139	36	45.0	60	1	H3NJ3C	cytotoxin 3 - Cape	212	35	43.8	201	2	S37847	hypothetical prote
140	36	45.0	60	1	H3NJ3M	cytotoxin 3 - Moza	213	35	43.8	211	2	C81001	probable pyrazinam
141	36	45.0	60	1	H3NJ3E	cytotoxin 4 - cobr	214	35	43.8	211	2	H82018	probable nicotinam
142	36	45.0	60	1	H3NJ5E	cytotoxin 5 - cobr	215	35	43.8	247	2	T27205	hypothetical prote
143	36	45.0	60	1	H3NJ5Y	cytotoxin 5 - Egyp	216	35	43.8	258	1	C69175	heat shock protein
144	36	45.0	60	1	H3NJ6E	cytotoxin 6 - cobr	217	35	43.8	258	2	S33535	myosin heavy chain
145	36	45.0	60	1	H3NJ6M	cytotoxin 6, minor	218	35	43.8	293	2	T47708	hypothetical prote
146	36	45.0	60	1	H3NJ7E	cytotoxin 7 - cobr	219	35	43.8	300	2	T27158	hypothetical prote
147	36	45.0	60	1	H3NJ7M	cytotoxin 7, minor	220	35	43.8	300	2	G87959	protein Y5485A.1 l
148	36	45.0	60	1	H3NJ8E	cytotoxin 8 - cobr	221	35	43.8	309	2	B87457	hypothetical prote
149	36	45.0	60	1	H3NJ8E	cytotoxin 8 - cobr	222	35	43.8	311	2	T27203	hypothetical prote
150	36	45.0	85	2	S51156	MHC class II beta	223	35	43.8	320	2	T33303	hypothetical prote
151	36	45.0	138	2	T34049	hypothetical prote	224	35	43.8	325	2	T14227	NADH2 dehydrogenas
152	36	45.0	144	2	B84450	hypothetical prote	225	35	43.8	329	2	T47795	hypothetical prote
153	36	45.0	163	2	S48050	cholecystokinin B	226	35	43.8	346	2	T26097	hypothetical prote
154	36	45.0	175	2	T17890	hypothetical prote	227	35	43.8	360	2	G84060	hypothetical prote
155	36	45.0	218	2	T03383	zinc-induced prote	228	35	43.8	369	2	T24022	hypothetical prote
156	36	45.0	221	2	T27271	hypothetical prote	229	35	43.8	386	2	A35693	NADH2 dehydrogenas
157	36	45.0	246	2	T51418	hypothetical prote	230	35	43.8	398	2	C71682	ubiquinol-cytochro
158	36	45.0	281	2	C82547	hypothetical prote	231	35	43.8	419	2	T25565	hypothetical prote
159	36	45.0	300	2	A09556	dynein beta heavy	232	35	43.8	428	2	T46046	hypothetical prote
160	36	45.0	306	2	T45899	hypothetical prote	233	35	43.8	430	2	T16715	hypothetical prote
161	36	45.0	330	2	JC7703	TASK-5 protein - h	234	35	43.8	431	2	A64658	LPS biosynthesis p
162	36	45.0	335	2	A13453	transcription regu	235	35	43.8	456	2	F84472	probable replicati
163	36	45.0	344	2	JC6100	CACCC-box binding	236	35	43.8	461	1	KXHU	protein C (activat
164	36	45.0	353	2	JC4875	zinc-finger protei	237	35	43.8	512	2	JC4164	catalase (EC 1.11.
165	36	45.0	400	2	C70082	multidrug-efflux t	238	35	43.8	517	2	T22707	hypothetical prote
166	36	45.0	404	2	C84597	lipopolyaccharide	239	35	43.8	531	2	T40575	major facilitator
167	36	45.0	411	2	G97802	tyrosine-tRNA liga	240	35	43.8	531	2	T11596	hypothetical prote
168	36	45.0	411	2	C71660	tyrosine-tRNA liga	241	35	43.8	532	2	T42369	catalase (EC 1.11.
169	36	45.0	444	2	F71916	probable lipopolys	242	35	43.8	537	2	B33485	spore coat protein
170	36	45.0	447	2	I56511	Zic protein - mous	243	35	43.8	549	2	T49298	hypothetical prote
171	36	45.0	497	2	T27169	hypothetical prote	244	35	43.8	566	2	A81682	conserved hypother
172	36	45.0	499	2	T00858	hypothetical prote	245	35	43.8	566	2	G71525	probable outer mem
173	36	45.0	530	2	G02091	pancreatic zymogen	246	35	43.8	577	2	T43207	nuclear fusion pro
174	36	45.0	552	2	T23755	hypothetical prote	247	35	43.8	588	2	H84902	hypothetical prote
175	36	45.0	571	2	T29751	hypothetical prote	248	35	43.8	590	2	T156526	interleukin 1 rece

249	35	43.8	592	2	F71423	hypotheical prote	322	34	42.5	252	2	I50126	MHC class II hista
250	35	43.8	597	2	S65673	GABA transport pro	323	34	42.5	255	2	E82813	hypotheical prote
251	35	43.8	598	2	I51368	gamma-aminobutyric	324	34	42.5	298	2	T21203	hypotheical prote
252	35	43.8	598	2	F46027	gamma-aminobutyric	325	34	42.5	322	2	AF1031	hypotheical prote
253	35	43.8	599	1	ACRTGT	gamma-aminobutyric	326	34	42.5	322	2	T25648	hypotheical prote
254	35	43.8	599	2	S11073	gamma-aminobutyric	327	34	42.5	331	2	T13198	hypotheical prote
255	35	43.8	602	2	A44409	gamma-aminobutyric	328	34	42.5	332	2	A81667	conserved hypotet
256	35	43.8	602	2	A45078	gamma-aminobutyric	329	34	42.5	332	2	B71508	hypotheical prote
257	35	43.8	606	2	H88649	protein C09G12.6 [330	34	42.5	334	2	JC4681	bradykinin B1 rece
258	35	43.8	609	2	E81500	conserved hypotet	331	34	42.5	334	2	G86565	CT484 hypotheical
259	35	43.8	609	2	H72038	ct651 hypotheical	332	34	42.5	334	2	D72057	conserved hypotet
260	35	43.8	609	2	R86584	CT651 hypotheical	333	34	42.5	337	2	I38500	interferon gamma r
261	35	43.8	611	2	S46260	creatine transport	334	34	42.5	352	2	F96548	probable DNA-bindi
262	35	43.8	614	2	S68236	betaine transport	335	34	42.5	361	2	D86327	protein F18014.17
263	35	43.8	614	2	A41757	betaine transport	336	34	42.5	367	2	AD3631	nitrous-oxide redu
264	35	43.8	622	2	A43390	gamma-aminobutyric	337	34	42.5	370	2	T33975	hypotheical prote
265	35	43.8	622	2	S63539	GABA/beta-alanine	338	34	42.5	396	2	T19294	hypotheical prote
266	35	43.8	627	2	B44409	gamma-aminobutyric	339	34	42.5	398	2	T19293	hypotheical prote
267	35	43.8	627	2	JH0695	gamma-aminobutyric	340	34	42.5	441	2	H84576	diacylglycerol O-a
268	35	43.8	636	2	A84903	hypotheical prote	341	34	42.5	442	2	D82936	hemolysin U0072 [i
269	35	43.8	675	2	S59379	probable membrane	342	34	42.5	448	1	WMBP89	gene 8 protein - p
270	35	43.8	685	2	E82297	C-di-GMP phosphodi	343	34	42.5	448	1	WMBP82	gene 8 protein - p
271	35	43.8	728	2	I65413	sodium-dependent n	344	34	42.5	452	2	C85024	probable polygalac
272	35	43.8	730	2	I52632	sodium-dependent n	345	34	42.5	457	2	T39751	major facilitator
273	35	43.8	732	2	S77565	hypotheical prote	346	34	42.5	470	2	A65168	hypotheical 49.9
274	35	43.8	790	2	I50178	cadherin-6B - chic	347	34	42.5	491	2	A71533	probable phospholi
275	35	43.8	817	2	S51445	probable membrane	348	34	42.5	491	2	B86155	probable polygalac
276	35	43.8	861	2	T23810	hypotheical prote	349	34	42.5	496	2	T21140	hypotheical prote
277	35	43.8	901	2	C96696	protein F1N21.6 [i	350	34	42.5	496	2	A88763	protein F21P5.7 [i
278	35	43.8	903	2	T20804	hypotheical prote	351	34	42.5	501	2	T23011	hypotheical prote
279	35	43.8	972	2	T39876	hypotheical prote	352	34	42.5	504	2	S54143	SRP 54 protein - h
280	35	43.8	1327	2	T09402	immunoglobulin-lik	353	34	42.5	504	2	S05197	signal recognition
281	35	43.8	1360	2	T12064	DNA binding protei	354	34	42.5	504	2	S05198	signal recognition
282	35	43.8	1374	2	D85390	myosin-like protei	355	34	42.5	506	2	A40679	transcription enha
283	35	43.8	1375	2	T05200	myosin heavy chain	356	34	42.5	507	2	S54303	zinc transport pro
284	35	43.8	1379	2	JC4954	vascular endotheli	357	34	42.5	520	2	T52584	diacylglycerol O-a
285	35	43.8	1879	2	T19481	hypotheical prote	358	34	42.5	521	2	A29249	RNA-directed RNA p
286	35	43.8	2183	1	GNNY94	genome polyprotein	359	34	42.5	523	2	B40679	transcription enha
287	35	43.8	2185	1	GNNYBT	genome polyprotein	360	34	42.5	524	2	S07168	probable maturase,
288	35	43.8	2185	1	GNNYB3	genome polyprotein	361	34	42.5	529	2	JE0200	orphan UDP-glucuro
289	35	43.8	2233	2	T28669	surface protein 51	362	34	42.5	558	2	T40651	pre-mrna splicing
290	35	43.8	2957	2	T33152	hypotheical prote	363	34	42.5	587	2	S37927	hypotheical prote
291	35	43.8	3020	2	A43932	mucin 2 precursor,	364	34	42.5	627	2	AF1074	lytic murein trans
292	34.5	43.1	261	2	I78559	cyclic nucleotide-	365	34	42.5	634	1	S24384	nitrous-oxide redu
293	34.5	43.1	502	1	I30010	NADH2 dehydrogenas	366	34	42.5	635	2	A46061	Na(+)-dependent cr
294	34.5	43.1	513	2	P96735	hypotheical prote	367	34	42.5	635	2	JC2386	creatine transport
295	34.5	43.1	562	2	S56145	B569 protein - hum	368	34	42.5	635	2	G02095	creatine transport
296	34.5	43.1	663	2	S11521	cAMP-gated channel	369	34	42.5	635	2	S23431	choline transport
297	34.5	43.1	664	2	S35691	cyclic nucleotide-	370	34	42.5	636	2	C83222	nitrous-oxide redu
298	34.5	43.1	732	2	S35691	cyclic nucleotide-	371	34	42.5	638	1	A31845	nitrous-oxide redu
299	34	42.5	57	2	D49056	T-cell receptor al	372	34	42.5	639	2	C95342	nitrous-oxide redu
300	34	42.5	71	2	AF0683	NADH2 dehydrogenas	373	34	42.5	650	2	T44660	nitrous-oxide redu
301	34	42.5	91	2	T11163	GR1-related finger	374	34	42.5	650	2	T00617	endothyle-specific
302	34	42.5	100	2	A31201	Ig kappa chain V r	375	34	42.5	654	1	Q0ECW1	soluble lytic tran
303	34	42.5	108	2	S19112	hypotheical prote	376	34	42.5	654	2	F91297	soluble lytic mure
304	34	42.5	109	2	B86050	hypotheical prote	377	34	42.5	654	2	H86138	soluble lytic mure
305	34	42.5	115	1	KVMSK2	Ig kappa chain pre	378	34	42.5	696	2	T01951	hypotheical prote
306	34	42.5	122	2	S10213	hypotheical prote	379	34	42.5	716	2	JQ1366	polypeptin - hepa
307	34	42.5	129	1	F7SHB	foliitropin beta c	380	34	42.5	777	2	T04768	hypotheical prote
308	34	42.5	129	2	A23550	foliitropin beta c	381	34	42.5	788	2	T25061	hypotheical prote
309	34	42.5	141	2	D69160	hypotheical prote	382	34	42.5	840	2	T33217	hypotheical prote
310	34	42.5	141	2	H91203	hypotheical prote	383	34	42.5	848	2	B89042	protein F14F9.3 [i
311	34	42.5	144	2	S14156	hypotheical prote	384	34	42.5	918	2	A89042	protein F14F9.4 [i
312	34	42.5	152	1	VCBEY9	early glycoprotein	385	34	42.5	948	2	S26945	DNA ADP-directed RNA p
313	34	42.5	159	2	S18345	environmental stre	386	34	42.5	1013	1	S04200	NAD ADP-ribosyltra
314	34	42.5	161	1	T3BP79	gene 49.1 protein	387	34	42.5	1014	1	A29725	NAD ADP-ribosyltra
315	34	42.5	162	2	S68401	epiregulin precurs	388	34	42.5	1054	2	S48397	hypotheical prote
316	34	42.5	190	1	A44593	endo-1,4-beta-xyla	389	34	42.5	1165	1	S45879	chitin synthase (E
317	34	42.5	199	2	F91162	hypotheical membr	390	34	42.5	1181	2	B64516	hypotheical prote
318	34	42.5	200	2	G86008	hypotheical prote	391	34	42.5	1188	2	T38467	probable nuclear p
319	34	42.5	231	2	T26380	hypotheical prote	392	34	42.5	1238	2	T40120	CxH2 type zinc fin
320	34	42.5	231	2	T01294	sterol O-acyltrans	393	34	42.5	2195	2	T34264	hypotheical prote
321	34	42.5	234	2	T48454	hypotheical prote	394	34	42.5	2302	2	T14328	protein-tyrosine-p

395	34	42.5	2643	2	T29149	hypothetical prote	468	33	41.2	329	2	F64356	translation initia
396	34	42.5	2652	1	VRIHB2	genome polyprotein	469	33	41.2	332	2	A57055	melanocortin recep
397	34	42.5	2783	1	A41948	alpha-fetoprotein	470	33	41.2	334	2	D71044	tRNA-pseudouridine
398	34	42.5	2875	1	RRVUTW	genome polyprotein	471	33	41.2	334	2	E75170	probable pseudouri
399	33.5	41.9	2925	2	T00133	RNA-directed RNA p	472	33	41.2	335	2	D71275	hypothetical prote
400	33.5	41.9	42	2	T07581	hypothetical prote	473	33	41.2	341	2	G71313	hypothetical prote
401	33.5	41.9	80	2	A05185	hypothetical prote	474	33	41.2	342	2	T26677	hypothetical prote
402	33.5	41.9	347	2	T41962	hypothetical prote	475	33	41.2	344	1	TWXL3	transcription fact
403	33.5	41.9	357	2	T34012	hypothetical prote	476	33	41.2	344	2	T18019	probable site-spec
404	33.5	41.9	650	2	T00094	endostyle-specific	477	33	41.2	344	2	T28729	hypothetical prote
405	33.5	41.9	2395	1	S50820	surface protein ty	478	33	41.2	356	2	G97072	uncharacterized con
406	33	41.2	12	2	G54003	hypothetical prote	479	33	41.2	365	2	T28184	hypothetical prote
407	33	41.2	26	2	C39414	electron transport	480	33	41.2	391	2	T32601	hypothetical prote
408	33	41.2	27	2	T13836	NADH2 dehydrogenas	481	33	41.2	402	2	A70982	probable ppg prote
409	33	41.2	29	2	B43937	endo-1,4-beta-xyla	482	33	41.2	405	2	T42927	hypothetical prote
410	33	41.2	40	2	PQ0202	endo-1,4-beta-xyla	483	33	41.2	406	2	A41734	beta-galactoside a
411	33	41.2	62	2	S62862	toxin III-8 - fity	484	33	41.2	409	2	T28355	ORF MSV194 Ali mot
412	33	41.2	62	2	S62866	toxin III-8 - fity	485	33	41.2	415	2	F91209	low affinity trypt
413	33	41.2	62	2	A61484	toxin VI - Brazili	486	33	41.2	415	2	A86056	low affinity trypt
414	33	41.2	62	2	B39510	toxin III-8 - Braz	487	33	41.2	415	2	A39412	tryptophan transpo
415	33	41.2	63	2	A97346	hypothetical prote	488	33	41.2	424	2	JC5921	non-selective cati
416	33	41.2	76	2	T28486	hypothetical prote	489	33	41.2	426	2	T15285	hypothetical prote
417	33	41.2	76	2	F72156	C7L protein - vari	490	33	41.2	428	2	T48284	hypothetical prote
418	33	41.2	78	2	C90872	hypothetical prote	491	33	41.2	437	2	D84619	probable serine ca
419	33	41.2	84	2	S62868	toxin gamma precu	492	33	41.2	450	2	T39088	probable vacuolar
420	33	41.2	84	2	S62867	toxin gamma precu	493	33	41.2	451	1	S68455	serine/threonine-s
421	33	41.2	84	2	S21158	neurotoxin TeVII p	494	33	41.2	454	1	IQTJBA	replication initia
422	33	41.2	99	2	S33472	hypothetical prote	495	33	41.2	454	2	D84931	chromosomal replic
423	33	41.2	108	2	S69873	hypothetical prote	496	33	41.2	466	2	T33574	hypothetical prote
424	33	41.2	108	2	G69261	hypothetical prote	497	33	41.2	467	2	B87637	aminotransferase,
425	33	41.2	116	2	A82400	hypothetical prote	498	33	41.2	468	2	F82012	hypothetical prote
426	33	41.2	121	2	PH1661	Ig heavy chain V r	499	33	41.2	478	2	T31955	hypothetical prote
427	33	41.2	124	1	MLHUTL	Ig heavy chain V-I	500	33	41.2	487	2	F72126	ct339 hypothetical
428	33	41.2	128	2	S69856	hypothetical prote	501	33	41.2	487	2	E86495	CT339 hypothetical
429	33	41.2	138	2	S78252	ribosomal protein	502	33	41.2	487	2	A81545	conserved hypothet
430	33	41.2	145	2	S51907	cryptogene protei	503	33	41.2	492	2	S28007	probable ATP-bindi
431	33	41.2	145	2	A44385	iron-sulfur protei	504	33	41.2	503	2	S54302	zinc transporter Z
432	33	41.2	146	2	T01683	immobilization ant	505	33	41.2	505	2	C84949	NADH2 dehydrogenas
433	33	41.2	158	2	E90198	hypothetical prote	506	33	41.2	510	2	B88381	protein T2287.1 [i
434	33	41.2	171	2	G81783	hypothetical prote	507	33	41.2	525	2	T41663	probable transcrip
435	33	41.2	171	2	S35248	nifQ protein - Ent	508	33	41.2	562	2	B70081	hypothetical prote
436	33	41.2	172	2	T25500	hypothetical prote	509	33	41.2	576	2	A32604	interleukin-1 rece
437	33	41.2	215	2	B57055	melanocortin-4 rec	510	33	41.2	581	2	C96538	hypothetical prote
438	33	41.2	219	2	S71472	endo-1,4-beta-xyla	511	33	41.2	607	2	A44490	retrovirus-related
439	33	41.2	221	2	S76798	hypothetical prote	512	33	41.2	612	2	T05750	auxin-regulated pr
440	33	41.2	234	2	S01320	Ig kappa chain pre	513	33	41.2	623	1	GVGNBS	spike glycoprotein
441	33	41.2	240	2	B90739	probable enzyme [i	514	33	41.2	627	2	S37954	RNA polymerase I t
442	33	41.2	242	2	S73698	hypothetical prote	515	33	41.2	633	2	T52506	hypothetical prote
443	33	41.2	248	2	T26584	hypothetical prote	516	33	41.2	637	2	T20981	hypothetical prote
444	33	41.2	249	2	T04939	hypothetical prote	517	33	41.2	639	2	A10055	probable soluble l
445	33	41.2	251	2	T49370	hypothetical prote	518	33	41.2	644	1	T40712	endo-1,4-beta-xyla
446	33	41.2	253	2	T47303	hypothetical prote	519	33	41.2	652	1	S39409	nitrous-oxide redu
447	33	41.2	262	2	H91264	ATP-binding compon	520	33	41.2	658	2	T24851	hypothetical prote
448	33	41.2	262	2	E86105	ATP-binding compon	521	33	41.2	664	2	AB1430	hypothetical prote
449	33	41.2	262	2	A56220	phosphonates trans	522	33	41.2	664	2	AH1803	hypothetical prote
450	33	41.2	273	1	B64623	lipopolysaccharide	523	33	41.2	683	2	T01442	hypothetical prote
451	33	41.2	273	2	E71890	probable lipopolys	524	33	41.2	690	2	G84638	hypothetical prote
452	33	41.2	278	2	E71293	probable nicotinam	525	33	41.2	691	2	S46585	outward-rectifier
453	33	41.2	284	1	E64620	lipopolysaccharide	526	33	41.2	703	2	T15503	hypothetical prote
454	33	41.2	292	2	D71894	probable lipopolys	527	33	41.2	703	2	A54766	metastasis-associ
455	33	41.2	295	1	S29399	homeotic protein m	528	33	41.2	706	2	T51432	cyclic nucleotide
456	33	41.2	296	2	D70465	hypothetical prote	529	33	41.2	710	2	S22673	ferrioxamine recep
457	33	41.2	299	2	AE1341	fructose-1,6-bipho	530	33	41.2	715	2	T22787	hypothetical prote
458	33	41.2	299	2	AC1712	fructose-1,6-bipho	531	33	41.2	727	2	T18600	hypothetical prote
459	33	41.2	299	2	AD0058	transcription acti	532	33	41.2	733	2	B85357	hypothetical prote
460	33	41.2	314	2	H88991	protein K08D9.1 [i	533	33	41.2	747	2	T52572	cyclic nucleotide
461	33	41.2	314	2	T39510	probable mitochond	534	33	41.2	775	2	A61228	collagen alpha 2(I
462	33	41.2	320	2	G89898	protein C36C5_8 [i	535	33	41.2	795	2	S62464	conserved hypothet
463	33	41.2	320	2	AB1550	hypothetical prote	536	33	41.2	810	1	A33380	interleukin-4 reca
464	33	41.2	324	2	B25102	reaction center pr	537	33	41.2	839	2	F85334	myosin heavy chain
465	33	41.2	325	2	JC7560	cellulase (EC 3.2.	538	33	41.2	854	2	T52472	RAD16 nucleotide e
466	33	41.2	325	2	G70421	probable endogluc	539	33	41.2	880	2	B87222	probable iron-sulp
467	33	41.2	328	2	T30999	hypothetical prote	540	33	41.2	880	2	S56828	finger protein YJL

541	33	41.2	882	2	A70507	probable reductase	614	32	40.0	159	1	S27195	transforming growt
542	33	41.2	891	2	JC6519	DNA topoisomerase	615	32	40.0	159	1	WFR1	transforming growt
543	33	41.2	963	2	T41479	RAD16 nucleotide e	616	32	40.0	159	1	WFR1	transforming growt
544	33	41.2	971	2	T00268	hypothetical prote	617	32	40.0	164	2	AC0537	hypothetical prote
545	33	41.2	975	2	AC2517	hypothetical prote	618	32	40.0	173	2	A81923	probable membrane
546	33	41.2	982	2	T15967	hypothetical prote	619	32	40.0	176	2	S40726	hypothetical prote
547	33	41.2	994	2	T21356	hypothetical prote	620	32	40.0	183	2	T22604	hypothetical prote
548	33	41.2	996	2	T25512	hypothetical prote	621	32	40.0	186	2	S46450	hypothetical prote
549	33	41.2	1023	2	T18520	transhydrogenase h	622	32	40.0	197	1	A44597	endo-1,4-beta-xyla
550	33	41.2	1027	2	A56533	chromatin remodell	623	32	40.0	200	2	T27250	hypothetical prote
551	33	41.2	1043	2	T13733	Frz-P1 protein - f	624	32	40.0	202	2	AF0604	probable permease
552	33	41.2	1115	2	S40241	G protein-coupled	625	32	40.0	205	2	AF0532	hypothetical prote
553	33	41.2	1158	2	E86327	protein F180L4.19	626	32	40.0	213	2	T35433	hypothetical prote
554	33	41.2	1377	2	A38926	DNA-binding protei	627	32	40.0	214	2	T34069	hypothetical prote
555	33	41.2	1381	2	S55619	capsid protein 25	628	32	40.0	219	2	H71477	probable set domai
556	33	41.2	1402	2	T17456	cell surface prote	629	32	40.0	219	2	G81740	conserved hypotet
557	33	41.2	1446	2	T04528	myosin heavy chain	630	32	40.0	221	2	D86600	SR domain protein
558	33	41.2	1477	2	T00957	myosin heavy chain	631	32	40.0	221	2	B81514	conserved hypotet
559	33	41.2	1490	2	E84726	probable unconvet	632	32	40.0	221	2	D72024	set domain protein
560	33	41.2	1502	2	T14278	myosin-like protei	633	32	40.0	238	2	JC4503	macrophage maturat
561	33	41.2	1502	2	D84587	probable myosin he	634	32	40.0	243	1	D70456	gufa protein homol
562	33	41.2	1515	2	S51824	myosin heavy chain	635	32	40.0	245	2	T10407	immediate early pr
563	33	41.2	1611	2	A84743	probable myosin he	636	32	40.0	260	2	I49049	Ly-49D-GS antigen
564	33	41.2	1712	1	CSHU28	collagen alpha 2(I	637	32	40.0	261	2	D86149	TiN6.19 protein -
565	33	41.2	1736	2	E86178	hypothetical prote	638	32	40.0	262	2	S59078	conserved hypotet
566	33	41.2	1839	1	RRWPM	genome polypeptin	639	32	40.0	267	2	T32063	hypothetical prote
567	33	41.2	1872	2	S64851	probable membrane	640	32	40.0	272	2	T05498	hypothetical prote
568	33	41.2	1976	2	I56555	sodium channel pro	641	32	40.0	286	2	AE2459	hypothetical prote
569	33	41.2	2410	1	J01948	genome polypeptin	642	32	40.0	288	2	S36955	cytochrome-c oxida
570	33	41.2	2412	1	J01537	genome polypeptin	643	32	40.0	288	2	I78556	membrane glycoprot
571	33	41.2	2482	2	I48922	cation-independent	644	32	40.0	288	2	A45803	B-cell-restricted
572	33	41.2	2483	1	A49617	insulin-like growt	645	32	40.0	288	2	B43253	zinc finger protei
573	33	41.2	2704	2	S09118	G surface protein	646	32	40.0	289	2	G00031	B7 protein - red-c
574	33	41.2	2718	2	A23475	G surface protei	647	32	40.0	289	2	T24475	hypothetical prote
575	32.5	40.6	79	2	S59090	hypothetical prote	648	32	40.0	292	2	T16085	hypothetical prote
576	32.5	40.6	96	2	S55366	Ig kappa chain v r	649	32	40.0	295	2	E84425	probable homeodoma
577	32.5	40.6	101	2	S39490	hypothetical prote	650	32	40.0	303	2	T19310	hypothetical prote
578	32.5	40.6	221	2	T29509	hypothetical prote	651	32	40.0	304	2	C71637	rod shape-determin
579	32.5	40.6	258	2	C86541	Cr105 hypothetical	652	32	40.0	310	2	A70449	hypothetical prote
580	32.5	40.6	258	2	D72082	hypothetical prote	653	32	40.0	311	2	B84428	hypothetical prote
581	32.5	40.6	331	2	S43070	hypothetical prote	654	32	40.0	315	2	H96935	magnesium and coba
582	32.5	40.6	358	2	I50506	gene wnt8b protein	655	32	40.0	317	2	S57546	hypothetical prote
583	32.5	40.6	377	2	A49885	MHC class I histoc	656	32	40.0	326	2	C87578	ISCCs, transposase
584	32.5	40.6	379	2	A35878	class I major hist	657	32	40.0	330	2	S55595	G protein-coupled
585	32.5	40.6	379	2	E35878	class I major hist	658	32	40.0	335	2	T18032	probable site-spec
586	32.5	40.6	406	2	B35878	class I major hist	659	32	40.0	336	2	T22680	hypothetical prote
587	32.5	40.6	591	2	H72474	probable acylamino	660	32	40.0	339	1	RRVQBM	RNA-directed RNA p
588	32.5	40.6	634	2	H64508	hypothetical prote	661	32	40.0	340	2	S75099	hypothetical prote
589	32.5	40.6	1145	1	GNLJ5V	HIV-1 retropepsin	662	32	40.0	342	2	A45678	probable transmemb
590	32.5	40.6	1146	1	GNLJ22	HIV-1 retropepsin	663	32	40.0	343	2	S09777	hypothetical prote
591	32.5	40.6	1146	1	GNLJ2V	HIV-1 retropepsin	664	32	40.0	354	2	JC4152	Wnt-11 protein pre
592	32.5	40.6	3341	1	A42996	testis-specific pr	665	32	40.0	354	2	S34378	wnt-11 protein - m
593	32	40.0	55	2	S25774	hypothetical prote	666	32	40.0	354	2	S28765	hypothetical prote
594	32	40.0	63	2	G82084	hypothetical prote	667	32	40.0	354	2	B88650	protein C09G12.4 [
595	32	40.0	66	2	A29386	neurotoxin III - s	668	32	40.0	357	1	CQ8EG4	WLF3 protein - hu
596	32	40.0	67	2	JN0378	neurotoxin III - s	669	32	40.0	361	2	C85430	MAP kinase like pr
597	32	40.0	76	2	A48784	Ig kappa V regions	670	32	40.0	365	2	B97315	membrane protease
598	32	40.0	88	2	H91290	hypothetical prote	671	32	40.0	368	2	B84561	MAP kinase (ATMPK7
599	32	40.0	100	1	TNLJ3T	trans-activating t	672	32	40.0	368	2	S40473	mitogen-activated
600	32	40.0	106	2	JQ0234	hypothetical prote	673	32	40.0	373	2	JC7289	G-protein coupled
601	32	40.0	109	2	PH1671	Ig heavy chain v r	674	32	40.0	380	2	S34964	rhc protein - Shig
602	32	40.0	127	2	S26491	probable membrane	675	32	40.0	381	2	D89922	conserved hypotet
603	32	40.0	137	2	B34903	Ig heavy chain pre	676	32	40.0	381	2	F59101	hypothetical prote
604	32	40.0	143	1	PSGHA5	phospholipase A2 (677	32	40.0	385	2	A82388	conserved hypotet
605	32	40.0	144	2	S36322	T-cell receptor de	678	32	40.0	386	2	S60846	NADH2 dehydrogenas
606	32	40.0	144	2	T26605	hypothetical prote	679	32	40.0	389	2	T05782	hypothetical prote
607	32	40.0	145	1	TNLJBT	trans-activating t	680	32	40.0	392	2	T45032	hypothetical prote
608	32	40.0	147	2	F84869	hypothetical prote	681	32	40.0	392	2	T33444	hypothetical prote
609	32	40.0	152	2	T34649	hypothetical prote	682	32	40.0	392	2	T46418	hypothetical prote
610	32	40.0	153	2	H86034	hypothetical prote	683	32	40.0	395	2	T09654	polysaccharonase
611	32	40.0	153	2	G91187	hypothetical prote	684	32	40.0	398	2	AE3577	sugar-binding prot
612	32	40.0	153	2	S47817	hypothetical 18.1K	685	32	40.0	401	2	S09626	prrB protein - Esc
613	32	40.0	154	2	S76466	hypothetical prote	686	32	40.0	413	2	G84994	exodeoxyribonuclea

687	32	40.0	413	2	T10593	hypothetical prote	760	32	40.0	774	2	T22309	hypothetical prote
688	32	40.0	422	2	P86581	CHLPP 76 kDa homol	761	32	40.0	796	2	E96654	hypothetical prote
689	32	40.0	422	2	E72042	conserved hypothet	762	32	40.0	798	2	T34248	hypothetical prote
690	32	40.0	426	2	G02217	creatine transport	763	32	40.0	816	2	C69493	hypothetical prote
691	32	40.0	426	2	S28374	genome polyprotein	764	32	40.0	852	1	GNLJGB	pol polyprotein -
692	32	40.0	428	2	T48008	hypothetical prote	765	32	40.0	852	1	GNLJGB	pol polyprotein -
693	32	40.0	428	2	C69991	conserved hypothet	766	32	40.0	852	2	S29358	pol protein - bovi
694	32	40.0	429	2	S20050	transcription fact	767	32	40.0	874	2	T29548	hypothetical prote
695	32	40.0	434	2	T26275	hypothetical prote	768	32	40.0	886	2	T39229	hypothetical prote
696	32	40.0	441	2	H96968	integral membrane	769	32	40.0	893	2	T36795	probable penicilli
697	32	40.0	442	2	T18917	hypothetical prote	770	32	40.0	912	2	T02892	hypothetical prote
698	32	40.0	446	2	T31539	hypothetical prote	771	32	40.0	919	2	T16459	hypothetical prote
699	32	40.0	451	2	C38386	sugar transporter,	772	32	40.0	921	2	H84921	hypothetical prote
700	32	40.0	451	2	P83793	DNA-damage-inducib	773	32	40.0	923	2	S09583	peptidylglycine mo
701	32	40.0	454	2	T49117	hypothetical prote	774	32	40.0	946	2	G71617	SERA antigen/papai
702	32	40.0	465	2	T29257	hypothetical prote	775	32	40.0	972	1	URBOAP	peptidylglycine mo
703	32	40.0	465	2	T37415	hypothetical prote	776	32	40.0	974	1	URHUAP	peptidylglycine mo
704	32	40.0	475	2	T33943	hypothetical prote	777	32	40.0	976	1	URRTAP	peptidylglycine mo
705	32	40.0	485	1	VHVUWJ	nucleoprotein - Ha	778	32	40.0	1024	2	G72041	exodeoxyribonuclea
706	32	40.0	487	2	T06040	hypothetical prote	779	32	40.0	1024	2	P86582	exodeoxyribonuclea
707	32	40.0	497	2	T33013	hypothetical prote	780	32	40.0	1024	2	D81824	exodeoxyribonuclea
708	32	40.0	508	2	PC6300	synaptotagmin X -	781	32	40.0	1025	2	T21319	hypothetical prote
709	32	40.0	508	2	AH2688	Na+/H+ antiporter	782	32	40.0	1043	2	T19734	hypothetical prote
710	32	40.0	509	2	A96563	probable protein k	783	32	40.0	1110	2	A43253	large tra-1 protei
711	32	40.0	511	2	S49151	maturase matK, int	784	32	40.0	1113	2	JB0315	low-density lipopr
712	32	40.0	521	2	T38466	probable NRAMP-fam	785	32	40.0	1132	2	S60433	probable membrane
713	32	40.0	523	2	E70188	DNA primase (dnaG)	786	32	40.0	1177	2	L64233	hypothetical prote
714	32	40.0	523	2	T05692	hypothetical prote	787	32	40.0	1224	2	E71611	hypothetical prote
715	32	40.0	525	2	C97470	probable NADH dehy	788	32	40.0	1242	2	T45976	myosin heavy chain
716	32	40.0	527	1	K1BEHS	thymidine kinase (789	32	40.0	1260	2	T14276	myosin-like protei
717	32	40.0	527	1	T42934	thymidine kinase (790	32	40.0	1268	2	T50252	probable transcrip
718	32	40.0	529	2	C59280	conserved hypothet	791	32	40.0	1273	2	T42405	sax-3 protein - Ca
719	32	40.0	532	2	T28784	hypothetical prote	792	32	40.0	1291	1	S05465	retrovirus-related
720	32	40.0	536	2	G64752	xylian 1,4-beta-xy	793	32	40.0	1360	2	P96596	hypothetical prote
721	32	40.0	543	2	S65462	glucose transport	794	32	40.0	1363	1	A55875	xanthine dehydrog
722	32	40.0	555	2	H96720	probable peptide t	795	32	40.0	1428	2	T39475	probable ATP-depen
723	32	40.0	559	2	H71983	DNA primase - Heli	796	32	40.0	1520	2	S46444	myosin MV1, class
724	32	40.0	560	2	S23313	hypothetical prote	797	32	40.0	1528	2	T14279	myosin-like protei
725	32	40.0	561	2	T27318	hypothetical prote	798	32	40.0	1556	2	P96587	hypothetical prote
726	32	40.0	577	2	C84936	DNA primase [impor	799	32	40.0	1583	2	T00727	myosin heavy chain
727	32	40.0	578	2	T15958	hypothetical prote	800	32	40.0	1658	2	D86890	DNA-directed DNA p
728	32	40.0	581	2	H70125	hypothetical prote	801	32	40.0	1691	1	CGHU6B	collagen alpha 6(I
729	32	40.0	588	1	A37008	neopullulanase (EC	802	32	40.0	1707	2	A33526	collagen alpha 2(I
730	32	40.0	590	2	G86317	protein F15H18.15	803	32	40.0	1711	1	A47392	chromodomain-helic
731	32	40.0	597	2	A30814	development-specif	804	32	40.0	2164	1	GNX899	genome polyprotein
732	32	40.0	607	2	H88065	protein t16A1.1 [i	805	32	40.0	2505	1	XIRTPA	enoyl-[acyl-carrie
733	32	40.0	608	2	T25018	hypothetical prote	806	31.5	39.4	65	2	A38394	neurotoxin AaH IT4
734	32	40.0	609	2	A49839	odd-paired - fruit	807	31.5	39.4	100	2	A10092	probable membrane
735	32	40.0	611	2	D82881	zinc metalloprotei	808	31.5	39.4	116	2	I38410	RP3 candidate gene
736	32	40.0	616	2	T11850	DNA primase (EC 2.	809	31.5	39.4	188	2	P95944	hypothetical prote
737	32	40.0	619	2	A36519	CDC16 protein - hu	810	31.5	39.4	198	2	E69192	hypothetical prote
738	32	40.0	625	2	S48941	regulatory protein	811	31.5	39.4	259	2	JN0099	SPO7 protein - yea
739	32	40.0	627	2	T27319	hypothetical prote	812	31.5	39.4	262	2	T01562	hypothetical wtfl1
740	32	40.0	626	2	B84482	probable gag-prote	813	31.5	39.4	264	2	T40927	hypothetical prote
741	32	40.0	630	2	G87753	protein C43B11.8 [814	31.5	39.4	275	2	P86894	hypothetical prote
742	32	40.0	638	2	D86477	protein F1504.27 [815	31.5	39.4	367	2	AF2494	hypothetical prote
743	32	40.0	648	1	NPVZAM	nucleoside-triphos	816	31.5	39.4	424	2	T25774	hypothetical prote
744	32	40.0	651	2	F64417	probable ATP-depen	817	31.5	39.4	480	2	T01207	cysteine proteinas
745	32	40.0	657	2	B84460	hypothetical prote	818	31.5	39.4	502	2	T24817	hypothetical prote
746	32	40.0	659	2	A45184	protein-tyrosine k	819	31.5	39.4	527	2	T05828	hypothetical prote
747	32	40.0	659	2	I49553	protein-tyrosine k	820	31.5	39.4	538	2	B84863	hypothetical prote
748	32	40.0	661	2	B86596	hypothetical prote	821	31.5	39.4	559	2	S29305	poly(3-hydroxyalka
749	32	40.0	664	2	E83572	DNA primase PA0577	822	31.5	39.4	590	1	S34960	NADH2 dehydrogenas
750	32	40.0	669	2	S65551	factor H - bovine	823	31.5	39.4	965	2	S62935	hypothetical prote
751	32	40.0	669	2	B70186	translation elonga	824	31.5	39.4	1021	2	T10748	mannan endo-1,4-be
752	32	40.0	684	2	C96596	hypothetical prote	825	31.5	39.4	1124	2	G91055	hypothetical prote
753	32	40.0	687	2	T27533	hypothetical prote	826	31.5	39.4	1124	2	C85900	hypothetical prote
754	32	40.0	710	2	T52573	cyclic nucleotide	827	31.5	39.4	1504	2	T49896	glycine/proline-ri
755	32	40.0	712	2	S50969	probable membrane	828	31	38.8	29	2	S58388	T-cell receptor be
756	32	40.0	715	2	I40729	hypothetical 76k p	829	31	38.8	36	2	E70238	hypothetical prote
757	32	40.0	715	2	S08450	hypothetical prote	830	31	38.8	64	2	S28486	hypothetical prote
758	32	40.0	725	2	E96596	hypothetical prote	831	31	38.8	69	2	B70117	hypothetical prote
759	32	40.0	763	2	T27620	hypothetical prote	832	31	38.8	70	2	T17811	hypothetical prote

833	31	38.8	84	2	G95202	conserved hypochet	906	31	38.8	249	2	T19088	hypothetical prote
834	31	38.8	84	2	G98069	conserved hypochet	907	31	38.8	250	2	T30124	hypothetical prote
835	31	38.8	89	1	HVRK1	Ig heavy chain v r	908	31	38.8	252	2	AG1423	hypothetical prote
836	31	38.8	89	2	F69268	hypothetical prote	909	31	38.8	252	2	AE1797	hypothetical prote
837	31	38.8	89	2	S08578	hypothetical prote	910	31	38.8	260	2	T12395	NADH2 dehydrogenas
838	31	38.8	102	2	T45500	hypothetical prote	911	31	38.8	262	2	I49361	natural killer cel
839	31	38.8	102	2	F90052	hypothetical prote	912	31	38.8	262	2	A45813	T-cell surface gly
840	31	38.8	103	2	H11134	hypothetical prote	913	31	38.8	262	2	A30573	T-cell surface gly
841	31	38.8	105	2	H75046	pyruvate synthase	914	31	38.8	263	2	T32081	hypothetical prote
842	31	38.8	105	2	T45087	pyruvate synthase	915	31	38.8	266	2	I49363	natural killer cel
843	31	38.8	108	2	C71114	probable ferredoxi	916	31	38.8	266	2	I49114	Ly49H - mouse
844	31	38.8	110	2	D48562	hypothetical nucle	917	31	38.8	266	2	I49051	Ly49F-G8 antigen
845	31	38.8	114	2	S07898	endothelin 3 - rab	918	31	38.8	266	2	I49059	Ly49C - mouse
846	31	38.8	114	2	S09828	hypothetical prote	919	31	38.8	267	2	T30007	hypothetical prote
847	31	38.8	115	2	PL0246	Ig heavy chain v r	920	31	38.8	267	2	S66945	hypothetical prote
848	31	38.8	119	2	D64404	hypothetical prote	921	31	38.8	268	2	AG1408	transcription regu
849	31	38.8	128	2	AP2394	hypothetical prote	922	31	38.8	270	2	B48826	high choriolytic h
850	31	38.8	129	2	S39445	DNA-directed RNA p	923	31	38.8	274	2	A72241	endoglucanase - Th
851	31	38.8	132	2	A90364	hypothetical prote	924	31	38.8	277	2	H86622	dimethyladenosine
852	31	38.8	134	2	E83011	phosphoribosyl-AMP	925	31	38.8	277	2	H72001	dimethyladenosine
853	31	38.8	136	2	G64248	hypothetical prote	926	31	38.8	283	2	F88087	protein B0454.5 [i
854	31	38.8	136	2	S73520	MG441 homolog 809	927	31	38.8	283	2	JE0235	HIV-promoter GC-ri
855	31	38.8	137	2	S28705	hypothetical prote	928	31	38.8	287	2	F69413	oxygen-independent
856	31	38.8	137	2	AG1821	hypothetical prote	929	31	38.8	288	2	I49058	Ly49C - mouse
857	31	38.8	137	2	A99908	conserved hypochet	930	31	38.8	288	2	T32212	hypothetical prote
858	31	38.8	143	2	G71060	hypothetical prote	931	31	38.8	290	2	E96706	probable bifunctio
859	31	38.8	146	2	T10325	hypothetical prote	932	31	38.8	291	2	G71300	probable protein-m
860	31	38.8	150	2	B70892	hypothetical prote	933	31	38.8	292	2	F84951	hypothetical prote
861	31	38.8	155	1	W6WL43	E6 protein - human	934	31	38.8	294	1	MUSNM1	lysosome (EC 3.2.1
862	31	38.8	159	2	D90336	hypothetical prote	935	31	38.8	294	2	T32170	hypothetical prote
863	31	38.8	159	2	E82692	hypothetical prote	936	31	38.8	296	1	S37312	transcription acti
864	31	38.8	161	2	C71818	probable ribonucle	937	31	38.8	298	2	AD3336	sulfate transport
865	31	38.8	161	2	H64700	ribonuclease P, pr	938	31	38.8	310	2	T47675	glycoprotein-like
866	31	38.8	164	2	T44054	hypothetical prote	939	31	38.8	313	2	T28728	hypothetical prote
867	31	38.8	165	2	T29176	hypothetical prote	940	31	38.8	315	2	T15460	hypothetical prote
868	31	38.8	167	1	JC1102	endothelin 3 precu	941	31	38.8	318	2	T50039	beta-1,4-galactosy
869	31	38.8	167	2	D81049	hypothetical prote	942	31	38.8	318	2	S38511	adenosine receptor
870	31	38.8	172	2	B81828	hypothetical integ	943	31	38.8	319	2	T26888	hypothetical prote
871	31	38.8	177	2	H64423	hypothetical prote	944	31	38.8	320	1	A39479	homeotic protein m
872	31	38.8	189	2	JK0235	core protein MGC-2	945	31	38.8	320	2	T45909	hypothetical prote
873	31	38.8	194	2	AC0370	hypothetical prote	946	31	38.8	321	1	S28390	homeotic protein m
874	31	38.8	195	2	I46272	trophoblast interf	947	31	38.8	322	2	AD1535	hypothetical prote
875	31	38.8	195	2	S39967	hypothetical prote	948	31	38.8	322	2	AH1177	hypothetical prote
876	31	38.8	197	2	T37739	hypothetical prote	949	31	38.8	325	2	T32282	hypothetical prote
877	31	38.8	199	2	T32960	hypothetical prote	950	31	38.8	328	2	T32218	hypothetical prote
878	31	38.8	202	2	S11434	proteinase - bovin	951	31	38.8	329	2	T21872	hypothetical prote
879	31	38.8	202	2	T10387	hypothetical prote	952	31	38.8	332	2	T32219	hypothetical prote
880	31	38.8	202	2	T32159	hypothetical prote	953	31	38.8	335	2	T40160	conserved hypochet
881	31	38.8	202	2	AH3407	hypothetical cytos	954	31	38.8	337	2	T33209	hypothetical prote
882	31	38.8	209	2	T10295	hepatic lectin - c	955	31	38.8	338	2	S55657	transcription fact
883	31	38.8	209	2	LNCHL	hypothetical prote	956	31	38.8	339	2	B34895	capsid protein 62
884	31	38.8	209	2	JO2031	hypothetical prote	957	31	38.8	340	2	C72851	AcOrf-11 protein -
885	31	38.8	212	2	E91046	transcription regu	958	31	38.8	340	2	T41757	AcMNPV orf11 - Bom
886	31	38.8	212	2	F65023	gcvR protein - Esc	959	31	38.8	341	2	H48563	GI protein - fowlp
887	31	38.8	212	2	A85891	transcription regu	960	31	38.8	342	2	T16735	hypothetical prote
888	31	38.8	214	2	I49351	endothelin 3 precu	961	31	38.8	342	2	T37207	hypothetical prote
889	31	38.8	219	2	T47318	hypothetical prote	962	31	38.8	342	2	C72313	hypothetical prote
890	31	38.8	219	2	S25643	EBF2 protein - hu	963	31	38.8	345	2	T33706	hypothetical prote
891	31	38.8	220	2	S25005	nodulin-30 (Np30)	964	31	38.8	345	2	T32203	hypothetical prote
892	31	38.8	223	2	S77837	hypothetical prote	965	31	38.8	346	2	T20458	hypothetical prote
893	31	38.8	225	2	B65127	type 4 prepllin-li	966	31	38.8	348	2	D90522	restriction-modifi
894	31	38.8	228	2	G90316	hypothetical prote	967	31	38.8	350	2	B33319	microtubule-associ
895	31	38.8	228	2	T34197	hypothetical prote	968	31	38.8	355	2	E75577	conserved hypochet
896	31	38.8	230	2	B86563	phosphoglycolate p	969	31	38.8	356	2	T19015	hypothetical prote
897	31	38.8	230	2	B72062	phosphoglycolate p	970	31	38.8	357	2	T40410	hypothetical prote
898	31	38.8	232	2	A60095	larval glue protei	971	31	38.8	362	2	T45072	erythroid kruppel-
899	31	38.8	234	2	T32226	hypothetical prote	972	31	38.8	370	2	JC7998	platelet-derived g
900	31	38.8	238	1	A34378	endothelin 3 precu	973	31	38.8	370	2	JC7592	spinal cord-derive
901	31	38.8	239	2	B84257	hypothetical prote	974	31	38.8	373	2	A96927	probable N6-adenin
902	31	38.8	239	2	T26798	hypothetical prote	975	31	38.8	374	2	T37676	zinc-finger protei
903	31	38.8	244	2	S03215	hypothetical prote	976	31	38.8	374	2	T21734	hypothetical prote
904	31	38.8	244	2	A39365	cyanamide hydratas	977	31	38.8	380	2	G97828	hypothetical prote
905	31	38.8	246	2	I51325	proteolipid protei	978	31	38.8	383	2	T23182	hypothetical prote

979 31 38.8 387 2 T38876 probable ribosomal
 980 31 38.8 387 2 T26735 hypothetical prote
 981 31 38.8 387 2 D84700 hypothetical prote
 982 31 38.8 391 2 T51609 polygalacturonase
 983 31 38.8 397 2 S42549 polygalacturonase
 984 31 38.8 401 2 T24929 hypothetical prote
 985 31 38.8 405 2 A13148 conserved hypotet
 986 31 38.8 407 2 S52006 polygalacturonase
 987 31 38.8 409 2 AF2233 hypothetical prote
 988 31 38.8 410 2 T15442 hypothetical prote
 989 31 38.8 415 2 T38334 probable trna meth
 990 31 38.8 416 2 T50279 hypothetical serin
 991 31 38.8 417 2 T20199 hypothetical prote
 992 31 38.8 420 2 T25689 hypothetical prote
 993 31 38.8 425 2 B98139 bme3 protein (AF07
 994 31 38.8 425 2 C87619 hypothetical prote
 995 31 38.8 425 2 T38548 hypothetical zinc-
 996 31 38.8 430 2 G83710 hypothetical prote
 997 31 38.8 434 2 T19205 hypothetical prote
 998 31 38.8 436 2 B82431 regulatory protein
 999 31 38.8 439 2 S78378 maturase-like prot
 1000 31 38.8 439 2 F69216 conserved hypotet

ALIGNMENTS

RESULT 1
 H88124
 protein T12C9.3 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: H88124
 R:anonymouse, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome number: of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; MUID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: H88124
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1910 <STO>
 A:Cross-references: UNIPARC:UPI000017A592; GB:chr_II; PIDN:AC71141.1; PID:g1086770; GSPD
 A:Note: proline-rich
 C:Genetics:
 A:Gene: T12C9.3
 A:Map position: 2

Query Match 62.5%; Score 50; DB 2; Length 1910;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
 :|:|||||
 Db 1378 YYSFWKTKCT 1386

RESULT 2
 JH0560
 cyclic nucleotide-gated channel - channel catfish
 C:Species: Ictalurus punctatus (channel catfish)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: JH0560
 R:Goulding, E.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Siegelbaum, S.A.; Ches
 Neuron 8, 45-58, 1992
 A:Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated
 A:Reference number: JH0560; MUID:92110008; PMID:1370374
 A:Accession: JH0560
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-682 <GOU>
 A:Cross-references: UNIPROT:P55934; UNIPARC:UPI0000127C25; GB:M83111

A:Experimental source: olfactory epithelium
 C:Comment: This cyclic nucleotide-gated channel is activated equally well by both cAMP ar
 C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-g
 C:Keywords: cAMP binding; cGMP binding; ion channel; ion transport; olfaction; transmembr
 F:137-157/Domain: transmembrane #status predicted <TS1>
 F:173-193/Domain: transmembrane #status predicted <TS2>
 F:217-236/Domain: transmembrane #status predicted <TS3>
 F:241-261/Domain: transmembrane #status predicted <TS4>
 F:277-297/Domain: transmembrane #status predicted <TS5>
 F:319-337/Domain: transmembrane #status predicted <TS6>
 F:350-370/Domain: transmembrane #status predicted <TS6>
 F:447-571/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 58.1%; Score 46.5; DB 1; Length 682;
 Best Local Similarity 66.7%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 CYYVCF-WKTKCT 11
 :|:|||||
 Db 316 CYYVCFWSTLT 327

RESULT 3

T28166
 hypothetical protein ORF5 - Melanoplus sanguinipes entomopoxvirus (isolate Tuscon)
 C:Species: Melanoplus sanguinipes entomopoxvirus
 A:Variety: isolate Tuscon
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T28166
 R:Afonso, C.L.; Tullman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
 J. Virol. 73, 533-552, 1999
 A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
 A:Reference number: Z20484; MUID:99102612; PMID:9847359

A:Accession: T28166
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-246 <APO>
 A:Cross-references: UNIPROT:Q9YW87; UNIPARC:UPI00000F11B2; EMBL:AF063866; NID:G4049647; I
 A:Experimental source: isolate Tuscon
 C:Genetics:
 A:Note: MSV005

Query Match 55.0%; Score 44; DB 2; Length 246;
 Best Local Similarity 83.3%; Pred. No. 30;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YYTCFW 7
 :|:||||
 Db 224 YYTCYW 229

RESULT 4

JN0302
 hypothetical 237 protein (paba 5' region) - rye chloroplast (fragment)
 C:Species: chloroplast Secale cereale (rye)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 11-Jan-2000
 C:Accession: JN0302
 R:Koloso, V.L.; Zolotarev, A.S.
 Bioorg. Khim. 16, 1060-1068, 1990
 A:Title: Rye photosystem II: cloning and sequencing fragments of chloroplast DNA compris
 A:Reference number: JN0300; MUID:91136592; PMID:2285424

A:Accession: JN0302
 A:Molecule type: DNA
 A:Residues: 1-237 <KOL>
 A:Cross-references: UNIPARC:UPI0000017918C
 C:Genetics:

A:Genome: chloroplast
 C:Superfamily: barley chloroplast maturase matK
 C:Keywords: chloroplast

Query Match 53.8%; Score 43; DB 2; Length 237;
 Best Local Similarity 83.3%; Pred. No. 40;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YYCFW 7
|:|:|
Db 37 YYCFW 42

RESULT 5

S35716
glycine-rich protein (clone DC 9.1), embryonic - carrot
C;Species: Daucus carota (carrot)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: S35716
R;Alcith, F.; Richter, G.
Planta 183, 17-24, 1990
A;Title: Gene expression during induction of somatic embryogenesis in carrot cell suspension
A;Reference number: S35714
A;Accession: S35716
A;Molecule type: mRNA
A;Residues: 1-144 <ALE>
A;Cross-references: UNIPROT:P37703; UNIPARC:UPI000012BB0C
C;Superfamily: Arabidopsis glycine-rich protein 3
C;Keywords: embryo; transmembrane protein
F;5-25/Domain: transmembrane #status predicted <TMM>
F;37-107/Region: 6-residue repeat

Query Match 52.5%; Score 42; DB 2; Length 144;
Best Local Similarity 45.5%; Pred. No. 38;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CYYCFWKTCT 11
|:|:|:|
Db 116 CYYCHGRCCS 126

RESULT 6

S04069
glycine-rich protein - red goosefoot
C;Species: Chenopodium rubrum (red goosefoot)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S04069
R;Kaldenhoff, R.; Richter, G.
Nucleic Acids Res. 17, 2853, 1989
A;Title: Sequence of cDNA for a novel light-induced glycine-rich protein.
A;Reference number: S04069; MUID:89240041; PMID:2717413
A;Accession: S04069
A;Molecule type: mRNA
A;Residues: 1-144 <KAL>
A;Cross-references: UNIPROT:P11898; UNIPARC:UPI000012BAFB; EMBL:X14067; NID:G18147; PIDN
A;Note: the authors translated the codon ATC for residue 5 as Asn
C;Superfamily: Arabidopsis glycine-rich protein 3
C;Keywords: transmembrane protein

Query Match 52.5%; Score 42; DB 2; Length 144;
Best Local Similarity 45.5%; Pred. No. 38;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CYYCFWKTCT 11
|:|:|:|
Db 116 CYYCHGRCCS 126

RESULT 7

H96707
probable receptor kinase T2E12.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C;Accession: H96707
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96707
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-670 <STO>
A;Cross-references: UNIPROT:Q9M9C5; UNIPARC:UPI0000048421; GB:A8005173; NID:G6714351; PIDN
C;Genetics:
A;Gene: T2E12.5
A;Map position: 1
C;Superfamily: Receptor-like protein kinase

Query Match 52.5%; Score 42; DB 2; Length 670;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWK 8
|:|:|:|
Db 296 YYCFWR 301

RESULT 8

A36368
transcription factor CBF, CCAAT-binding - human
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: A36368
R;Lum, L.S.Y.; Sultzman, L.A.; Kaufman, R.J.; Linzer, D.I.H.; Wu, B.J.
Mol. Cell. Biol. 10, 6709-6717, 1990
A;Title: A cloned human CCAAT-box-binding factor stimulates transcription from the human
A;Reference number: A36368; MUID:91061780; PMID:2247079
A;Accession: A36368
A;Molecule type: mRNA
A;Residues: 1-998 <LUM>
A;Cross-references: UNIPROT:Q03701; UNIPARC:UPI0000127180; GB:M37197; NID:G179968; PIDN
C;Genetics:
A;Gene: GDB:CEBPA; CEBP
A;Cross-references: GDB:128839; OMIM:116897
A;Map position: 19q13.1-19q13.1

Query Match 52.5%; Score 42; DB 2; Length 998;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWTC 10
|:|:|:|
Db 465 YFCFFTC 472

RESULT 9

A35349
H+-transporting ATP synthase protein 6 homolog - Trypanosoma brucei mitochondrion
C;Species: mitochondrion Trypanosoma brucei
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 07-Dec-1999
C;Accession: A35349
R;Bhat, G.J.; Koslowsky, D.J.; Feagin, J.E.; Smiley, B.L.; Stuart, K.
Cell 61, 885-894, 1990
A;Title: An extensively edited mitochondrial transcript in kinetoplastids encodes a protein
A;Reference number: A35349; MUID:90263114; PMID:2140530
A;Accession: A35349
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-214 <BHA>
A;Cross-references: UNIPARC:UPI000017B5A6
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC6
C;Keywords: mitochondrion

Query Match 51.2%; Score 41; DB 2; Length 214;

Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYYICFW 7
| | | | |
Db 17 CMYICVW 23

RESULT 10
A:Accession: A49677
endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana
N:Alternate names: 26K endoplasmic reticulum retention receptor
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A:Accession: A49677
R:Lee, H.I.; Gal, S.; Newman, T.C.; Raikhel, N.V.
Proc. Natl. Acad. Sci. U.S.A. 90, 11433-11437, 1993
A:Title: The Arabidopsis endoplasmic reticulum retention receptor functions in yeast.
A:Reference number: A49677; MUID:94068617; PMID:8248265
A:Contents: ecotype Columbia
A:Accession: A49677
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-215 <LSE>
A:Cross-references: UNIPROT:P35402; UNIPARC:UPI000000117D
A:Note: sequence extracted from NCBI backbone (NCBIP:140528)
C:Function:
A:Description: achieves retention of proteins specific to the lumen of the endoplasmic r
usually KDEL in animal cells and HDEL in budding yeasts
C:Superfamily: KDEL receptor
C:Keywords: Golgi apparatus; protein trafficking; sorting signal recognition; transmembr

Query Match 51.2%; Score 41; DB 2; Length 215;
Best Local Similarity 70.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YYICFWKTC 11
| | | | |
Db 200 YYISWKNT 209

RESULT 11
T21586
hypothetical protein F31B9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T21586
R:Steward, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: 219445
A:Accession: T21586
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-399 <WLI>
A:Cross-references: UNIPROT:O62189; UNIPARC:UPI000007522C; EMBL:281520; PIDN:CAB04223.1;
A:Experimental source: clone F31B9
C:Genetics:
A:Gene: CESP:F31B9.1
A:Map position: X
A:Introns: 151/3; 176/3; 218/2; 263/3; 293/1; 322/2
C:Superfamily: neurokinin 1 receptor

Query Match 51.2%; Score 41; DB 2; Length 399;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYICFWK 8
| | | | |
Db 206 YFCFWK 211

RESULT 12
G96816

hypothetical protein F9K20.19 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A:Accession: G96816
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Matti, R.; Marzfall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G96816
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-521 <STO>
A:Cross-references: UNIPROT:Q9ZV95; UNIPARC:UPI000009C868; GB:AE005173; NID:g3834317; PI
C:Genetics:
A:Gene: F9K20.19
A:Map position: 1

Query Match 51.2%; Score 41; DB 2; Length 521;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYYICFWK 8
| | | | |
Db 295 CYYICWK 302

RESULT 13
T00602
hypothetical protein Atg202620 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T8K22.8
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
A:Accession: T00602; G84438
R:Roundley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence.
A:Reference number: Z14192
A:Accession: T00602
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-635 <ROU>
A:Cross-references: UNIPROT:O64715; UNIPARC:UPI00000A3670; EMBL:AC004136; NID:g3184270; I
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; I
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.
euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84438
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-635 <STO>
A:Cross-references: UNIPARC:UPI00000A3670; GB:AE002093; NID:g3184278; PIDN:AAC18925.1; G
C:Genetics:
A:Gene: T8K22.8; Atg202620
A:Map position: 2
A:Introns: 18/3

Query Match 51.2%; Score 41; DB 2; Length 635;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 CYYICFWKTC 10
| | | | |
Db 136 CYYICV--TC 143

RESULT 14

A54895
mucin 2, intestinal/tracheal - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 31-Dec-2004
C/Accession: A54895
J. Ohmori, H.; Dohman, A.F.; Gallup, M.; Tsuda, T.; Kai, H.; Gum Jr., J.R.; Kim, Y.S.; H
J. Biol. Chem. 269, 17833-17840, 1994
A/Title: Molecular cloning of the amino-terminal region of a rat MUC 2 mucin gene homolog
A/Reference number: A54895; MUID:94299489; PMID:8027037
A/Accession: A54895
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1513 <OHM>
A/Cross-references: UNIPARC:Q62635; UNIPARC:UPI0000012P8D0; GB:U07615
C/Superfamily: von Willebrand factor type C repeat homology
C/Keywords: intestine

Query Match 51.2%; Score 41; DB 2; Length 1513;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKC 10

Db 1234 FCYWC 1240

RESULT 15

S58014
probable olfactory receptor tpr120 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S58014
R/Vanderhaeghe, P.; Schurmans, S.; Vassart, G.; Parmentier, M.
submitted to the EMBL Data Library, July 1995
A/Description: Male germ cells from several mammalian species express a specific receptor
A/Reference number: S57995
A/Accession: S58014
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-157 <VAN>
A/Cross-references: UNIPROT:Q15614; UNIPARC:UPI0000041D67; EMBL:X89669; NID:G902321; PIN
C/Superfamily: olfactory receptor OR14

Query Match 50.0%; Score 40; DB 2; Length 157;
Best Local Similarity 62.5%; Pred. No. 76;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YYCFCWKT 9

Db 13 YHHCFWLT 20

RESULT 16

JQ1301
hemorrhagic proteinase (EC 3.4.24.-) / rhodostomin precursor - Malayan pit viper
N/Alternate names: kistrin precursor; rhodostomin precursor
N/Contains: hemorrhagic proteinase (EC 3.4.24.-); platelet aggregation inhibitor (disint
C/Species: Calloselasma rhodostoma (Malayan pit viper)
C/Date: 31-Mar-1992 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: S33792; JQ1301; A37480; A61579; B35982; S68308; S33726
R/Au, L.C.; Chou, J.S.; Chang, K.J.; Teh, G.W.; Lin, S.B.
Biochim. Biophys. Acta 1173, 243-245, 1993
A/Title: Nucleotide sequence of a full-length cDNA encoding a common precursor of plate
A/Reference number: S33792; MUID:93277962; PMID:7916635
A/Accession: S33792
A/Molecule type: mRNA
A/Residues: 1-478 <AVA>
A/Cross-references: UNIPROT:P30403; UNIPARC:UPI0000012941F; GB:L08780; GB:W75916; NID:930
R/Au, L.C.; Huang, Y.B.; Huang, T.F.; Teh, G.W.; Lin, H.H.; Choo, K.B.
Biochem. Biophys. Res. Commun. 181, 585-593, 1991

A/Title: A common precursor for a putative hemorrhagic protein and rhodostomin, a platelet
A/Reference number: JQ1301; MUID:92095959; PMID:1755841
A/Contents: venom gland
A/Accession: JQ1301
A/Molecule type: mRNA
A/Residues: 77-478 <AUL>
A/Cross-references: UNIPARC:UPI0000175DB5; GB:W75916
A/Experimental source: venom gland
R/Ponnudurai, G.; Chung, M.C.M.; Tan, N.H.
Toxicol 31, 997-1005, 1993
A/Title: Isolation and characterization of a hemorrhagin from the venom of Calloselasma
A/Reference number: A37480; MUID:94024951; PMID:8212052
A/Accession: A37480
A/Molecule type: protein
A/Residues: 189-201, 'X', '203-209 <PON>
A/Cross-references: UNIPARC:UPI0000175DB6
A/Note: this sequence was derived from the amino end of a 34K form designated rhodostoxin
R/Bando, E.; Nikai, T.; Sugihara, H.
Int. J. Biochem. 23, 1193-1199, 1991
A/Title: Hemorrhagic protease from the venom of Calloselasma rhodostoma.
A/Reference number: A61579; MUID:92175156; PMID:1794444
A/Accession: A61579
A/Molecule type: protein
A/Residues: 189, 'L', '191-200, 'XX', '203-204, 'Y', '206, 'X', '208 <BAN>
A/Cross-references: UNIPARC:UPI0000175DB7
R/Dennis, M.S.; Hensel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Deisher, T.A.; Bur
Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990
A/Title: Platelet glycoprotein IIB-IIIa protein antagonists from snake venoms: evidence f
A/Reference number: A35982; MUID:90207217; PMID:2320569
A/Accession: B35982
A/Molecule type: protein
A/Residues: 408-475 <DEN>
A/Cross-references: UNIPARC:UPI00001133F8
R/Chung, M.C.M.; Ponnudurai, G.; Kataoka, M.; Shimizu, S.; Tan, N.H.
Arch. Biochem. Biophys. 325, 199-208, 1996
A/Title: Structural studies of a major hemorrhagin (rhodostoxin) from the venom of Callor
A/Reference number: S68308; MUID:96139300; PMID:8561498
A/Accession: S68308
A/Molecule type: protein
A/Residues: 189-286, 'T', '288-391 <CHU>
A/Cross-references: UNIPARC:UPI0000175DB8
C/Comment: Rhodostomin (kistrin) is a human platelet aggregation inhibitor.
C/Superfamily: trigramin precursor; disintegrin homology
C/Keywords: anticoagulant; glycoprotein; hydrolase; metalloproteinase; venom; zinc
F/1-18/Domain: signal sequence #status predicted <SIG>
F/19-188/Domain: propeptide #status predicted <PRO>
F/189-391/Product: hemorrhagic proteinase #status predicted <HEM>
F/396-474/Domain: disintegrin homology <DIS>
F/408-475/Product: rhodostomin (kistrin) #status experimental <RHO>
F/456-458/Region: cell attachment (R-G-D) motif
F/207-248, 305-386/Disulfide bonds: #status experimental
F/279, 369/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/330, 334, 340/Binding site: zinc (His) #status predicted
F/331/Active site: Glu #status predicted
F/345-386, 347-353/Disulfide bonds: #status predicted

Query Match 50.0%; Score 40; DB 2; Length 478;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYYCFCWK 8

Db 370 CSYYQFCWK 377

RESULT 17

Q1AD52
early E1B 55K protein 1 - human adenovirus 2
C/Species: Mastadenovirus h2 (human adenovirus 2)
A/Note: host Homo sapiens (man)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: B03809; A03809
R/Gingerae, T.R.; Sciaky, D.; Gelinae, R.E.; Bing-Dong, J.; Yen, C.E.; Kelly, M.M.; Bull

probable membrane protein YCR001w - yeast (Saccharomyces cerevisiae)
 N;Alternate names: protein 21
 C;Species: Saccharomyces cerevisiae
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: S19430; S20186
 R;van der Aart, Q.J.M.; Steensma, H.Y.
 submitted to the Protein Sequence Database, March 1992
 A;Reference number: S19400
 A;Accession: S19430
 A;Molecule type: DNA
 A;Residues: 1-104 <AAR>
 A;Cross-references: UNIPROT:P25347; UNIPARC:UPI000013A6F4; EMBL:X59720; NID:gl1907116; PI
 R;Steensma, H.Y.; van der Aart, Q.J.M.
 Yeast 7, 425-429, 1991
 A;Title: Sequence of the CDC10 region at chromosome III of Saccharomyces cerevisiae.
 A;Reference number: S20186; MUID:91335898; PMID:1872033
 A;Accession: S20186
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-104 <STE>
 A;Cross-references: UNIPARC:UPI000013A6F4; EMBL:S48552; NID:G233477; PIDN:AAD13855.1; PI
 C;Genetics:
 A;Cross-references: SGD:S0000594
 A;Map position: 3R
 C;Superfamily: Saccharomyces cerevisiae probable membrane protein YCR001w
 C;Keywords: transmembrane protein
 F;70-86/Domain: transmembrane #status predicted <TM>
 Query Match 48.8%; Score 39; DB 2; Length 104;
 Best Local Similarity 62.5%; Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 YYCFWKTC 10
 :|||
 Db 26 FYCFWKLC 33
 :|||
 RESULT 23
 S70222
 hypothetical protein YDR271c - yeast (Saccharomyces cerevisiae)
 C;Species: Saccharomyces cerevisiae
 C;Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C;Accession: S70222
 R;Le, T.
 submitted to the EMBL Data Library, May 1996
 A;Description: The sequence of S. cerevisiae cosmid 9954.
 A;Reference number: S70124
 A;Accession: S70222
 A;Molecule type: DNA
 A;Residues: 1-123 <LET>
 A;Cross-references: UNIPROT:P87282; UNIPARC:UPI000006BB75; EMBL:U51030; NID:gl1332633; PI
 C;Genetics:
 A;Gene: MIPS:YDR271c
 A;Cross-references: SGD:S0002679
 A;Map position: 4R
 C;Superfamily: Saccharomyces hypothetical protein YDR271c
 Query Match 48.8%; Score 39; DB 2; Length 123;
 Best Local Similarity 50.0%; Pred. No. 87;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 YYCFWKTC 11
 :|||
 Db 5 YYCYKSKS 14
 :|||
 RESULT 24
 C87585
 hypothetical protein CC2714 [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: C87585
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: C87585
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-212 <STO>
 A;Cross-references: UNIPROT:Q9A4W1; UNIPARC:UPI00000C7801; GB:AB005673; NID:gl13424303; P
 C;Genetics:
 A;Gene: CC2714
 Query Match 48.8%; Score 39; DB 2; Length 212;
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 CFWKTC 11
 :|||
 Db 202 CFWRSCS 208
 :|||
 RESULT 25
 AG1214
 methylases homolog lmo119 [imported] - *Listeria monocytogenes* (strain EGD-e)
 C;Species: *Listeria monocytogenes*
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
 C;Accession: AG1214
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, P.; Berche, P.; Bloecker
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
 D.; Jones, L.N.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A;Title: Comparative genomics of *Listeria species*.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AG1214
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-285 <GLA>
 A;Cross-references: UNIPROT:Q8Y800; UNIPARC:UPI0000055118; GB:NC_003210; PIDN:CAC99197.1
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: lmo119
 C;Superfamily: modification methylase (adenine-specific), M.EcoRV type
 Query Match 48.8%; Score 39; DB 2; Length 285;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YCFWKT 9
 :|||
 Db 64 YCFWKS 69
 :|||
 RESULT 26
 A46355
 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) - *Chlorella virus*
 N;Alternate names: cytosine-specific DNA methylase; cytosine-specific DNA methyltransferase
 C;Species: *Chlorella virus* IL-3A
 C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 31-Dec-2004
 C;Accession: A46355
 R;Shields, S.L.; Burbank, D.E.; Grabherr, R.; van Etten, J.L.
 Virology 176, 16-24, 1990
 A;Title: Cloning and sequencing the cytosine methyltransferase gene M.CviJI from *Chlorella*
 A;Reference number: A46355; MUID:90232725; PMID:2158687
 A;Accession: A46355
 A;Molecule type: DNA
 A;Residues: 1-367 <GHI>
 A;Cross-references: UNIPROT:P36216; UNIPARC:UPI000012F77F; GB:M27265; NID:g323314; PIDN:
 C;Superfamily: modification methylase (cytosine-specific), M.EcoRII type
 C;Keywords: methyltransferase; restriction modification system; S-adenosylmethionine
 F;73/Active site: Cys #status predicted

Query Match 48.8%; Score 39; DB 1; Length 367;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YYCFWKC 10
 | : | : | : |
 Db 134 YFCRWVTC 141

RESULT 27
 T18185
 probable site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) - Chlorella
 C;Species: Chlorella virus PBCV-1
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
 C;Accession: T18185
 R;Graves, M.V.; Van Etten, J.L.
 submitted to the EMBL Data Library, May 1999
 A;Reference number: Z18806
 A;Accession: T18185
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-367 <GRA>
 A;Cross-references: UNIPROT:O41165; UNIPARC:UPI00000F3484; EMBL:U42580; NID:G4028896; P1
 A;Experimental source: specific host Chlorella strain NC64A
 C;Genetics:
 A;Notes: A683L
 C;Superfamily: modification methylase (cytosine-specific), M.EcoRII type
 C;Keywords: methyltransferase; restriction modification system; S-adenosylmethionine

Query Match 48.8%; Score 39; DB 2; Length 367;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YYCFWKC 10
 | : | : | : |
 Db 134 YFCRWVTC 141

RESULT 28
 T38012
 longevity-assurance protein 1 - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T38012
 R;Churcher, C.W.
 submitted to the EMBL Data Library, September 1997
 A;Reference number: Z21761
 A;Accession: T38012
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-390 <CHU>
 A;Cross-references: UNIPROT:P78970; UNIPARC:UPI000012E1PA; EMBL:Z99258; PIDN:CAB16359.1
 A;Experimental source: strain 972h-; cosmid c1A6
 C;Genetics:
 A;Gene: lag1; SPDB:SPAC1A6.09c
 A;Map position: 1

Query Match 48.8%; Score 39; DB 2; Length 390;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YYCFW 7
 | : | : | : |
 Db 164 YYLCFW 169

RESULT 29
 T37888
 hypothetical protein SPAC1805.03c - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T37888

R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, September 1999
 A;Reference number: Z21752
 A;Accession: T37888
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-407 <RIE>
 A;Cross-references: UNIPROT:Q9UTH1; UNIPARC:UPI000006AA2F; EMBL:AL117390; PIDN:CAB55844.1
 A;Experimental source: strain 972h-; cosmid c1805
 C;Genetics:
 A;Gene: SPDB:SPAC1805.03c
 A;Map position: 1
 A;Introns: 32/2; 148/2; 160/3

Query Match 48.8%; Score 39; DB 2; Length 407;
 Best Local Similarity 44.4%; Pred. No. 2.1e+02;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYYCFWKT 9
 | : | : | : |
 Db 293 CHHCRTWT 301

RESULT 30
 T10541
 cyclic nucleotide gated channel homolog F313.30 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
 C;Accession: T10541
 R;Bavan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Voickaert, G.; Bai
 submitted to the Protein Sequence Database, June 1999
 A;Reference number: Z17080
 A;Accession: T10541
 A;Molecule type: DNA
 A;Residues: 1-698 <BEV>
 A;Cross-references: UNIPARC:UPI000017AF4E; EMBL:AL080237; GSPDB:GN00062; ATSP:F313.30
 A;Experimental source: cultivar Columbia; BAC clone F313
 C;Genetics:
 A;Gene: ATSP:F313.30
 A;Map position: 4
 A;Introns: 30/1; 186/3; 357/2; 394/3; 473/3; 605/2

Query Match 48.8%; Score 39; DB 2; Length 698;
 Best Local Similarity 66.7%; Pred. No. 3.1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YYCFW 7
 | : | : | : |
 Db 345 PFYCFW 350

RESULT 31
 F86143
 hypothetical protein F6F3.13 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: F86143
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: F86143
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-706 <STO>
 A;Cross-references: UNIPROT:Q9LNJ0; UNIPARC:UPI00000A02DE; GB:AE005172; NID:g9665147; PI

C;Genetics:
A;Map position: 1

Query Match 48.8%; Score 39; DB 2; Length 706;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YYICFW 7
:|||||
Db 337 FFYCFW 342

RESULT 32

T51354

cyclic nucleotide-regulated ion channel 1 [validated] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
A;Accession: T51354
R;Kohler, C.; Neuhaus, G.
Plant Physiol. 116, 1604, 1998
A;Title: Cloning and partial characterization of two putative cyclic nucleotide-regulated ion channels from Arabidopsis thaliana
A;Reference number: Z25380
A;Accession: T51354
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-716 <KOH>
A;Cross-references: UNIPROT:O65717; UNIPARC:UPI0000048CSD; EMBL:Y16327; PIDN:CAA76178.1
A;Experimental source: cultivar Columbia; whole plant; 14 day old seedlings
C;Genetics:
A;Gene: cngcl
A;Function:
A;Description: can partly complement the K(+) uptake-deficient yeast mutant CY162 [valid]

Query Match 48.8%; Score 39; DB 2; Length 716;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YYICFW 7
:|||||
Db 355 FFYCFW 360

RESULT 33

G84902

hypothetical protein At2g46430 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84902
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-718 <STO>
A;Cross-references: UNIPROT:Q9SKD7; UNIPARC:UPI000004866C; GB:AE002093; NID:G4559385; PID:G4559385

Query Match 48.8%; Score 39; DB 2; Length 718;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YYICFW 7
:|||||
Db 358 FFYCFW 363

RESULT 34

S65938

nitrate reductase [NAD(P)H] (EC 1.7.1.2) - yeast (Pichia angusta)
N;Alternate names: assimilatory nitrate reductase
C;Species: Pichia angusta

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A;Accession: S65938; T43157
R;Avila, J.; Perez, M.D.; Brito, N.; Gonzalez, C.; Siverio, J.M.
FEBS Lett. 366, 137-142, 1995

A;Title: Cloning and disruption of the YNR1 gene encoding the nitrate reductase apoenzyme
A;Reference number: S65938; MUID:95309418; PMID:7789531
A;Accession: S65938
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-859 <AVI>

A;Cross-references: UNIPROT:P49050; UNIPARC:UPI000000094B; EMBL:Z49110; NID:G902625; PID:R;Siverio, J.M.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z22318
A;Accession: T43157
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-859 <SIV>
A;Cross-references: UNIPARC:UPI000000094B; EMBL:AJ223294; PIDN:CAA11232.1
C;Genetics:
A;Gene: YNR1

C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C;Keywords: heme; iron; metalloprotein; molybdenum; molybdopterin; NADP; oxidoreductase;
F;30-432/Domain: molybdopterin-binding domain homology <PCO>
F;504-577/Domain: cytochrome b5 core homology <CBS>
F;609-859/Domain: cytochrome-b5 reductase homology <CBR>
F;137/Binding site: molybdopterin (Cys) (covalent) #status predicted
F;538,561/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 48.8%; Score 39; DB 1; Length 859;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYYICFWK 8
:|||||
Db 381 CLCFCFWK 388

RESULT 35

S52857

nitrate reductase (NADH) (EC 1.7.1.1) - Beauveria bassiana

C;Species: Beauveria bassiana
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S52857
R;Maurer, P.
submitted to the EMBL Data Library, February 1995
A;Reference number: S52857
A;Accession: S52857
A;Molecule type: DNA
A;Residues: 1-894 <HAU>
A;Cross-references: UNIPROT:P43100; UNIPARC:UPI000013005F; EMBL:X84950; NID:G693925; PID:G693925

A;Genetics:

A;Introns: 593/1

C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C;Keywords: heme; iron; metalloprotein; molybdenum; molybdopterin; oxidoreductase; phospho
F;62-467/Domain: molybdopterin-binding domain homology <PCO>
F;535-609/Domain: cytochrome b5 core homology <CBS>
F;645-894/Domain: cytochrome-b5 reductase homology <CBR>
F;169/Binding site: molybdopterin (Cys) (covalent) #status predicted
F;570,593/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 48.8%; Score 39; DB 2; Length 894;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYYICFWK 8
:|||||
Db 416 CFCFCFWK 423

```

RESULT 36
T21267
hypochemical protein F22E10.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
C/Accession: T21267
R/Gardner, A.
submitted to the EMBL Data Library, November 1995
A/Reference number: Z19398
A/Accession: T21267
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1291 <WIL>
A/Cross-references: UNIPROT:Q19734; UNIPARC:UPI000007DFD5; EMBL:Z67882; PIDN:CAA91800.1;
A/Experimental source: clone F22E10
C/Genetics:
A/Gene: CRGP:F22E10.2
A/Map position: X
A/Introns: 19/3; 63/2; 81/3; 114/2; 156/3; 201/2; 258/3; 354/1; 642/2; 724/1; 791/3; 912/3
Query Match 48.8%; Score 39; DB 2; Length 1291;
Best Local Similarity 45.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CYVYCFWKTC 11
Db 155 CQYMCQFQVCS 165

RESULT 37
T00368
hypochemical protein KIAA0663 - human
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C/Accession: T00368
R/Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 169-176, 1998
A/Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A/Reference number: Z14142; MUID:98403880; PMID:9734811
A/Accession: T00368
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-810 <ISH>
A/Cross-references: UNIPROT:O75152; UNIPARC:UPI000006F3FD; EMBL:AB014563; NID:G3327139;
A/Experimental source: brain
C/Genetics:
A/Note: KIAA0663
Query Match 48.1%; Score 38.5; DB 2; Length 810;
Best Local Similarity 54.5%; Pred. No. 4e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
Qy 1 CYVYCFWKTC 11
Db 8 CYFP-FYSTCT 17

RESULT 38
UOQMG2
urotensin II - long-jawed mudsucker
C/Species: Gillichthys mirabilis (long-jawed mudsucker)
C/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C/Accession: A01409
R/Pearson, D.; Shively, J.E.; Clark, B.R.; Geschwind, I.I.; Barkley, M.; Nishioka, R.; B
Proc. Natl. Acad. Sci. U.S.A. 77, 5021-5024, 1980
A/Title: Urotensin II: a somatostatin-like peptide in the caudal neurosecretory system c
A/Reference number: A01409; MUID:81054904; PMID:6107911
A/Accession: A01409
A/Molecule type: protein
A/Residues: 1-12 <PEA>
A/Cross-references: UNIPROT:P01147; UNIPARC:UPI0000035102
A/Note: the proposed sequence was confirmed by synthesis of a peptide with the same stru

C/Comment: Urotensin II is found in the teleost caudal neurosecretory system and is invo
C/Superfamily: urotensin II
C/Keywords: neuropeptide; osmoregulation
F:6-11/Disulfide bonds: #status experimental
Query Match 47.5%; Score 38; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CFWKTC 10
Db 6 CFWKYC 11

RESULT 39
JS0423
urotensin II-A peptide - white sucker
C/Species: Catostomus commersoni (white sucker)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: JS0423
R/McMaster, D.; Lederis, K.
Peptides 4, 367-373, 1983
A/Title: Isolation and amino acid sequence of two urotensin II peptides from Catostomus
A/Reference number: JS0423; MUID:84041959; PMID:6138758
A/Accession: JS0423
A/Molecule type: protein
A/Residues: 1-12 <MCM>
A/Cross-references: UNIPROT:P04558; UNIPARC:UPI0000137D4F
C/Comment: This peptide has smooth muscle-stimulating activity.
C/Superfamily: urotensin II
F:6-11/Disulfide bonds: #status experimental
Query Match 47.5%; Score 38; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CFWKTC 10
Db 6 CFWKYC 11

RESULT 40
S42765
urotensin II - teleostean fish
C/Species: teleostean fish
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
R/Bhaskaran, R.; Arunkumar, A.I.; Yu, C.
Biochim. Biophys. Acta 1199, 115-122, 1994
A/Title: NMR and dynamical simulated annealing studies on the solution conformation of u
A/Reference number: S42765; MUID:94169160; PMID:8123660
A/Accession: S42765
A/Molecule type: protein
A/Residues: 1-12 <BHA>
A/Cross-references: UNIPROT:P01147; UNIPARC:UPI0000035102
C/Superfamily: urotensin II
C/Keywords: neuropeptide; osmoregulation
F:6-11/Product: urotensin II #status experimental <MAT>
Query Match 47.5%; Score 38; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CFWKTC 10
Db 6 CFWKYC 11

RESULT 41
JS0424
urotensin II-B peptide - white sucker
C/Species: Catostomus commersoni (white sucker)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

```

C;Accession: JS0424
R;McMaster, D.; Lederis, K.
Peptides 4, 367-373, 1983
A;Title: Isolation and amino acid sequence of two urotensin II peptides from Catostomus
A;Reference number: JS0423; MUID:84041959; PMID:6138758
A;Accession: JS0424
A;Molecule type: protein
A;Residues: 1-12 <MC>
A;Cross-references: UNIPROT:P04559; UNIPARC:UPI0000137D51
C;Comment: This peptide has smooth muscle-stimulating activity.
F;6-11/Disulfide bonds: #status experimental

Query Match 47.5%; Score 38; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
Db 6 CFWKYC 11

RESULT 42
PQ0445
urotensin II - laughing frog
C;Species: Rana ridibunda (laughing frog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-1995
C;Accession: PQ0445
R;Conlon, J.M.; O'Harte, F.; Smith, D.D.; Tonon, M.C.; Vaudry, H.
Biochem. Biophys. Res. Commun. 188, 578-583, 1992
A;Title: Isolation and primary structure of urotensin II from the brain of a tetrapod, t
A;Reference number: PQ0445; MUID:93075134; PMID:1445302
A;Accession: PQ0445
A;Molecule type: protein
A;Residues: 1-13 <CON>
A;Cross-references: UNIPARC:UPI0000035103
A;Experimental source: brain
C;Superfamily: urotensin II

Query Match 47.5%; Score 38; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
Db 7 CFWKYC 12

RESULT 43
NTSR1C
neurotoxin 1 - bark scorpion (tentative sequence)
C;Species: Centruroides sculpturatus (bark scorpion)
C;Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 09-Jul-2004
C;Accession: A01752
R;Babin, D.R.; Watt, D.D.; Goos, S.M.; Mlejnek, R.V.
Arch. Biochem. Biophys. 164, 694-706, 1974
A;Title: Amino acid sequences of neurotoxic protein variants from the venom of Centruroid
A;Reference number: A90058; MUID:75163395; PMID:4460885
A;Accession: A01752
A;Molecule type: protein
A;Residues: 1-65 <BAB>
A;Cross-references: UNIPROT:P01492; UNIPARC:UPI00001735F2
C;Superfamily: scorpion neurotoxin
C;Keywords: neurotoxin; venom
F;12-64,16-41,27-46,29-48/Disulfide bonds: #status predicted

Query Match 47.5%; Score 38; DB 1; Length 65;
Best Local Similarity 43.8%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 3; Indels 6; Gaps 1;

Qy 1 CYYCYFW-----KTC 10
Db 12 KYYDCFWLGNKNEHTC 27

C;Accession: JS0424
R;McMaster, D.; Lederis, K.
Peptides 4, 367-373, 1983
A;Title: Isolation and amino acid sequence of two urotensin II peptides from Catostomus
A;Reference number: JS0423; MUID:84041959; PMID:6138758
A;Accession: JS0424
A;Molecule type: protein
A;Residues: 1-12 <MC>
A;Cross-references: UNIPROT:P04559; UNIPARC:UPI0000137D51
C;Comment: This peptide has smooth muscle-stimulating activity.
F;6-11/Disulfide bonds: #status experimental

Query Match 47.5%; Score 38; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
Db 6 CFWKYC 11

RESULT 42
PQ0445
urotensin II - laughing frog
C;Species: Rana ridibunda (laughing frog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-1995
C;Accession: PQ0445
R;Conlon, J.M.; O'Harte, F.; Smith, D.D.; Tonon, M.C.; Vaudry, H.
Biochem. Biophys. Res. Commun. 188, 578-583, 1992
A;Title: Isolation and primary structure of urotensin II from the brain of a tetrapod, t
A;Reference number: PQ0445; MUID:93075134; PMID:1445302
A;Accession: PQ0445
A;Molecule type: protein
A;Residues: 1-13 <CON>
A;Cross-references: UNIPARC:UPI0000035103
A;Experimental source: brain
C;Superfamily: urotensin II

Query Match 47.5%; Score 38; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
Db 7 CFWKYC 12

RESULT 43
NTSR1C
neurotoxin 1 - bark scorpion (tentative sequence)
C;Species: Centruroides sculpturatus (bark scorpion)
C;Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 09-Jul-2004
C;Accession: A01752
R;Babin, D.R.; Watt, D.D.; Goos, S.M.; Mlejnek, R.V.
Arch. Biochem. Biophys. 164, 694-706, 1974
A;Title: Amino acid sequences of neurotoxic protein variants from the venom of Centruroid
A;Reference number: A90058; MUID:75163395; PMID:4460885
A;Accession: A01752
A;Molecule type: protein
A;Residues: 1-65 <BAB>
A;Cross-references: UNIPROT:P01492; UNIPARC:UPI00001735F2
C;Superfamily: scorpion neurotoxin
C;Keywords: neurotoxin; venom
F;12-64,16-41,27-46,29-48/Disulfide bonds: #status predicted

Query Match 47.5%; Score 38; DB 1; Length 65;
Best Local Similarity 43.8%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 3; Indels 6; Gaps 1;

Qy 1 CYYCYFW-----KTC 10
Db 12 KYYDCFWLGNKNEHTC 27

RESULT 44
S10706
urotensin II precursor - European flounder (fragments)
C;Species: Platichthys flesus (European flounder)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: S10706
R;Conlon, J.M.; Arnold-Reed, D.; Balmert, R.J.
FEBS Lett. 266, 37-40, 1990
A;Title: Post-translational processing of prepro-urotensin II.
A;Reference number: S10706; MUID:90306357; PMID:2365069
A;Accession: S10706
A;Molecule type: protein
A;Residues: 1-83 <CON>
A;Cross-references: UNIPROT:P21857; UNIPARC:UPI0000137D56
A;Experimental source: urophys
C;Superfamily: urotensin II
C;Keywords: neuropeptide; osmoregulation
F;1-71/Product: urotensin II #status experimental <MAT>
F;72-83/Domain: carboxyl-terminal propeptide #status experimental <PRO>
F;77-82/Disulfide bonds: #status predicted

Query Match 47.5%; Score 38; DB 2; Length 83;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
Db 77 CFWKYC 82

RESULT 45
I50499
urotensin II-gamma precursor - common carp
C;Species: Cyprinus carpio (common carp)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50499
R;Ohsako, S.; Ishida, I.; Ichikawa, T.; Deguchi, T.
J. Neurosci. 6, 2730-2735, 1986
A;Title: Cloning and sequence analysis of cDNAs encoding precursors of urotensin II-alpha
A;Reference number: I50498; MUID:86307061; PMID:2427672
A;Accession: I50499
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-125 <OHS>
A;Cross-references: UNIPROT:P06580; UNIPARC:UPI0000137D53; GB:M14088; NID:g213068; PIDN:
C;Superfamily: urotensin II

Query Match 47.5%; Score 38; DB 2; Length 125;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
Db 119 CFWKYC 124

RESULT 46
I50498
urotensin II-alpha precursor - common carp
C;Species: Cyprinus carpio (common carp)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50498
R;Ohsako, S.; Ishida, I.; Ichikawa, T.; Deguchi, T.
J. Neurosci. 6, 2730-2735, 1986
A;Title: Cloning and sequence analysis of cDNAs encoding precursors of urotensin II-alpha
A;Reference number: I50498; MUID:86307061; PMID:2427672
A;Accession: I50498
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-125 <OHS>
A;Cross-references: UNIPROT:P04560; UNIPARC:UPI0000137D50; GB:M14084; NID:g213066; PIDN:
C;Superfamily: urotensin II

Query Match 47.5%; Score 38; DB 2; Length 125;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
 |||||
 Db 119 CFWKYC 124

RESULT 47
 T16744
 hypothetical protein R13F6.5 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T16744
 R/Miller, N.
 submitted to the EMBL Data Library, April 1994
 A/Description: The sequence of *C. elegans* cosmid R13F6.
 A/Reference number: Z18570
 A/Accession: T16744
 A/Status: preliminary; translated from GB/EMBL/DBDJ
 A/Molecule type: DNA
 A/Residues: 1-210 <MIL>
 A/Cross-references: UNIPROT:Q21981; UNIPARC:UPI0000802F5; EMBL:U00046; NID:G470358; PID
 A/Experimental source: strain Bristol N2; clone R13F6
 C/Genetics:
 A/Gene: CESP:R13F6.5
 A/Map position: 3
 A/Introns: 77/3; 116/3; 151/3; 177/3

Query Match 47.5%; Score 38; DB 2; Length 210;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YCFWKT 9
 |||||
 Db 146 YDFWKT 152

RESULT 48
 I51323
 proteolipid protein DM alpha - spiny dogfish
 C/Species: *Squalus acanthias* (spiny dogfish)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C/Accession: I51323
 R/Kitagawa, K.; Sinoway, M.P.; Yang, C.; Gould, R.M.; Colman, D.R.
 Neuron 11, 433-448, 1993
 A/Title: A proteolipid protein gene family: expression in sharks and rays and possible e
 A/Reference number: I51323; MUID:94000810; PMID:8398138
 A/Accession: I51323
 A/Status: preliminary; translated from GB/EMBL/DBDJ
 A/Molecule type: mRNA
 A/Residues: 1-245 <KIT>
 A/Cross-references: UNIPROT:P36963; UNIPARC:UPI00001294CD; EMBL:U02973; NID:G409969; PID
 C/Superfamily: myelin proteolipid protein

Query Match 47.5%; Score 38; DB 2; Length 245;
 Best Local Similarity 62.5%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YCFWKT 10
 |||||
 Db 142 YTFWSTC 149

RESULT 49
 S76841
 hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
 C/Species: *Synechocystis* sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 31-Dec-2004
 C/Accession: S76841

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yaeuda
 DNA Res. 3, 109-136, 1996
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
 s.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S76841
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-285 <KAN>
 A/Cross-references: UNIPROT:P74637; UNIPARC:UPI00000C09E2; EMBL:D90917; GB:AB001339; NID
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Superfamily: modification methylase (adenine-specific), M.EcoRV type

Query Match 47.5%; Score 38; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWK 8
 |||||
 Db 83 YCFWK 87

RESULT 50
 T00399
 probable AP2 domain transcription factor [imported] - *Arabidopsis thaliana*
 N/Alternate names: transcription factor TINY homolog T13E15.5
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C/Accession: T00399; F84884
 R/Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masor
 submitted to the EMBL Data Library, July 1997
 A/Description: *Arabidopsis thaliana* chromosome II BAC T13E15 genomic sequence.
 A/Reference number: Z14146
 A/Accession: T00399
 A/Status: translated from GB/EMBL/DBDJ
 A/Molecule type: DNA
 A/Residues: 1-295 <ROU>
 A/Cross-references: UNIPROT:O22158; UNIPARC:UPI00000A8865; EMBL:AC002388; NID:G3420042; I
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A/Reference number: A84420; MUID:20083487; PMID:10617197
 A/Accession: T00399
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-295 <STO>
 A/Cross-references: UNIPARC:UPI00000A8865; GB:AE002093; NID:G4895256; PIDN:AAD32841.1; G
 C/Genetics:
 A/Gene: T13E15.5; Ac2g44940
 A/Map position: 2

Query Match 47.5%; Score 38; DB 2; Length 295;
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CYTCFWKTC 10
 |||||
 Db 270 CYTSSTWQLC 279

Search completed: May 9, 2006, 12:10:22
 Job time : 29.3333 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:05:00 ; Search time 67.3333 Seconds
(without alignments)
115.260 Million cell updates/sec

Title: US-10-796-158-6
Perfect score: 80
Sequence: 1 CYYCFWKTCT 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: uniprot_05.80.*

2: uniprot_sprot.*

3: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	66.2	652	Q4TB21	tetradon n
2	51	63.7	266	Q9SDR9	PRUDU
3	50	62.5	1302	Q22426	CABEL
4	48	60.0	507	Q7MNB7	VIBVY
5	47	58.8	811	ZC11A	PONPY
6	46.5	58.1	682	1	CNG1CTPU
7	45.5	56.9	2994	2	Q81124 PLAF7
8	45	56.2	53	Q4XHO9	PLACH
9	45	56.2	74	Q5K4V4	BARIN
10	45	56.2	189	Q581W3	9TRYP
11	45	56.2	334	2	Q96615_CABEL
12	44	55.0	74	2	Q5K4V7_BARIN
13	44	55.0	96	2	Q96CY8_HUMAN
14	44	55.0	231	2	Q86F16_SCHJA
15	44	55.0	234	2	Q7D3A0_AGR75
16	44	55.0	246	2	Q9YMB7_MSEPV
17	44	55.0	284	2	Q54B88_DICDI
18	44	55.0	384	2	Q54FT1_DICDI
19	44	55.0	393	2	Q61412_CABBR
20	44	55.0	599	2	Q52426_MAGGR
21	43.5	54.4	315	2	Q706P3_PSEPU
22	43	53.8	67	1	B009_MOUSE
23	43	53.8	104	2	Q7PF49_ANOGA
24	43	53.8	231	2	Q95Y29_CABEL
25	43	53.8	231	2	Q4N0N6_THEPA
26	43	53.8	329	2	Q6RUM6_9ROSI
27	43	53.8	395	2	Q61817_CABBR
28	43	53.8	423	2	Q5VH36_9ROSI
29	43	53.8	426	2	Q61L22_DROME
30	43	53.8	427	2	Q9DE40_BRARE
31	43	53.8	428	2	Q5VH38_9ROSI

32	43	53.8	511	1	MATK_PSAJU	Q85z66 peathyrosta
33	43	53.8	511	1	MATK_WHEAT	P58271 triticum ae
34	43	53.8	512	2	Q9MUY6	triticum ae
35	43	53.8	686	2	Q6K6P3	oryza sativ
36	43	53.8	762	2	Q7TOA0	mus musculus
37	43	53.8	773	2	Q7Q8P9	giardia lam
38	43	53.8	1026	2	Q6ZQD0	mus musculus
39	43	53.8	1317	2	Q7TQAI	mus musculus
40	43	53.8	1320	2	Q925N6	rattus norv
41	42.5	53.1	262	1	TRYT_DROER	P54628 drosophila
42	42.5	53.1	262	1	TRYT_DROME	P42278 drosophila
43	42	52.5	74	2	Q5K4X4	barbus inte
44	42	52.5	74	2	Q5K4X8	barbus inte
45	42	52.5	75	2	Q5K4Y2	barbus inte
46	42	52.5	95	2	Q4YX20	plasmodium
47	42	52.5	144	1	GRP1_CHERU	P11898 chenopodium
48	42	52.5	144	1	GRP9_DAUCA	P37703 daucus caro
49	42	52.5	201	2	Q5HZ64	oryza sativ
50	42	52.5	238	2	Q6IEM0	oryza sativ
51	42	52.5	267	2	Q5OY97	entamoeba h
52	42	52.5	280	2	Q5CSK4	cryptospori
53	42	52.5	280	2	Q5CMT5	cryptospori
54	42	52.5	352	2	Q84DD2	uncultured
55	42	52.5	444	2	Q9NXJ6	homo sapien
56	42	52.5	539	2	Q9HCC8	homo sapien
57	42	52.5	670	2	Q9M9C5	arabidopsis
58	42	52.5	671	2	Q94JL9	arabidopsis
59	42	52.5	869	2	Q6MYK4	aspergillus
60	42	52.5	869	2	Q8TGB7	aspergillus
61	42	52.5	869	2	Q4WSG7	aspergillus
62	42	52.5	998	1	CEBEP2	homo sapien
63	42	52.5	1054	2	Q8NE75	homo sapien
64	41.5	51.9	589	2	Q7RHR5	plasmodium
65	41	51.2	58	2	Q4Z7F2	barbus inte
66	41	51.2	74	2	Q5K4W4	barbus inte
67	41	51.2	74	2	Q5K4X5	barbus inte
68	41	51.2	75	2	Q5K4X1	barbus inte
69	41	51.2	88	2	Q7Y7J4	caenorhabdi
70	41	51.2	117	2	Q6G3K0	bartonella
71	41	51.2	129	1	FSHB_CAVPO	Q9Jk69 cavia porce
72	41	51.2	131	2	Q4L922	staphylococ
73	41	51.2	188	2	Q8NHA3	homo sapien
74	41	51.2	215	1	ERD2_ARATH	P35402 arabidopsis
75	41	51.2	235	2	Q70XU1	barbus inte
76	41	51.2	289	2	Q5OYX8	entamoeba h
77	41	51.2	327	2	Q8RCU3	thermoanaer
78	41	51.2	338	2	Q5AYA7	EMENI
79	41	51.2	358	2	Q6GR30	XENJIA
80	41	51.2	370	2	Q7QEG9	ANOGA
81	41	51.2	399	2	Q62189	CABEL
82	41	51.2	419	2	Q4K7T1	PSEF5
83	41	51.2	468	2	Q8I619	HALRO
84	41	51.2	470	2	Q6MMG4	EDEBA
85	41	51.2	521	2	Q9ZV95	ARATH
86	41	51.2	542	2	Q6L5J4	ARATH
87	41	51.2	635	2	Q64715	arabidopsis
88	41	51.2	740	2	Q8H013	oryza sativ
89	41	51.2	814	2	Q5R9U0	PONPY
90	41	51.2	833	2	Q537P7	9VIRU
91	41	51.2	1513	1	MUC3_RAT	Q62635 rattus norv
92	40	50.0	45	2	Q5C7A4	SCHJA
93	40	50.0	74	2	Q5K4W6	BARIN
94	40	50.0	74	2	Q5K4X6	barbus inte
95	40	50.0	74	2	Q5K4X9	barbus inte
96	40	50.0	99	2	Q4X4Y7	PLACH
97	40	50.0	122	2	Q8VEG9	MOUSE
98	40	50.0	157	1	OR8G2	HUMAN
99	40	50.0	163	2	Q55111	DICDI
100	40	50.0	163	2	Q8VB89	WSSV
101	40	50.0	177	2	Q738N9	BACCL
102	40	50.0	178	2	Q4M003	BACCL
103	40	50.0	178	2	Q6HJ36	BACHK
104	40	50.0	178	2	Q81DT7	BACCR

981 36 45.0 411 2 Q4UL45 RICPE Q4UL45 rickettsia
 982 36 45.0 411 2 Q68MH9 RICTV Q68MH9 rickettsia
 983 36 45.0 414 2 Q8NA57 HUMAN Q8NA57 homo sapien
 984 36 45.0 414 2 Q51GM1 ENTHI Q51GM1 entameoba h
 985 36 45.0 415 2 Q6AYU0 RAT Q6AYU0 rattus norv
 986 36 45.0 416 2 Q9LV89 ARATH Q9LV89 arabidopsis
 987 36 45.0 422 2 Q5M1P5 STRT1 Q5M1P5 streptococc
 988 36 45.0 422 2 Q5M686 STRET2 Q5M686 streptococc
 989 36 45.0 423 2 Q6BK22 DEBHA Q6BK22 debaryomyce
 990 36 45.0 423 2 Q4RW07 TETNG Q4RW07 tetradon n
 991 36 45.0 424 2 Q84QU5 ORYSA Q84QU5 oryza sativ
 992 36 45.0 426 2 Q84UM0 ORYSA Q84UM0 oryza sativ
 993 36 45.0 429 2 Q4VD14 9POAL Q4VD14 juncus oxyx
 994 36 45.0 431 2 Q4VD15 9POAL Q4VD15 juncus atyg
 995 36 45.0 437 2 Q413H9 GIBZE Q413H9 gibberella
 996 36 45.0 439 2 Q5Z3Z6 NOCPA Q5Z3Z6 nocardia fa
 997 36 45.0 442 2 Q93311 BRARE Q93311 brachydanio
 998 36 45.0 444 2 Q9ZLL6 HELPJ Q9ZLL6 helicobacte
 999 36 45.0 444 2 Q8JJC0 CHICK Q8JJC0 gallus gall
 1000 36 45.0 445 2 Q9IAT0 BRACHY Q9IAT0 brachydanio

ALIGNMENTS

RESULT 1
 Q4TB21_TETNG
 ID Q4TB21_TETNG PRELIMINARY; PRT; 652 AA.
 AC Q4TB21;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCA7P211, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG0003948001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]

NP NUCLEOTIDE SEQUENCE.
 RA Jallou O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA David C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Bottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Queller P., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Croliis H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype."
 RL Nature 431:946-957(2004).
 RN [2]

NP NUCLEOTIDE SEQUENCE.
 RP Genoscope, Whitehead Institute Centre for Genome Research;
 RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01007211; CAF89911.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 652 AA; 72726 MW; C95DCCFDEC2D8246 CRC64;

Query Match 66.2%; Score 53; DB 2; Length 652;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFWKT 9
 ||:||:|:
 DB 521 CYHYCWRT 529

RESULT 2

Q9SDR9_PRUDU
 ID Q9SDR9_PRUDU PRELIMINARY; PRT; 266 AA.
 AC Q9SDR9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Lecithin-cholesterol acyl transferase (Fragment).
 GN Names=LCAT1;
 OS Prunus dulcis (Almond) (Prunus amygdalus).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=3755;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ma R.C., Oliveira M.M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF209909; AAF22841.1; -; Genomic DNA.
 DR GO; GO:0004607; F:phosphatidylcholine-sterol O-acyltransferase. . .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR InterPro; IPR003386; LACT.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF02450; LACT; 1.
 KW Transferase.
 FT NON TER 1
 SQ SEQUENCE 266 AA; 29613 MW; 057533E294332F37 CRC64;

Query Match 63.7%; Score 51; DB 2; Length 266;
 Best Local Similarity 77.8%; Pred. No. 9.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YYCYCFWKT 10
 ||:||:|:
 DB 165 YYLCFWKC 173

RESULT 3

Q22426_CAEEL
 ID Q22426_CAEEL PRELIMINARY; PRT; 1302 AA.
 AC Q22426;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Twik family of potassium channels protein 2.
 GN Name=twk-2; ORFNames=TI2C9.3;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology".
 RL Science 282:2012-2018(1998).
 DR EMBL; U41104; AAK18976.2; -; Genomic DNA.
 DR EMBL; TI2C9.3; Caenorhabditis elegans.
 DR WormBase; WBGene00006657; twk-2.
 DR WormPep; T12C9.3; CE36894.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0005267; F:potassium channel activity; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR005560; DUF326.

```

DR InterPro; IPR001622; K-channel_pore.
DR Pfam; PF03860; DUF326; 3.
KW Complete proteome; Ionic channel.
SQ SEQUENCE 1302 AA; 148653 MW; DA737D251C81548A CRC64;

Query Match 62.5%; Score 50; DB 2; Length 1302;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YVCFWKTC 11
   :|||
Db 814 FYSPWKTC 822

RESULT 4
ID Q7MNB7 VIBVY PRELIMINARY; PRT; 507 AA.
AC Q7MNB7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VV0800.
OS OrderedLocusNames=VV0800;
GN Vibrio vulnificus (strain VJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chang H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL; BA000037; BAC93584.1; -, Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 507 AA; 58254 MW; PFFCAE282CC756EA CRC64;

Query Match 60.0%; Score 48; DB 2; Length 507;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
   :|||
Db 394 YCFWKSC 400

RESULT 5
ID ZC11A PONPY STANDARD; PRT; 811 AA.
AC Q5REG6;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Zinc finger CCH-type domain containing protein 11A.
GN Name=ZC3H11A;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Pongo.
OX NCBI_TaxID=96600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Kidney;
RG The German cDNA consortium;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 3 C3H1-type zinc fingers.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M83111; -, NOT_ANNOTATED_CDS; Genomic_RNA.
CC PIR; JH0560; JH0560.
CC InterPro; IPR000595; CNMP bd.
CC InterPro; IPR003938; EAG_ELK_ERG.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR001622; K-channel_pore.
CC InterPro; IPR001201; PAP_25A_core.
CC Pfam; PF00027; CNMP_binding; 1.
CC Pfam; PF00520; Ion_trans; 1.
CC PRINTS; PR01463; BAGCHANLFMLY.
CC PROSITE; PS00888; CNMP_BINDING_1; 1.
CC PROSITE; PS00889; CNMP_BINDING_2; 1.
CC PROSITE; PS00042; CNMP_BINDING_3; 1.

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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; CR857563; CAH89841.1; -, mRNA.
CC InterPro; IPR000571; Znf_CCCH.
CC Pfam; PF00642; zf-CCCH; 2.
CC SMART; SM00356; Znf_C3H1; 3.
KW Coiled coil; Metal-binding; Repeat; Zinc; Zinc-finger.
FT ZN_FING 3 29 C3H1-type 1.
FT ZN_FING 32 57 C3H1-type 2.
FT ZN_FING 61 87 C3H1-type 3.
FT COILED 363 424 Potential.
FT COMPTAS 162 169 Poly-Asp.
FT COMPTAS 688 691 Poly-Ser.
SQ SEQUENCE 811 AA; 89320 MW; 75155ADFD9838076 CRC64;

Query Match 58.8%; Score 47; DB 1; Length 811;
Best Local Similarity 54.5%; Pred. No. 11e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYYVCFWKTC 11
   :|||
Db 8 CYVFFVSTCT 18

RESULT 6
CNG ICTPU STANDARD; PRT; 682 AA.
ID CNG ICTPU STANDARD; PRT; 682 AA.
AC P55934;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cyclic-nucleotide-gated cation channel.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=92110008; PubMed=1370374;
RA Goulding E.H., Ngai J., Kramer R.H., Colicos S., Axel R.,
RA Siegelbaum S.A., Chess A.;
RT "Molecular cloning and single-channel properties of the cyclic
RT nucleotide-gated channel from catfish olfactory neurons.";
RL Neuron 8:45-58(1992).
CC -1- FUNCTION: This cyclic nucleotide-gated channel is activated
CC equally well by both cAMP and cGMP.
CC -1- TISSUE SPECIFICITY: Olfactory neurons.
CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M83111; -, NOT_ANNOTATED_CDS; Genomic_RNA.
CC PIR; JH0560; JH0560.
CC InterPro; IPR000595; CNMP bd.
CC InterPro; IPR003938; EAG_ELK_ERG.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR001622; K-channel_pore.
CC InterPro; IPR001201; PAP_25A_core.
CC Pfam; PF00027; CNMP_binding; 1.
CC Pfam; PF00520; Ion_trans; 1.
CC PRINTS; PR01463; BAGCHANLFMLY.
CC PROSITE; PS00888; CNMP_BINDING_1; 1.
CC PROSITE; PS00889; CNMP_BINDING_2; 1.
CC PROSITE; PS00042; CNMP_BINDING_3; 1.

```

KW CAMP; CAMP-binding; cGMP; cGMP-binding; Ion transport; Ionic channel;
 KW Nucleotide-binding; Olfaction; Sensory transduction; Transmembrane;
 KW Transport.
 FT TOPO_DOM 1 136 Cytoplasmic (Potential).
 FT TRANSMEM 137 157 H1 (Potential).
 FT TOPO_DOM 158 169 Extracellular (Potential).
 FT TRANSMEM 170 190 H2 (Potential).
 FT TOPO_DOM 191 218 Cytoplasmic (Potential).
 FT TRANSMEM 219 239 H3 (Potential).
 FT TOPO_DOM 240 272 Extracellular (Potential).
 FT TRANSMEM 273 293 H4 (Potential).
 FT TOPO_DOM 294 311 Cytoplasmic (Potential).
 FT TRANSMEM 312 332 H5 (Potential).
 FT TOPO_DOM 333 343 Extracellular (Potential).
 FT TRANSMEM 344 364 H6 (Potential).
 FT TOPO_DOM 365 682 Cytoplasmic (Potential).
 FT NP_BIND 455 577 CAMP (By similarity).
 FT BINDING 514 514 CAMP (Potential).
 FT BINDING 529 529 CAMP (Potential).
 SQ SEQUENCE 682 AA; 78020 MW; 2C78597DC2C74F75 CRC64;
 Query Match 58.1%; Score 46.5; DB 1; Length 682;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 CYVYCF-WKTCT 11
 Db 316 CYVCFYWSLT 327
 RESULT 7
 ID Q81124 PLAF7 PRELIMINARY; PRT; 2994 AA.
 AC Q81124;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythrocyte membrane protein 1 (pEMP1).
 GN ORFNames=PF1_0008;
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
 RA Gardner M.J., Hall N., Fung E., White O., Herriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
 RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrall B.G.;
 RT "Genome sequence of the human malaria parasite Plasmodium falciparum".
 RL Nature 415:458-511(2002).
 DR EMBL; AB014836; AAN35605.1; -; Genomic_DNA.
 DR GO; GO:0005539; F:glycoaminoglycan binding; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR02048; EF-hand.
 DR InterPro; IPR004258; PPEMP.
 DR Pfam; PF03011; PPEMP; 2.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
 SQ SEQUENCE 2994 AA; 345687 MW; A80E27F713FA9007 CRC64;
 Query Match 56.9%; Score 45.5; DB 2; Length 2994;
 Best Local Similarity 57.1%; Pred. No. 6e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
 Qy 1 CYVY---CFWKTCT 11
 Db 473 CFFYGVKCNWKTCT 486

RESULT 8
 Q4XHQ9 PLACH PRELIMINARY; PRT; 53 AA.
 AC Q4XHQ9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PC401301.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrall B., Turner C.M.K., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01006037; CAH83556.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 53 AA; 6513 MW; 069C2B1BEB7141A4 CRC64;
 Query Match 56.2%; Score 45; DB 2; Length 53;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CYVYCFW 7
 Db 28 CYVYFPW 34
 RESULT 9
 ID Q5K4V4 BARIN PRELIMINARY; PRT; 74 AA.
 AC Q5K4V4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN Name=babr-DAB*0103;
 OS Barbus intermedius (Lake tana barbels).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Barbus.
 OX NCBI_TaxID=40831;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kruiswijk C.P., Hermesen T., Heerwaarden J., Dixon B.,
 RA Savelkoul H.F.J., Stet R.J.M.;
 RT "Major histocompatibility genes in the Lake Tana African large barb species flock: evidence for complete partitioning of class II B, but not class I genes among different species.";
 RL Immunogenetics 56:894-908(2005).
 DR EMBL; AJ506706; CAD4914.1; -; Genomic_DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0045012; P:MHC class II receptor activity; IEA.
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000353; MHC_II_beta_N.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.


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KW MHC II; Transmembrane.
FT NON TER 1 1
PT NON TER 74 74
SQ SEQUENCE 74 AA; 8772 MW; 1D6C63BA9CF6B4F8 CRC64;

Query Match 56.2%; Score 45; DB 2; Length 74;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YYCFWKTC 10
   |||||
Db 3 YYFSWSEC 11

RESULT 10
ID Q581W3_9TRYP PRELIMINARY; PRT; 189 AA.
AC Q581W3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Tb927.8.2190;
OS Trypanosoma brucei.
OC Eukaryota; Ruglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA Shalton J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wanless D., White O., Workman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA El-Sayed N.M., Khalak H., Adams M.D.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Haas B., Blandin G., El-Sayed N.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC091701; AAK79440.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 189 AA; 21870 MW; 379004EF29F037FA CRC64;

Query Match 56.2%; Score 45; DB 2; Length 189;
Best Local Similarity 54.5%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CYYCFWKTC 11
   |:-|:-|:-|
Db 15 CFSFCWKECT 25

RESULT 11
ID Q96615 CAEBL PRELIMINARY; PRT; 334 AA.
AC Q96615;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serpentine receptor, class h protein 33.
GN Name=srh-33; ORFNames=M02H5.9;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peleoderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AC006675; AAK84559.1; -; Genomic_DNA.
DR Ensembl; M02H5.9; Caenorhabditis elegans.
DR WormBase; WBGene0005256; M02H5.9.
DR WormPep; M02H5.9; CE25956.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003003; 7TM chemrecept2.
DR InterPro; IPR000168; Nm7TM_chemrecept.
DR Pfam; PF01604; 7tm_5; 1.
KW Complete proteome; Receptor.
SQ SEQUENCE 334 AA; 38574 MW; 3FB75103857A17CE CRC64;

Query Match 56.2%; Score 45; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YYCFWKTC 10
   |:-|:-|:-|
Db 53 YLHCFWTC 61

RESULT 12
ID Q5K4V7 BARIN PRELIMINARY; PRT; 74 AA.
AC Q5K4V7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=bain-DAB*0105(Rb);
OS Barbus intermedius (Lake tana barbels).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=40831;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=fin;
RA Kruiswijk C.P., Hermesen T., Heerwaarden J., Dixon B.,
RA Savelkoul H.F.J., Stet R.J.M.;
RT "Major histocompatibility genes in the Lake Tana African large barb
RT speciesflock: evidence for complete partitioning of class II B, but
RT not class I genes among different species.";
RL Immunogenetics 56:894-908(2005).
DR EMBL; AJ506733; CAD4941.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON TER 1 1
FT NON TER 74 74
SQ SEQUENCE 74 AA; 8664 MW; 11411EAD18176FB9 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 74;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YYCFWKTC 10
   |||||
Db 3 YYSLWTC 11

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RESULT 13
Q96CV8_HUMAN
ID Q96CV8_HUMAN PRELIMINARY; PRT; 96 AA.
AC Q96CV8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MAX protein, isoform d.
GN Name=MAX;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
TISUS=Brain;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramo R.D., Mullahy S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,
RA Butterfield Y.S.N., Kryzyski M.I., Skalska U., Smail J.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Brain;
RA Director MGC Project;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC013669; AAH13669.1; -; mRNA.
DR HSBP; P61244; IHLO.
DR SMR; Q96CV8; 13-57.
DR Ensembl; ENSG00000125952; Homo sapiens.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006335; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001092; HLH basic.
DR Pfam; PF00010; HLH; 1.
DR PRINTS; PR00044; LEUZIPRMVC.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS50888; HLH; 1.
SQ SEQUENCE 96 AA; 11455 MW; D380F721DCF2D6C8 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 96;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YYCFWKTC 11
|:|:|:|
Db 59 YFLEWKLCT 67

RESULT 14
Q96F16_SCHJA
ID Q96F16_SCHJA PRELIMINARY; PRT; 231 AA.

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AC Q96F16;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Clone ZD120 mRNA sequence.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
RA Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
RA Xue C.L., Feng Z., Chen Z., Han Z.G.;
RT "Evolutionary and biomedical implications of a Schistosoma japonicum
RL Nat. Genet. 35:139-147(2003).
DR EMBL; AY223048; AAP06071.1; -; mRNA.
DR InterPro; IPR002893; Znf.MYND.
DR Pfam; PF01753; zf-MYND; 1.
DR PROSITE; PS01360; ZF_MYND_1; UNKNOWN_1.
DR PROSITE; PS0865; ZF_MYND_2; 1.
SQ SEQUENCE 231 AA; 27255 MW; D629D635C439D0FD CRC64;

Query Match 55.0%; Score 44; DB 2; Length 231;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YYCFWKTC 9
|:|:|:|
Db 82 YYFCWNT 89

RESULT 15
Q7D3A0_AGR75
ID Q7D3A0_AGR75 PRELIMINARY; PRT; 234 AA.
AC Q7D3A0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AGR PAT 516P.
GN OrderedLocustNames=AGR_PAT 516;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OX Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OX Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STAIN=Cereon;
RA MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmieu K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cleo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RL Science 294:2323-2328(2001).
DR EMBL; AB007905; AAK90732.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005293; F:lysine permease activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR001123; LysE.
DR Pfam; PF01810; LysE; 1.
KW Plasmid.
SQ SEQUENCE 234 AA; 25196 MW; C7CB898134263DA7 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 234;
Best Local Similarity 75.0%; Pred. No. 92;

```

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYYCFWK 8
| | | | |
Db 6 CYRYCCWK 13

RESULT 16

ID Q9YWB7 MSBPV PRELIMINARY; PRT; 246 AA.
AC Q9YWB7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein MSV005.
GN Name=MSV005;
OS Melanoplus sanguinipes entomopoxvirus (MsePV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Betaentomopoxvirus.
OX NCBI_TaxID=83191;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99102612; PubMed=9847359;
RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
RT "The genome of Melanoplus sanguinipes entomopoxvirus.";
RL J. Virol. 73:533-552(1999).
DR EMBL; AF063866; AAC97860.1; -; Genomic_DNA.
DR FIR; T28166; T28166.
KW Hypothetical protein.
SQ SEQUENCE 246 AA; 30090 MW; 098823A3ESD28ACB CRC64;

Query Match 55.0%; Score 44; DB 2; Length 246;
Best Local Similarity 83.3%; Pred. No. 97;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YYCYFW 7
| | | | |
Db 224 YYCYW 229

RESULT 17

ID Q54B88 DICDI PRELIMINARY; PRT; 284 AA.
AC Q54B88;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD80219788;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriam M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulseghe H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;

RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFI01000296; EAL60528.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 284 AA; 32024 MW; 04647225B348A4D6 CRC64;

Query Match 55.0%; Score 44; DB 2; Length 284;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CYYCFWTC 10
| | | | |
Db 88 CRYCQKTC 97

RESULT 18

Q54FTL DICDI PRELIMINARY; PRT; 384 AA.
ID Q54FTL;
AC Q54FTL;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD80188988;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriam M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulseghe H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;

RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFI01000235; EAL62163.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 384 AA; 44121 MW; 2435791B06CE3BEE CRC64;

Query Match 55.0%; Score 44; DB 2; Length 384;
Best Local Similarity 61.5%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 CYYCFP--WTC 11
| | | | |
Db 20 CYYLFRNWT 32

RESULT 19

Q61412 CAEBR PRELIMINARY; PRT; 393 AA.
ID Q61412 CAEBR
AC Q61412;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG15996 (fragment).
 GN Name=CBG15996;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CAAC0100076; CAB69725.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; C:receptor activity; IEA.
 DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP FL 1; UNKNOWN_1.
 DR PROSITE; PS02621; G-PROTEIN RECP FL 2; 1.
 KW G-protein coupled receptor; Hypothetical protein; Receptor;
 KW Transducer; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 393 AA; 44772 MW; 202E22EA48F5F9FE CRC64;

 Query Match 55.0%; Score 44; DB 2; Length 393;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 YYCFWK 8
 Db 198 YFFCFWK 204

 RESULT 20
 Q52426 MAGGR PRELIMINARY; PRT; 599 AA.
 ID Q52426 MAGGR PRELIMINARY;
 AC Q52426
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=MG09310.4;
 OS Magnaporthe grisea 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
 OX NCBI_TaxID=242507;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen C., Allen T., An P., Anderson M., Anderson S.,
 RA Archchi H., Armbruster J., Bachanteang P., Baldwin J., Barry A.,
 RA Bayul T., Blitshatayn B., Bloom T., Blye J., Boguslavskiy L.,
 RA Bowersky M., Boukhaltier B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawes T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Fato S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Gallagan J., Geatin G., Gnerre S.,
 RA Giralke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysellis M., Karlsson E.,
 RA Kells C., Kieu A., Kishner P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,

RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalov A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., Nieves C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotoho B.,
 RA O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schuppach R., Seaman C., Settillalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
 RA Towey S., Teamia T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Magnaporthe grisea."
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AACU01000661; EAA55503.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 599 AA; 67021 MW; FEA5E522ECF849C9 CRC64;

 Query Match 55.0%; Score 44; DB 2; Length 599;
 Best Local Similarity 62.5%; Pred. No. 2.2e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 CYYCFWK 8
 Db 570 CYFWCTWK 577

 RESULT 21
 Q706P3 PSEPU PRELIMINARY; PRT; 315 AA.
 ID Q706P3 PSEPU PRELIMINARY;
 AC Q706P3
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=strain R321;
 RA MEDLINE=99008981; PubMed=97910971;
 RA Ravatn R., Scuder S., Zender A.J.B., van der Meer J.R.;
 RT "Int-B13, an unusual site-specific recombinase of the bacteriophage P4
 RT integrase family is responsible for chromosomal insertion of the 105-
 RT kb c1c-element of Pseudomonas sp. strain B13."
 RL J. Bacteriol. 180:5505-5514(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=strain RR21;
 RA MEDLINE=22708816; PubMed=12823813;
 RX DOI=10.1046/j.1365-2958.2003.03548.x;

RA Senthillo V., Zehnder A.J.B., van der Meer J.R.;
 RT "Characterization of two alternative promoters and a transcription
 RT regulator for integrase expression in the clc catabolic genomic island
 RT of *Pseudomonas* sp. strain B13.";
 RL Mol. Microbiol. 49:93-104(2003).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=strain RR21;
 RA Gallard M., Werlen C., Vallaeys T., Vorhoefer F.J., Puehler A.,
 RA van der Meer J.R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ617740; CA92907.1; -; Genomic_DNA.
 DR InterPro: IPR011092; DUF1527.
 DR Pfam: PF07513; DUF1527; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 315 AA; 34504 MW; FA5324EAC85CA370 CRC64;
 Query Match 54.4%; Score 43.5; DB 2; Length 315;
 Best Local Similarity 58.3%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
 QY 1 CYY-YCFWKTCT 11
 ||: ||: ||: ||
 DB 52 CYWLYCTWTGCT 63

RESULT 22
 ID BD09 MOUSE STANDARD; PRT; 67 AA.
 AC Q8R2I6;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Beta-Defensin 9 precursor (Defensin, beta 9) (BD-9) (mBD-9).
 GN Name=Defb9;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6N; TISSUE=Testis;
 RX PubMed=12644567; DOI=10.1093/molbev/msg060;
 RA Morrison G.M., Sempke C.A.M., Kilanowski F.M., Hill R.E., Dorin J.R.;
 RT "Signal sequence conservation and mature peptide divergence within
 RT subgroups of the murine beta-defensin gene family.";
 RL Mol. Biol. Evol. 20:460-470(2003).
 CC -1- FUNCTION: Has antibacterial activity (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Weakly expressed in adult and neonatal brain.
 CC -1- SIMILARITY: Belongs to the beta-defensin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: AJ437647; CAD26896.1; -; mRNA.
 DR Ensembl: ENSMUSG00000047390; Mus musculus.
 DR MGI: MGI:2179198; Defb9.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR InterPro: IPR001855; Defensin_beta.
 DR Pfam: PF00711; Defensin_beta; 1.
 KW Antibiotic; Antimicrobial; Defensin; Multigene family; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 67 Beta-defensin 9.
 FT DISULFID 34 62 By similarity.
 FT DISULFID 41 55 By similarity.
 FT DISULFID 45 63 By similarity.
 SQ SEQUENCE 67 AA; 7682 MW; 35910A00DCBE1A74 CRC64;

Query Match 53.8%; Score 43; DB 1; Length 67;
 Best Local Similarity 31.8%; Pred. No. 40;
 Matches 7; Conservative 1; Mismatches 2; Indels 12; Gaps 1;
 QY 1 CYYVCF-----WKTC 10
 ||: ||: ||: ||
 DB 41 CYFCFSSHKKGSCPPWPRC 62

RESULT 23
 ID Q7PF49 ANOGA
 AC Q7PF49; ANOGA PRELIMINARY; PRT; 104 AA.
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE ENSANGP0000024722 (Fragment).
 GN ORPNames=ENSANGG00000019994;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT "Anopheles gambiae re-annotation.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAB0100807; EAA45465.2; -; Genomic_DNA.
 FT NON TER 1 1
 SQ SEQUENCE 104 AA; 12146 MW; 688BE1C6AD3E7858 CRC64;

Query Match 53.8%; Score 43; DB 2; Length 104;
 Best Local Similarity 54.5%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CYYVCFWKTCT 11
 ||: ||: ||: ||
 DB 44 CVTVCPLWLSCT 54

RESULT 24
 ID Q95Y29 CAEL PRELIMINARY; PRT; 231 AA.
 AC Q95Y29;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein Y34B4A.6.
 GN ORPNames=Y34B4A.6;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodirinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: AC024755; AAL65801.1; -; Genomic DNA.
 DR Ensembl: Y34B4A.6; Caenorhabditis elegans.

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DR WormBase; WBGene00021322; Y34B4A.6.
DR WormPep; Y34B4A.6; CE30215
DR InterPro; IPR009673; DUF1261.
DR Pfam; PF06879; DUF1261; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 231 AA; 25640 MW; C6C9643824F2E2EFA CRC64;

Query Match 53.8%; Score 43; DB 2; Length 231;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CYYCFWKC 10
||: |||
Db 187 CYQQLFWNAC 196

RESULT 25
Q4N0N6 THEPA PRELIMINARY; PRT; 231 AA.
AC Q4N0N6
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TP03_0080;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muga;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoibi A., Wasawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Fraser C.M., Nene V.;
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
lymphocytes."
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AAGX01000005; EAN30816.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 231 AA; 27477 MW; E9B3D65B62C03F59 CRC64;

Query Match 53.8%; Score 43; DB 2; Length 231;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YYCFW 7
|||||
Db 87 FYICFW 92

RESULT 26
Q6RUM6 THEPA PRELIMINARY; PRT; 329 AA.
AC Q6RUM6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Maturase (Fragment).
GN Name=matK;
OS Cleome hassleriana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Cleomaceae; Cleome.
OX NCBI_TaxID=28532;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hilu K.W., Borsch T., Mueller K., Soltis D.E., Soltis P.S.,
RA Savolainen V., Chase M., Powell M., Alice L.A., Evans R., Sanquet H.,
RA Neinhuis C., Slotta T.A.B., Rohwer J.G., Campbell C.S., Catrou L.W.;
RT "Angiosperm phylogeny based on matK sequence information.";
Am. J. Bot. 90:1758-1776(2003).
DR EMBL; AY491649; AAS76490.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0008380; P:RNA splicing; IEA.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast; mRNA processing.
FT NON_TER 1
FT NON_TER 329
SQ SEQUENCE 329 AA; 38954 MW; 1CPA9FC6A88B142 CRC64;

Query Match 53.8%; Score 43; DB 2; Length 329;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YYCFWKC 10
|||||
Db 40 YEYCNWKC 48

RESULT 27
Q61817 CAEBR PRELIMINARY; PRT; 395 AA.
ID Q61817
AC Q61817
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG14644.
GN Name=CBG14644;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC01000068; CAB68718.1; -; Genomic_DNA.
DR InterPro; IPR009673; DUF1261.
DR Pfam; PF06879; DUF1261; 2.
KW Hypothetical protein.
SQ SEQUENCE 395 AA; 44140 MW; EEB386DDDF197693 CRC64;

Query Match 53.8%; Score 43; DB 2; Length 395;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CYYCFWKC 10
||: |||

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Db 198 CYQLFWNAC 207

RESULT 28

Q5VH36_9ROSI
 ID Q5VH36_9ROSI PRELIMINARY; PRT; 423 AA.
 AC Q5VH36_9ROSI
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Maturase K (Fragment).
 GN Name=matK;
 OS Podandrogynae chiriquensis.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Cleomaceae; Podandrogynae.
 OX NCBI_TaxID=202666;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall J.C., Iltis H.H., Sytama K.J.;
 RT "Molecular phylogenetics of core Brassicales, placement of orphan
 RT genera, Emblingia, Forchhammeria, Tiranania, and character evolution.";
 RL Syst. Bot. 29:654-669(2004).
 DR EMBL; AY483233; AAS77388.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0008380; P:RNA splicing; IEA.
 DR InterPro; IPR000442; Intrin_maturase2.
 DR InterPro; IPR002866; MatK_N.
 DR Pfam; PF01348; Intrin_maturase2; 1.
 DR Pfam; PF01824; MatK_N; 1.
 KW Chloroplast; mRNA processing.
 FT NON TER 423 423
 SQ SEQUENCE 423 AA; 50867 MW; E3A444763F5A956E CRC64;

Query Match 53.8%; Score 43; DB 2; Length 423;

Best Local Similarity 66.7%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YYCYCFWKTC 10

|||||
 187 YEYCNWKNK 195

RESULT 29

Q6ILZ2_DROME
 ID Q6ILZ2_DROME PRELIMINARY; PRT; 426 AA.
 AC Q6ILZ2_DROME
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE HDC08032.
 GN Drosophila melanogaster (Fruit fly).
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
 RA Hild M., Beckmann B., Haas S.A., Koch B., Solovvey V., Busold C.,
 RA Fellenberg K., Boutros M., Vingron M., Sauer P., Hoheisel J.D.,
 RA Paro R.;
 RT "An integrated gene annotation and transcriptional profiling approach
 RT towards the full gene content of the Drosophila genome.";
 RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK001874; DAA02720.1; -; Genomic DNA.
 SQ SEQUENCE 426 AA; 50138 MW; 30479F5137F3FDB CRC64;

Query Match 53.8%; Score 43; DB 2; Length 426;

Best Local Similarity 83.3%; Pred. No. 2.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YYCYCFW 7

|||||
 53 YFYCFW 58

RESULT 30

Q9DE40_BRARE
 ID Q9DE40_BRARE PRELIMINARY; PRT; 427 AA.
 AC Q9DE40_BRARE
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Zinc finger protein Zic2 (Zic family member 2 (Odd-paired homolog,
 DE Drosophila) b).
 GN Name=zic2b; Synonyms=zic2;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kim C.H., Jiang D., Taang M., Itoh M., David I., Chitnis A.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RG NIH MGC Project;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF207751; AAG35717.2; -; mRNA.
 DR EMBL; BC098556; AAH98556.1; -; mRNA.
 DR HSSP; P08047; ISP2.
 DR ZFIN; ZDB-GENE-030219-92; zic2b.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0003576; F:nucleic acid binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 3.
 DR ProDom; PD000003; Znf_C2H2; 1.
 DR SMART; SM00355; Znf_C2H2; 5.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; Nuclear protein; zinc; zinc-finger.
 SQ SEQUENCE 427 AA; 47045 MW; 055C0CE595E12C5B CRC64;

CC -1- FUNCTION: Probably assists in splicing chloroplast group II


```
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YYICFW 7
DB 311 YYICFW 316

RESULT 34
Q9MUY6 WHEAT
ID Q9MUY6 WHEAT PRELIMINARY; PRT; 512 AA.
AC Q9MUY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Maturase.
GN Name=matk;
OS Triticum aestivum (Wheat).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OC NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hilu K.W., Alice L.A., Liang H.;
RT "Phylogeny of Poaceae inferred from matK sequences.";
RL Ann. Mo. Bot. Gard. 86:835-851(1999).
CC -1- FUNCTION: Probably assists in splicing chloroplast group II
CC introns (By similarity).
CC introns (By similarity).
DR EMBL; AF164405; AAF66192.1; -; Genomic_DNA.
DR Gramene; Q9MUY6; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0008380; P:RNA splicing; IEA.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01349; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
DR KEGG; K01824; MatK_N; 1.
KW Chloroplast; mRNA processing.
SQ SEQUENCE 512 AA; 61552 MW; 61D814A0F32DD11C CRC64;

Query Match 53.8%; Score 43; DB 2; Length 512;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YYICFW 7
DB 312 YYICFW 317

RESULT 35
Q6K6P3 ORYZA
ID Q6K6P3 ORYZA PRELIMINARY; PRT; 686 AA.
AC Q6K6P3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative cyclic nucleotide-gated calmodulin-binding ion channel.
GN Name=P0042D01.18;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005000; BAD23159.1; -; Genomic_DNA.
DR Gramene; Q6K6P3; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
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DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PSS0042; cNMP_BINDING_3; 1.
SQ SEQUENCE 686 AA; 79170 MW; 7FA896476FF6D9A4 CRC64;

Query Match 53.8%; Score 43; DB 2; Length 686;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YYICFW 7
DB 359 YYICFW 364

RESULT 36
Q7TQAO_MOUSE
ID Q7TQAO_MOUSE PRELIMINARY; PRT; 762 AA.
AC Q7TQAO;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inhibin binding protein/p120 variant 3.
GN Name=igsf1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=22716681; PubMed=12832474;
RX DOI=10.1128/MCB.23.14.4882-4891.2003;
RA Bernard D.J., Burns K.H., Haupt B., Matzuk M.M., Woodruff T.K.;
RT "Normal reproductive function in inhBP/p120-deficient mice.";
RL Mol. Cell. Biol. 23:4882-4891(2003).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; AY227773; AAF57081.1; -; mRNA.
DR HSPF; Q8NHL6; IG0X.
DR Ensemble; ENSMUSG00000031111; Mus musculus.
DR MGI; MGI:2147913; Igsf1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PSS0835; IG_LIKE; 3.
KW Immunoglobulin domain; Transmembrane.
SQ SEQUENCE 762 AA; 86396 MW; 4557846BED8C8814 CRC64;

Query Match 53.8%; Score 43; DB 2; Length 762;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYYICFWKT 9
DB 382 CHYLLTKT 390

RESULT 37
Q7QRF9_GIALA
ID Q7QRF9_GIALA PRELIMINARY; PRT; 773 AA.
AC Q7QRF9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 448 18533 20854.
OS Giardia_lambliA ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OC NCBI_TaxID=184922;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Alley S.B., Gillin P.D.,
EA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000134; EAA37615.1; -; Genomic DNA.
SQ SEQUENCE 773 AA; 87482 MW; C8ACIA09E34056AA CRC64;

Query Match 53.8%; Score 43; DB 2; Length 773;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YYCYCFWTKT 11
Db 659 YVYCYWDHCS 668

RESULT 38
Q6ZQD0_MOUSE
ID Q6ZQD0_MOUSE PRELIMINARY; PRT; 1026 AA.
AC Q6ZQD0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKTAA0364 protein (Fragment).
GN Name=Igsf1; Synonym=MKIAA0364;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryonic tail;
MEDLINE=22977043; PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hirakawa S.,
RA Soga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129126; BAC37936.1; -; -.
DR Ensembl; ENSMUSG00000031111; Mus musculus.
DR MGI; MGI:2147913; Igsf1.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IGC2; 5.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG LIKE; 4.
FT NON_TER 1
SQ SEQUENCE 1026 AA; 115029 MW; 31327447B7575992 CRC64;

Query Match 53.8%; Score 43; DB 2; Length 1026;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYYCYCFWTKT 9
Db 383 CHYYLTWTKT 391

RESULT 39
Q7TQAL_MOUSE
ID Q7TQAL_MOUSE PRELIMINARY; PRT; 1317 AA.
AC Q7TQAL;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inhibin binding protein/p120 long isoform.
GN Name=Igsf1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pituitary;
MEDLINE=22716681; PubMed=12832474;
RA DOI=10.1126/MBE.23.14.4882-4891.2003;
RA Bernard D.J., Burns K.H., Haupt B., Matzuk M.M., Woodruff T.K.;
RT "Normal reproductive function in Inhibin/p120-deficient mice.";
RL Mol. Cell. Biol. 23:4882-4891(2003).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; AY227771; AAP57079.1; -; mRNA.
DR HSSP; Q8NHL6; IGX.
DR Ensembl; ENSMUSG00000031111; Mus musculus.
DR MGI; MGI:2147913; Igsf1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 6.
KW Immunoglobulin domain; Transmembrane.
SQ SEQUENCE 1317 AA; 147010 MW; 09D1E7A89ADC804D CRC64;

Query Match 53.8%; Score 43; DB 2; Length 1317;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYYCYCFWTKT 9
Db 382 CHYYLTWTKT 390

RESULT 40
Q925N6_RAT
ID Q925N6_RAT PRELIMINARY; PRT; 1320 AA.
AC Q925N6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inhibin binding protein long isoform.
GN Name=Igsf1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=21168090; PubMed=11266515; DOI=10.1210/me.15.4.654;
RA Bernard D.J., Woodruff T.K.;
RT "Inhibin binding protein in rats: alternative transcripts and
RT regulation in the pituitary across the estrous cycle.";
RL Mol. Endocrinol. 15:654-667(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; AF322216; AAK40083.1; -; mRNA.
DR HSSP; Q8NHL6; IGX.
DR Ensembl; ENSRNORG00000007600; Rattus norvegicus.
DR RGD; 631402; Igsf1.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 5.
KW Immunoglobulin domain; Transmembrane.
SQ SEQUENCE 1320 AA; 147293 MW; F5F5B2AA77BA3C2A CRC64;

```

Query Match 53.8%; Score 43; DB 2; Length 1320;
 Best Local Similarity 66.7%; Pred. No. 6.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYYCPCWKT 9
 DB 383 CHYLTWKT 391

RESULT 41

TRYT_DROER
 ID TRYT_DROER STANDARD; PRT; 262 AA.
 AC P54628;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Trypsin theta precursor (EC 3.4.21.4).
 GN Name=theta-Try;

OS Drosophila erecta (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7220;
 RN [1]

NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RP MEDLINE=99416435; PubMed=10486967;
 RA Wang S., Magoullas C., Hickey D.A.;
 RT "Concerted evolution within a trypsin gene cluster in Drosophila.";
 RL Mol. Biol. Evol. 16:1117-1124 (1999).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.

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 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; U40653; AA83238.1; -; Genomic_DNA.
 DR HSP; P00760; IEXX.

DR MEROPS; S01.114; -.
 DR FlyBase; FBgn0015082; Dera\theta-Try.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.

DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Multigene family; Protease; Serine protease; Signal;

KW Zymogen.

FT SIGNAL 1 19 Probable.
 FT PROPEP 20 34 Activation peptide.
 FT CHAIN 35 262 Trypsin theta.
 FT DOMAIN 35 260 Peptidase S1.
 FT ACT_SITE 76 76 Charge relay system (By similarity).
 FT ACT_SITE 121 121 Charge relay system (By similarity).
 FT ACT_SITE 216 216 Charge relay system (By similarity).
 FT SITE 210 210 Required for specificity (By similarity).
 FT DISULFID 61 77 By similarity.
 FT DISULFID 186 203 By similarity.
 FT DISULFID 212 236 By similarity.
 SQ SEQUENCE 262 AA; 28210 MW; EF3BCABD1143F25D CRC64;

Query Match

Best Local Similarity 53.1%; Score 42.5; DB 1; Length 262;
 Matches 7; Conservative 2; Mismatches 1; Indels 15; Gaps 1;

QY 1 CYYCPCWKT 9

Db 162 CYFCWMTLPKTLQAVVYVIVDWKTC 186

RESULT 42

TRYT_DROME
 ID TRYT_DROME STANDARD; PRT; 262 AA.
 AC P42278; Q8S2Q7; Q9V5Y0;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Trypsin theta precursor (EC 3.4.21.4).
 GN Name=theta-Try; ORFNames=CG12385;

OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RP STRAIN=Oregon-R;
 RC MEDLINE=99416435; PubMed=10486967;
 RA Wang S., Magoullas C., Hickey D.A.;
 RT "Concerted evolution within a trypsin gene cluster in Drosophila.";
 RL Mol. Biol. Evol. 16:1117-1124 (1999).
 RN [2]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RP STRAIN=Berkely;
 RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananthides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-X., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195 (2000).
 RN [3]

GENOME REANNOTATION.

RP MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review",
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=Berkeley; TISSUE=Embryo;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarion H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.,
RT "A Drosophila full-length cDNA resource";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -|- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -|- SUBCELLULAR LOCATION: Extracellular.
CC -|- SIMILARITY: Belongs to the peptidase S1 family.
CC -|- SIMILARITY: Contains 1 peptidase S1 domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U04853; AAL17454.1; -, Genomic DNA.
DR EMBL; AB003826; AAF58661.1; -, Genomic DNA.
DR EMBL; AY070583; AAL48054.1; -, mRNA.
DR HSP; P00760; 1EZX.
DR M89PS; S01.114; -.
DR Ensembl; CG1385; Drosophila melanogaster.
DR Flybase; FBgn0011555; theta-try.
DR GO; GO:004295; F:trypsin activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Multigene family; Protease; Serine protease; Signal;
KW zymogen.
FT SIGNAL 1 19 Probable.
FT PROPEP 20 34 Activation peptide.
FT CHAIN 35 262 Trypsin theta.
FT DOMAIN 35 260 Peptidase S1.
FT ACT_SITE 76 76 Charge relay system (By similarity).
FT ACT_SITE 121 121 Charge relay system (By similarity).
FT ACT_SITE 216 216 Charge relay system (By similarity).
FT SITE 210 210 Required for specificity (By similarity).
FT DISULFID 61 77 By similarity.
FT DISULFID 186 203 By similarity.
FT DISULFID 212 236 By similarity.
FT CONFLICT 45 46 AH -> GD (in Ref. 1).
FT CONFLICT 73 73 T -> A (in Ref. 4).
SQ SEQUENCE 262 AA; 28378 MW; 440A6F07037C985 CRC64;

Query Match 53.1%; Score 42.5; DB 1; Length 262;
Best Local Similarity 28.0%; Pred. NO. 1.7e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 15; Gaps 1;
Qy 1 CVYTCF-----WKTC 10
Db 162 CYFWCMTLPKTLQEVYVNVIVDKTC 186
|||||
1 162

RESULT 43
ID Q5K4X4 BARIN PRELIMINARY; PRT; 74 AA.
AC Q5K4X4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE MHC class II antigen (Fragment).
GN Name=bame-DAB*0102;
OS Barbus intermedius (Lake tana barbels).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=40831;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RA Kruiswijk C.P., Hermesen T., Heerwaarden J., Dixon B.,
RA Savelkoul H.F.J., Stet R.J.M.;
RT "Major histocompatibility genes in the Lake Tana African large barb
RT speciesflock: evidence for complete partitioning of class II B, but
RT not class I genes among different species";
RL Immunogenetics 56:894-908(2005).
DR EMBL; AJ506712; CAD44920.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON_TER 1 74
FT NON_TER 74 74
SQ SEQUENCE 74 AA; 8791 MW; E6E3BB8D6049AE74 CRC64;

Query Match 52.5%; Score 42; DB 2; Length 74;
Best Local Similarity 55.6%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 2 YYTCFWKTC 10
Db 3 YYTSYWSKC 11
|||||
2 3

RESULT 44
ID Q5K4X8 BARIN PRELIMINARY; PRT; 74 AA.
AC Q5K4X8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE MHC class II antigen (Fragment).
GN Name=bame-DAB*0102;
OS Barbus intermedius (Lake tana barbels).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=40831;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RA Kruiswijk C.P., Hermesen T., Heerwaarden J., Dixon B.,
RA Savelkoul H.F.J., Stet R.J.M.;
RT "Major histocompatibility genes in the Lake Tana African large barb
RT speciesflock: evidence for complete partitioning of class II B, but
RT not class I genes among different species";
RL Immunogenetics 56:894-908(2005).
DR EMBL; AJ506712; CAD44920.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.

GN Name=bame-DAB*0102;
OS Barbus intermedius (Lake tana barbels).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=40831;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RA Kruiswijk C.P., Hermesen T., Heerwaarden J., Dixon B.,
RA Savelkoul H.F.J., Stet R.J.M.;
RT "Major histocompatibility genes in the Lake Tana African large barb
RT speciesflock: evidence for complete partitioning of class II B, but
RT not class I genes among different species";
RL Immunogenetics 56:894-908(2005).
DR EMBL; AJ506712; CAD44920.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON_TER 1 74
FT NON_TER 74 74
SQ SEQUENCE 74 AA; 8791 MW; E6E3BB8D6049AE74 CRC64;

Query Match 52.5%; Score 42; DB 2; Length 74;
Best Local Similarity 55.6%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 2 YYTCFWKTC 10
Db 3 YYTSYWSKC 11
|||||
2 3

RESULT 44
ID Q5K4X8 BARIN PRELIMINARY; PRT; 74 AA.
AC Q5K4X8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE MHC class II antigen (Fragment).
GN Name=bame-DAB*0102;
OS Barbus intermedius (Lake tana barbels).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=40831;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RA Kruiswijk C.P., Hermesen T., Heerwaarden J., Dixon B.,
RA Savelkoul H.F.J., Stet R.J.M.;
RT "Major histocompatibility genes in the Lake Tana African large barb
RT speciesflock: evidence for complete partitioning of class II B, but
RT not class I genes among different species";
RL Immunogenetics 56:894-908(2005).
DR EMBL; AJ506712; CAD44920.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.

```

FT NON TER 1 1
FT NON TER 74 74
SQ SEQUENCE 74 AA; 9074 MW; 12BE7B260ED6B8A0 CRC64;

Query Match 52.5%; Score 42; DB 2; Length 74;
Best Local Similarity 55.6%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YYCYFWKTC 10
   ||| :|
Db 3 YYYSWSKC 11

RESULT 45
Q5K4Y2 BARIN PRELIMINARY; PRT; 75 AA.
AC Q5K4Y2
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=bama-DAB*0102;
OS Barbus intermedius (Lake tana barbels).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=40831;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RA Kruijswijk C.F., Hermesen T., Heerwaarden J., Dixon B.,
RA Savellkoul H.F.J., Stet R.J.M.;
RT "Major histocompatibility genes in the Lake Tana African large barb
RT speciesflock: evidence for complete partitioning of class II B, but
RT not class I, genes among different species.";
RL Immunogenetics 58:894-908(2005).
DR EMBL; AJ506708; CAD44916.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC II beta_N.
DR Pfam; PF00969; MHC II beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR MHC II; Transmembrane.
KW MHC II; Transmembrane.
FT NON TER 1 1
FT NON TER 75 75
SQ SEQUENCE 75 AA; 9074 MW; D82E2164809462E3 CRC64;

Query Match 52.5%; Score 42; DB 2; Length 75;
Best Local Similarity 55.6%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YYCYFWKTC 10
   ||| :|
Db 4 YYYSWSKC 12

RESULT 46
Q4YX20 PLABE PRELIMINARY; PRT; 95 AA.
ID Q4YX20 PLABE
AC Q4YX20
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PB104828.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; CAA101001987; CAH97436.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 95 AA; 11446 MW; 97D0437AD73EB810 CRC64;

Query Match 52.5%; Score 42; DB 2; Length 95;
Best Local Similarity 71.4%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYIYCFW 7
   ||| :|
Db 14 CYIYFIFW 20

RESULT 47
GRP1_CHERU STANDARD; PRT; 144 AA.
ID GRP1_CHERU
AC P11898;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Glycine-rich protein HCl.
OS Chenopodium rubrum (Red goosefoot) (Pigweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Amaranthaceae; Chenopodium.
OX NCBI_TaxID=3560;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89240041; PubMed=2717413;
RA Kaldenhoff R., Richter G.;
RT "Sequence of cDNA for a novel light-induced glycine-rich protein.";
RL Nucleic Acids Res. 17:2853-2853(1989).
CC -1- INDUCTION: By light.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; X14067; CAA32230.1; -; mRNA.
DR PIR; S04069; S04069.
DR InterPro; IPR010800; GRP.
DR Pfam; PF07172; GRP; 1.
DR Repeat; Transmembrane.
KW TRANSMEM 5 25 Potential.
FT REPEAT 37 42 1.
FT REPEAT 43 48 2.
FT REPEAT 50 55 3.
FT REPEAT 56 61 4.
FT REPEAT 63 68 5.
FT REPEAT 69 74 6.
FT REPEAT 76 81 7.
FT REPEAT 82 87 8.
FT REPEAT 89 94 9.
FT REPEAT 102 107 10.
FT REPEAT 108 113 11.
FT REPEAT 37 113 11 X 6 AA tandem repeats of G-Y-[NH]-N-G
FT REGION -G.
SQ SEQUENCE 144 AA; 14137 MW; 5B4D62D4A61621B0 CRC64;

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Query Match      52.5%; Score 42; DB 1; Length 144;
Best Local Similarity 45.5%; Pred. No. 1.2e+02;
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Db 116 CYHYCHGRCCS 126

RESULT 48
GRP9 DAUCA
ID _GRP9 DAUCA STANDARD; PRT; 144 AA.
AC P37703;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Glycine-rich protein DC9.1.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Apiales; Apiaceae; Scandiceae;
OC Daucinae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Alsieth F., Richter G.;
RT "Gene expression during induction of somatic embryogenesis in carrot
cell suspensions.";
RL Planta 183:17-24(1990).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; S35716; S35716.
DR InterPro; IPR010800; GRP.
DR Pfam; PF01712; GRP; 1.
KW Repeat; Transmembrane.
FT TRANSMEM 5 25
FT REPEAT 37 42
FT REPEAT 43 48
FT REPEAT 50 55
FT REPEAT 56 61
FT REPEAT 63 68
FT REPEAT 69 74
FT REPEAT 76 81
FT REPEAT 82 87
FT REPEAT 89 94
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Db 116 CYHYCHGRCCS 126

RESULT 49
QSHZ64 ORYSA
ID QSHZ64_ORYSA PRELIMINARY; PRT; 201 AA.
AC QSHZ64;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)

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DE WRKY transcription factor 81.
GN Name=WRKY81;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15618416; DOI=10.1104/pp.104.054312;
RA Zhen X., Zhang Z.-L., Zou X., Huang J., Ruas P., Thompson D.,
RA Shen Q.J.;
RT "Annotations and Functional Analyses of the Rice WRKY Gene Superfamily
Reveal Positive and Negative Regulators of Abscisic Acid Signaling in
Arabidopsis Cells.";
RL Plant Physiol. 137:176-189(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Xie Z., Zhang Z.-L., Ruas P., Hall T., Zou X., Shen Q.J.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK005215; DAA05639.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR003657; WRKY.
DR Pfam; PF03106; WRKY; 2.
DR PROSITE; PS0811; WRKY; 2.
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Qy 1 CYYICFWKTCT 11
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RESULT 50
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ID Q6IEMO_ORYSA PRELIMINARY; PRT; 238 AA.
AC Q6IEMO;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE WRKY transcription factor 61.
GN Name=WRKY61;
OS Oryza sativa (indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39946;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15047897; DOI=10.1104/pp.103.034967;
RA Zhang Z.-L., Xie Z., Zou X., Casaretto J., Ho T.H., Shen Q.J.;
RT "A rice WRKY gene encodes a transcriptional repressor of the
glutathione S-transferase pathway in aleurone cells.";
RL Plant Physiol. 134:1500-1513(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Zhang Z.-L., Xie Z., Zou X., Casaretto J., Ho T.-h.D., Shen Q.J.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK005064; DAA05126.1; -; Genomic_DNA.
DR Gramene; Q6IEMO; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR003657; WRKY.
DR Pfam; PF03106; WRKY; 2.
DR PROSITE; PS0811; WRKY; 2.
SQ SEQUENCE 238 AA; 26575 MW; 619466FF5EFPFAES CRC64;

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Query Match 52.5%; Score 42; DB 2; Length 238;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CYYICFWKTCT 11
||| | |||
Db 136 CYYRCIHKTIT 146

Search completed: May 9, 2006, 12:09:48
Job time : 95.3333 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:05:44 ; Search time 14.6667 Seconds
(without alignments)
62.007 Million cell updates/sec

Title: US-10-796-158-6

Perfect score: 80

Sequence: 1 CYYCFWKTCT 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

- Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	66.2	8	2	US-09-528-200-158
2	53	66.2	8	2	US-09-734-583B-4
3	53	66.2	9	2	US-09-586-670A-16
4	50	62.5	8	2	US-09-484-318-1
5	50	62.5	8	2	US-09-484-318-8
6	50	62.5	8	2	US-09-484-319-1
7	50	62.5	8	2	US-09-484-319-8
8	50	62.5	8	2	US-09-484-320-1
9	50	62.5	8	2	US-09-484-320-8
10	50	62.5	8	2	US-09-484-321-1
11	50	62.5	8	2	US-09-484-321-8
12	50	62.5	8	2	US-09-484-323-1
13	50	62.5	8	2	US-09-484-323-8
14	50	62.5	8	2	US-09-325-769-1
15	50	62.5	8	2	US-09-325-769-2
16	50	62.5	8	2	US-09-636-170-1
17	50	62.5	8	2	US-09-636-170-8
18	50	62.5	8	2	US-09-637-518-1
19	50	62.5	8	2	US-09-637-518-8
20	50	62.5	8	2	US-09-528-200-159
21	48	60.0	8	2	US-09-528-200-156
22	45	56.2	6	2	US-09-734-583B-2
23	45	56.2	8	2	US-09-528-200-157
24	45	56.2	8	2	US-09-898-659-15
25	45	56.2	277	2	US-09-489-039A-7268
26	44.5	55.6	34	2	US-09-985-526-15
27	43	53.8	8	2	US-09-467-472C-2

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29	43	53.8	8	2	US-09-852-870A-2	Sequence 2, Appli
30	42	52.5	7	2	US-09-623-548A-640	Sequence 640, App
31	42	52.5	7	2	US-09-657-276-640	Sequence 640, App
32	42	52.5	8	1	US-08-286-748B-7	Sequence 7, Appli
33	42	52.5	8	2	US-08-586-670A-13	Sequence 13, Appli
34	42	52.5	8	2	US-08-586-670A-14	Sequence 14, Appli
35	42	52.5	9	2	US-08-586-670A-11	Sequence 11, Appli
36	42	52.5	9	2	US-08-586-670A-15	Sequence 15, Appli
37	42	52.5	66	2	US-09-248-796A-27573	Sequence 27573, A
38	42	52.5	144	2	US-10-190-902B-7	Sequence 7, Appli
39	42	52.5	144	2	US-10-190-902B-8	Sequence 8, Appli
40	42	52.5	217	2	US-09-270-767-60201	Sequence 60201, A
41	42	52.5	361	2	US-09-270-767-44745	Sequence 44745, A
42	41.5	51.9	374	2	US-09-270-767-36720	Sequence 36720, A
43	41.5	51.9	374	2	US-09-270-767-51937	Sequence 51937, A
44	41	51.2	71	2	US-09-248-796A-23946	Sequence 23946, A
45	41	51.2	312	2	US-09-270-767-59311	Sequence 59311, A
46	41	51.2	534	2	US-09-270-767-43905	Sequence 43905, A
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49	40	50.0	8	2	US-08-467-472C-4	Sequence 4, Appli
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73	40	50.0	347	2	US-09-103-330-13	Sequence 13, Appli
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84	39	48.8	114	2	US-09-270-767-34608	Sequence 34608, A
85	39	48.8	114	2	US-09-270-767-49825	Sequence 49825, A
86	39	48.8	134	2	US-09-270-767-33414	Sequence 33414, A
87	39	48.8	134	2	US-09-270-767-48631	Sequence 48631, A
88	39	48.8	148	2	US-09-248-796A-15527	Sequence 15527, A
89	39	48.8	151	2	US-09-134-001C-5595	Sequence 5595, Ap
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94	39	48.8	390	2	US-08-977-865-2	Sequence 2, Appli
95	39	48.8	416	2	US-09-270-767-41063	Sequence 41063, A
96	39	48.8	416	2	US-09-270-767-56279	Sequence 56279, A
97	38.5	48.1	93	2	US-09-270-767-61228	Sequence 61228, A
98	38.5	48.1	157	2	US-09-270-767-60822	Sequence 60822, A
99	38.5	48.1	299	2	US-09-270-767-45708	Sequence 45708, A
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427 35 43.8 5179 2 US-09-538-092-1258 Sequence 1258, App 500
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459 34 42.5 75 2 US-09-248-796A-27065 Sequence 27065, A 532
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464 34 42.5 84 2 US-09-270-767-46822 Sequence 46822, A 537
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Sequence 27251, A
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Sequence 94, Appli
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Sequence 3, Appli
Sequence 38330, A
Sequence 53547, A
Sequence 3, Appli
Sequence 3, Appli

977 32 40.0 79 2 US-09-513-999C-6319 Sequence 6319, Ap
978 32 40.0 80 2 US-09-599-632-12 Sequence 12, Appl
979 32 40.0 80 2 US-09-107-433-4711 Sequence 4711, Ap
980 32 40.0 88 2 US-09-270-767-41252 Sequence 41252, A
981 32 40.0 88 2 US-09-270-767-56468 Sequence 56468, A
982 32 40.0 89 2 US-09-513-999C-6890 Sequence 6890, Ap
983 32 40.0 90 2 US-09-270-767-60113 Sequence 60113, A
984 32 40.0 92 2 US-09-270-767-36989 Sequence 36989, A
985 32 40.0 92 2 US-09-270-767-52206 Sequence 52206, A
986 32 40.0 95 2 US-09-270-767-38877 Sequence 38877, A
987 32 40.0 95 2 US-09-270-767-54094 Sequence 54094, A
988 32 40.0 101 2 US-09-319-588C-14 Sequence 14, Appl
989 32 40.0 102 2 US-09-461-697-441 Sequence 441, App
990 32 40.0 103 2 US-10-104-047-2826 Sequence 2826, Ap
991 32 40.0 105 2 US-08-248-796A-14161 Sequence 14161, A
992 32 40.0 106 1 US-08-553-501A-84 Sequence 84, Appl
993 32 40.0 106 1 US-08-553-501A-86 Sequence 86, Appl
994 32 40.0 106 2 US-09-205-231-84 Sequence 84, Appl
995 32 40.0 106 2 US-09-205-231-86 Sequence 86, Appl
996 32 40.0 107 2 US-10-104-047-2260 Sequence 2260, Ap
997 32 40.0 108 2 US-09-107-532A-6130 Sequence 6130, Ap
998 32 40.0 108 2 US-09-898-659-27 Sequence 27, Appl
999 32 40.0 108 2 US-09-513-999C-4717 Sequence 4717, Ap
1000 32 40.0 108 2 US-09-232-290-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-528-200-158
; Sequence 158, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFGANG
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR FILING DATE: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 158
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-158

Query Match 66.2%; Score 53; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
:|||||
Db 1 FCFWKTKCT 8

RESULT 2
US-09-734-583B-4
; Sequence 4, Application US/09734583B
; Patent No. 6930088

; GENERAL INFORMATION:
; APPLICANT: Hornik, Vered
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOG
; FILE REFERENCE: 87534-3000
; CURRENT APPLICATION NUMBER: US/09/734,583B
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: The Phe residue is a D isomer
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (8)-(8)
; OTHER INFORMATION: The Thr residue ends with CH2OH
; FEATURE:
; NAME/KEY: DISULFIDE BRIDGE
; LOCATION: (2)-(2)
; OTHER INFORMATION: A disulfide bridge is formed between Cys residues 2 and 7
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)-(4)
; OTHER INFORMATION: The Trp residue is a D isomer
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-734-583B-4

Query Match 66.2%; Score 53; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
:|||||
Db 1 FCFWKTKCT 8

RESULT 3
US-08-586-670A-16
; Sequence 16, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/586,670A
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000


```

; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2..5
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Phe is in the D conformation; the Trp
; OTHER INFORMATION: is in the D conformation;"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7..9
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The sulfur atom of the cysteine is
; OTHER INFORMATION: methylated; the carboxyl group of the C-
; OTHER INFORMATION: terminal Thr is reduced to an alcohol;"
; US-08-586-670A-16

Query Match 66.2%; Score 53; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
Db 2 FCFWKTKT 9
; :|:|:|:|:|

RESULT 4
US-09-484-318-1
; Sequence 1, Application US/09484318
; Patent No. 6180085
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,318
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
; US-09-484-318-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
Db 1 FCFWKTKT 8
; :|:|:|:|:|

RESULT 6
US-09-484-319-1
; Sequence 1, Application US/09484319
; Patent No. 6180086
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,319
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
```

```
, OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-319-1
Query Match          62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTKT 11
       :|:|||||
Db      1 FCYWKTKT 8

RESULT 7
US-09-484-319-8
; Sequence 8, Application US/09484319
; Patent No. 6180086
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,319
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-484-319-8
Query Match          62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTKT 11
       :|:|||||
Db      1 FCYWKTKT 8

RESULT 8
US-09-484-320-1
; Sequence 1, Application US/09484320
; Patent No. 6180087
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastring
; CURRENT APPLICATION NUMBER: US/09/484,320
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-484-319-8
Query Match          62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTKT 11
       :|:|||||
Db      1 FCYWKTKT 8

RESULT 8
US-09-484-320-1
; Sequence 1, Application US/09484320
; Patent No. 6180087
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastring
; CURRENT APPLICATION NUMBER: US/09/484,320
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-484-320-8
Query Match          62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTKT 11
       :|:|||||
Db      1 FCYWKTKT 8

RESULT 10
US-09-484-321-1
; Sequence 1, Application US/09484321
; Patent No. 6183726
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
; FILE REFERENCE: DNA STRING
```

```
, NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-320-1
Query Match          62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTKT 11
       :|:|||||
Db      1 FCYWKTKT 8

RESULT 9
US-09-484-320-8
; Sequence 8, Application US/09484320
; Patent No. 6180087
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastring
; CURRENT APPLICATION NUMBER: US/09/484,320
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-484-320-8
Query Match          62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTKT 11
       :|:|||||
Db      1 FCYWKTKT 8

RESULT 10
US-09-484-321-1
; Sequence 1, Application US/09484321
; Patent No. 6183726
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
; FILE REFERENCE: DNA STRING
```

; CURRENT APPLICATION NUMBER: US/09/484,321
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-321-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
:|:|||||
Db 1 FCYWKTKT 8

RESULT 11

US-09-484-321-8
; Sequence 8, Application US/09484321
; Patent No. 6183726
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,321
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-484-321-8

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
:|:|||||
Db 1 FCYWKTKT 8

RESULT 12

US-09-484-323-1
; Sequence 1, Application US/09484323
; Patent No. 6190641
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,323
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-323-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
:|:|||||
Db 1 FCYWKTKT 8

RESULT 13

US-09-484-323-8
; Sequence 8, Application US/09484323
; Patent No. 6190641
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,323
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-484-323-8

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
Db 1 FCYWKTCCT 8

RESULT 14
US-09-325-769-1
; Sequence 1, Application US/09325769
; Patent No. 6217848
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Dorshow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; APPLICANT: Rajagopalan, Raghavan
; TITLE OF INVENTION: NOVEL CYANINE AND INDOCYANINE DYE BIOCONJUGATES FOR
; TITLE OF INVENTION: BIOMEDICAL APPLICATIONS
; FILE REFERENCE: 1668-286
; CURRENT APPLICATION NUMBER: US/09/325,769
; CURRENT FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: ATTY DOCKET 1668-284
; EARLIER FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine.
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; FEATURE:
; LOCATION: (4)
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This is D-tryptophan.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate.
US-09-325-769-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
Db 1 FCYWKTCCT 8

RESULT 15
US-09-325-769-2
; Sequence 2, Application US/09325769
; Patent No. 6217848
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Dorshow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; APPLICANT: Rajagopalan, Raghavan
; TITLE OF INVENTION: NOVEL CYANINE AND INDOCYANINE DYE BIOCONJUGATES FOR
; TITLE OF INVENTION: BIOMEDICAL APPLICATIONS
; FILE REFERENCE: 1668-286
; CURRENT APPLICATION NUMBER: US/09/325,769
; CURRENT FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: ATTY DOCKET 1668-284
; EARLIER FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine.
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue has had the terminal COOH
; OTHER INFORMATION: reduced to CH2OH.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide.
US-09-325-769-2

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
Db 1 FCYWKTCCT 8

RESULT 16
US-09-636-170-1
; Sequence 1, Application US/09636170
; Patent No. 6264919
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/636,170
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
; OTHER INFORMATION: US-09-636-170-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
Db 1 FCYWKTCCT 8

```
Db      1 FCYWKTCCT 8

RESULT 17
US-09-636-170-8
; Sequence 8, Application US/09636170
; Patent No. 6264919
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/636,170
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-636-170-8

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
       :|:|||||
Db      1 FCYWKTCCT 8

RESULT 18
US-09-637-518-8
; Sequence 1, Application US/09637518
; Patent No. 6264920
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastrng
; CURRENT APPLICATION NUMBER: US/09/637,518
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-637-518-8

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
       :|:|||||
Db      1 FCYWKTCCT 8

RESULT 19
US-09-637-518-8
; Sequence 8, Application US/09637518
; Patent No. 6264920
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastrng
; CURRENT APPLICATION NUMBER: US/09/637,518
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-637-518-8

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
       :|:|||||
Db      1 FCYWKTCCT 8

RESULT 20
US-09-528-200-159
; Sequence 159, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
```

; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-159

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||
Db 1 FCFWKVCT 8

RESULT 21

US-09-528-200-156
; Sequence 156, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHIA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH

; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-528-200-156

Query Match 60.0%; Score 48; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||
Db 1 FCFWKVCT 8

RESULT 22

US-09-734-583B-2
; Sequence 2, Application US/09734583B
; Patent No. 6930088
; GENERAL INFORMATION:
; APPLICANT: Hornik, Vered
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOG
; FILE REFERENCE: 87534-3000
; CURRENT APPLICATION NUMBER: US/09/734,583B
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: DISULFIDE BRIDGE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Cys residues at amino acid positions 1 and 6 form a disulfide bridge
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Trp residue is the D isomer
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-734-583B-2

Query Match 56.2%; Score 45; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
|||||
Db 1 CFWKTC 6

RESULT 23

US-09-528-200-157
; Sequence 157, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHIA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH

; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-528-200-157

Query Match 56.2%; Score 45; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||
Db 1 FCFWKVCT 8

RESULT 24

US-09-898-659-15
; Sequence 15, Application US/09898659
; Patent No. 6756524
; GENERAL INFORMATION:
; APPLICANT: Tanksley, Steven D.
; TITLE OF INVENTION: GENE CONTROLLING FRUIT SIZE AND CELL DIVISION IN PLANTS
; FILE REFERENCE: 19603/3211

; CURRENT APPLICATION NUMBER: US/09/898,659
; FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,824
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum3
US-09-898-659-15

Query Match 56.2%; Score 45; DB 2; Length 134;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CYYVCFWKTC 10
| :||| :
Db 98 CLVHCFWEAC 107

RESULT 25

US-09-489-039A-7268
; Sequence 7268, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7268
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7268

Query Match 56.2%; Score 45; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYYVCF 6
| :||| :
Db 1 CYYVCF 6

RESULT 26

US-08-985-526-15
; Sequence 15, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:

; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-15

Query Match 55.6%; Score 44.5; DB 2; Length 34;
Best Local Similarity 35.3%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 7; Gaps 1;

QY 1 CYY-----YCFWKTC 10
| :||| :
Db 3 CYWKVWGKSFYWKVC 19

RESULT 27

US-08-467-472C-2
; Sequence 2, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:

; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: N/A
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A

FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- Bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
US-08-467-472C-2

Query Match 53.8%; Score 43; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTC 11
:|||||
Db 1 FCFWKTC 8

RESULT 28
US-09-384-061-2
; Sequence 2, Application US/09384061

Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAPFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- Bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
PUBLICATION INFORMATION:

AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
US-09-384-061-2

Query Match 53.8%; Score 43; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTKTCT 11
Db 1 FCFWKTKTST 8

RESULT 29

US-09-852-870A-2
Sequence 2, Application US/09852870A
Patent No. 6673769
GENERAL INFORMATION:
APPLICANT: Goodman, Murray
APPLICANT: Oesapay, George
TITLE OF INVENTION: Lanthionin Bridged Proteins
FILE REFERENCE: LKR 9122-D
CURRENT APPLICATION NUMBER: US/09/852.870A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/384,601
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-2

Query Match 53.8%; Score 43; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTKTCT 11
Db 1 FCFWKTKTST 8

RESULT 30

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-623-548A-640
Sequence 640, Application US/09623548A
Patent No. 6849714
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/623,548A
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 640
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-640

Query Match 52.5%; Score 42; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTKTCT 11
Db 1 CYWKVKCT 7

RESULT 31

US-09-657-276-640
Sequence 640, Application US/09657276
Patent No. 6887470
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/657,276
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 640
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-657-276-640
Sequence 640, Application US/09657276
Patent No. 6887470
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/657,276
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 640
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide
US-09-657-276-640

Query Match 52.5%; Score 42; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTCCT 11
|:|:|
Db 1 CYWKVCT 7

RESULT 32
US-08-286-748B-7
; Sequence 7, Application US/08286748B
; Patent No. 5759542
; GENERAL INFORMATION:
; APPLICANT: Victor Gurewlich
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
; OF DRUGS BY PLATELETS FOR THE TREATMENT OF
; TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
; TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 558X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.748B
; FILING DATE: August 5, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: J. Peter Rasse
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04547/013001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa is D- -Naphthylalanine

Query Match 52.5%; Score 42; DB 1; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTCCT 11
|:|:|
Db 2 CYWKVCT 8

RESULT 33
US-08-586-670A-13
; Sequence 13, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: MCBride, William
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; APPLICANT: MCBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586.670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "Xaa is D-naphthylalanine and is linked
; OTHER INFORMATION: to DTPA; Trp is in the D conformation;

US-08-586-670A-13
Query Match 52.5%; Score 42; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTCCT 11
|:|:|
Db 2 CYWKVCT 8

RESULT 34
US-08-586-670A-14
; Sequence 14, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: MCBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "Xaa is D-naphthylalanine and is linked
; OTHER INFORMATION: to 2-ketogulonyl; Trp is in the D conformation;
; US-08-586-670A-14

Query Match 52.5%; Score 42; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CPWKTCCT 11
Db 2 CYMKVCT 8

RESULT 35
US-08-586-670A-11
; Sequence 11, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "Lys is linked to a BAT chelator
; OTHER INFORMATION: through the side chain nitrogen and to DTPA
```

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Lys is linked to a BAT chelator
; OTHER INFORMATION: through the side chain nitrogen; Xaa is
; OTHER INFORMATION: D-naphthylalanine; the Cys sulfur is methylated;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5..8
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Trp residue is in the D conformation;
; OTHER INFORMATION: the Cys side chain sulfur is methylated;
; US-08-586-670A-11

Query Match 52.5%; Score 42; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CPWKTCCT 11
Db 3 CYMKVCT 9

RESULT 36
US-08-586-670A-15
; Sequence 15, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "Lys is linked to a BAT chelator
; OTHER INFORMATION: through the side chain nitrogen and to DTPA
```

```
, OTHER INFORMATION: at the N-terminus; Xaa is D-naphthylalanine;
, FEATURE:
, NAME/KEY: Modified-site
, LOCATION: 3..8
, OTHER INFORMATION: /label= Variant residues
, OTHER INFORMATION: /note= "The Trp residue is in the D conformation;
, OTHER INFORMATION: each of the Cys side chain sulfur atoms are
, OTHER INFORMATION: methylated;
US-08-586-670A-15

Query Match 52.5%; Score 42; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTCT 11
|:|:|
Db 3 CYMKVCT 9

RESULT 37
US-09-248-796A-27573
; Sequence 27573, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinatock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27573
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27573

Query Match 52.5%; Score 42; DB 2; Length 66;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYYCFWKT 9
|:|:|
Db 4 CYYCWSNT 12

RESULT 38
US-10-190-902B-7
; Sequence 7, Application US/10190902B
; Patent No. 6861573
; GENERAL INFORMATION:
; APPLICANT: Chen, Chao-Ying
; TITLE OF INVENTION: NOVEL GLYCINE-RICH GENE
; FILE REFERENCE: 10/190,902
; CURRENT APPLICATION NUMBER: US/10/190,902B
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Chenopodium rubrum
US-10-190-902B-7

Query Match 52.5%; Score 42; DB 2; Length 144;
Best Local Similarity 45.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 CYYCFWKTCT 11
|:|:|
Db 116 CYHYCHGRCS 126

RESULT 39
US-10-190-902B-8
; Sequence 8, Application US/10190902B
; Patent No. 6861573
; GENERAL INFORMATION:
; APPLICANT: Chen, Chao-Ying
; TITLE OF INVENTION: NOVEL GLYCINE-RICH GENE
; FILE REFERENCE: 10/190,902
; CURRENT APPLICATION NUMBER: US/10/190,902B
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Daucus carota
US-10-190-902B-8

Query Match 52.5%; Score 42; DB 2; Length 144;
Best Local Similarity 45.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CYYCFWKTCT 11
|:|:|
Db 116 CYHYCHGRCS 126

RESULT 40
US-09-270-767-60201
; Sequence 60201, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60201
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60201

Query Match 52.5%; Score 42; DB 2; Length 217;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CYYCFWKTCT 10
|:|:|
Db 152 CCYYCYTYXC 161

RESULT 41
US-09-270-767-44745
; Sequence 44745, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44745
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44745

Query Match      52.5%; Score 42; DB 2; Length 361;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CYYICFWKTC 10
      | |||::: |
Db      296 CCYCYCYXK 305

RESULT 42
US-09-270-767-36720
; Sequence 36720, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36720
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-36720

Query Match      51.9%; Score 41.5; DB 2; Length 374;
Best Local Similarity 53.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy      2 YYICFWK---TCT 11
      : | ||| |||
Db      46 HYXCFWSASLTCT 58

RESULT 43
US-09-270-767-51937
; Sequence 51937, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51937
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-51937

Query Match      51.9%; Score 41.5; DB 2; Length 374;
Best Local Similarity 53.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy      2 YYICFWK---TCT 11
      : | ||| |||
```

```
Db      46 HYXCFWSASLTCT 58

RESULT 44
US-09-248-796A-23946
; Sequence 23946, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23946
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23946

Query Match      51.2%; Score 41; DB 2; Length 71;
Best Local Similarity 50.0%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CYYICFWKTC 10
      | |||: |
Db      4 CYYMCWVKC 13

RESULT 45
US-09-270-767-59311
; Sequence 59311, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59311
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-59311

Query Match      51.2%; Score 41; DB 2; Length 312;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      5 CFWKTC 10
      |||: ||
Db      225 CFWETC 230

RESULT 46
US-09-270-767-43905
; Sequence 43905, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
```

NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43905
LENGTH: 534
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43905

Query Match 51.2%; Score 41; DB 2; Length 534;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
Db 347 CFWKTC 352

RESULT 47

US-09-528-200-160
Sequence 160, Application US/09528200
Patent No. 6630570
GENERAL INFORMATION:
APPLICANT: LICA, KAI
APPLICANT: BECKER, ANDREAS
APPLICANT: SEMMLER, WOLFHARD
APPLICANT: WEIDENMANN, BERTRAM
APPLICANT: HESSNIUS, CARTSEN
APPLICANT: VOLKMER-ENGERT, RUDOLF
APPLICANT: SCHNEIDER-MERGENER, JENS
APPLICANT: BHARGAVA, SARAH
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
FILE REFERENCE: SCH-1731
CURRENT APPLICATION NUMBER: US/09/528,200
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: DE 199 17 713.9
PRIOR FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 160
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: MOD RES
LOCATION: (6)
OTHER INFORMATION: Abu
US-09-528-200-160

Query Match 50.0%; Score 40; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
Db 1 FCYWKXC 7

RESULT 48

US-08-467-472C-3
Sequence 3, Application US/08467472C
Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAPFNER & DELAHUNTY
STREET: 99 PARK AVENUE

CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a-S-bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:

;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
;; PUBLICATION INFORMATION:
;; AUTHORS: BEAN, MARK F.
;; TITLE: IDENTIFICATION OF A THIOETHER
;; TITLE: BY-PRODUCT
;; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
;; TITLE: BY
;; TITLE: TANDEN MASS SPECTROMETRY
;; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
;; JOURNAL: PEPTIDE
;; JOURNAL: SYMPOSIUM
;; VOLUME: ESCOM (LEIDEN 1990)
;; ISSUE:
;; PAGES: 443 - 445
;; DATE: 1990
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
;; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-3

Query Match 50.0%; Score 40; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 11
Db 2 CFWKTS 8

RESULT 49

US-08-467-472C-4
;; Sequence 4, Application US/08467472C
;; Patent No. 6028168
;; GENERAL INFORMATION:
;; APPLICANT: GOODMAN, MURRAY
;; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
;; NUMBER OF SEQUENCES: 24
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROOKS HAIDT HAPFNER & DELAHUNTY
;; STREET: 99 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10016
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" FLOPPY DISC
;; COMPUTER: COMPAQ - IBM COMPATIBLE
;; OPERATING SYSTEM: MS-DOS Version 6.2
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/467,472C
;; FILING DATE: 6-JUNE-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/742,908
;; FILING DATE: 9-AUGUST-1991
;; APPLICATION NUMBER: US 08/021,606
;; FILING DATE: 28-JANUARY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ROBINSON, WILLIAM R.
;; REGISTRATION NUMBER: 27,224
;; REFERENCE/DOCKET NUMBER: LKR-9122B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 697-3355
;; TELEFAX: (212) 557-5635
;; TELEX: NONE
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8

;; TYPE: AMINO ACID
;; TOPOLOGY: LINEAR
;; MOLECULE TYPE:
;; DESCRIPTION: PEPTIDE
;; HYPOTHETICAL: N/A
;; ANTI-SENSE: N/A
;; FRAGMENT TYPE: INTERNAL
;; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
;; ORIGINAL SOURCE: INC.,
;; IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
;; POSITION IN GENOME: N/A
;; FEATURE:
;; NAME/KEY: ENANTIOMER
;; LOCATION: -4
;; IDENTIFICATION METHOD: amino acid analysis
;; IDENTIFICATION METHOD: and
;; IDENTIFICATION METHOD: mass spectrometry
;; OTHER INFORMATION: water is removed and
;; OTHER INFORMATION: thereby
;; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
;; PUBLICATION INFORMATION:
;; AUTHORS: JUNG, GUNTHER
;; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
;; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
;; JOURNAL: PEPTIDE
;; JOURNAL: SYMPOSIUM
;; VOLUME: ESCOM (LEIDEN 1990)
;; ISSUE:
;; PAGES: 865 - 869
;; DATE: 1990
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO: 4: CYS-SER
;; PUBLICATION INFORMATION:
;; AUTHORS: SHIBA, TETSUO
;; JOURNAL: BIOPOLYMERS
;; VOLUME: JOHN WILEY AND SONS, INC.
;; ISSUE: SUPPLEMENTARY
;; PAGES: 511 - 519
;; DATE: 1986
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO: 4: CYS-SER
;; PUBLICATION INFORMATION:
;; AUTHORS: BEAN, MARK F.
;; TITLE: IDENTIFICATION OF A THIOETHER
;; TITLE: BY-PRODUCT
;; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
;; TITLE: BY
;; TITLE: TANDEN MASS SPECTROMETRY
;; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
;; JOURNAL: PEPTIDE
;; JOURNAL: SYMPOSIUM
;; VOLUME: ESCOM (LEIDEN 1990)
;; ISSUE:
;; PAGES: 443 - 445
;; DATE: 1990
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO: 4: CYS-SER
;; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-4

Query Match 50.0%; Score 40; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 11

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Db      2 CPWKST 8
|||||
RESULT 50
US-09-384-061-3
; Sequence 3, Application US/09384061
; Patent No. 6268339
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/384,061
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,472
; FILING DATE:
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHEICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:

; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; TITLE: TANDEM MASS SPECTROMETRY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
; US-09-384-061-3

Query Match 50.0%; Score 40; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CPWKST 11
Db 2 CPWKST 8

Search completed: May 9, 2006, 12:09:12
Job time : 18.6667 secs
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:10:26 ; Search time 99.3333 Seconds
(without alignments)
46.270 Million cell updates/sec

Title: US-10-796-158-6
Perfect score: 80
Sequence: 1 CYYCFWKTCT 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 segs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications_AA_Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	64	80.0	15	5	US-10-490-326-27
5	64	80.0	20	5	US-10-490-326-37
6	64	80.0	20	5	US-10-490-326-38
7	64	80.0	20	5	US-10-490-326-45
8	64	80.0	22	5	US-10-490-326-22
9	64	80.0	25	5	US-10-490-326-43
10	64	80.0	25	5	US-10-490-326-46
11	64	80.0	30	5	US-10-490-326-44
12	62	77.5	11	5	US-10-796-158-7
13	55	68.8	12	5	US-10-490-326-24
14	55	68.8	12	5	US-10-490-326-30
15	55	68.8	12	5	US-10-490-326-31
16	55	68.8	12	5	US-10-490-326-32
17	55	68.8	12	5	US-10-490-326-41
18	55	68.8	15	5	US-10-490-326-21
19	55	68.8	15	5	US-10-490-326-23
20	55	68.8	15	5	US-10-490-326-35
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22	55	68.8	15	5	US-10-490-326-47
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31	55	68.8	18	5	US-10-490-326-56	Sequence 56, Appl
32	55	68.8	19	5	US-10-490-326-26	Sequence 26, Appl
33	55	68.8	19	5	US-10-490-326-58	Sequence 58, Appl
34	55	68.8	20	5	US-10-490-326-40	Sequence 40, Appl
35	55	68.8	21	5	US-10-490-326-29	Sequence 29, Appl
36	55	68.8	21	5	US-10-490-326-39	Sequence 39, Appl
37	55	68.8	22	5	US-10-490-326-57	Sequence 57, Appl
38	53	66.2	8	3	US-09-781-980-5	Sequence 5, Appl
39	53	66.2	8	3	US-10-818-246-1	Sequence 1, Appl
40	53	66.2	8	5	US-10-473-721A-15	Sequence 15, Appl
41	53	66.2	8	5	US-10-473-721A-16	Sequence 16, Appl
42	53	66.2	8	5	US-10-916-522A-4	Sequence 4, Appl
43	53	66.2	8	5	US-10-505-239-12	Sequence 12, Appl
44	53	66.2	9	6	US-11-006-071-7	Sequence 7, Appl
45	50	62.5	7	5	US-10-490-326-34	Sequence 34, Appl
46	50	62.5	7	5	US-10-796-158-4	Sequence 4, Appl
47	50	62.5	8	3	US-09-781-980-6	Sequence 6, Appl
48	50	62.5	9	4	US-10-427-160A-22	Sequence 22, Appl
49	50	62.5	9	4	US-10-444-853A-515	Sequence 515, App
50	50	62.5	9	5	US-10-780-447-22	Sequence 22, Appl
51	50	62.5	9	5	US-10-757-803-515	Sequence 515, App
52	50	62.5	9	5	US-10-826-966-515	Sequence 515, App
53	50	62.5	14	4	US-10-258-766A-1	Sequence 1, Appl
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58	50	62.5	14	4	US-10-258-766A-14	Sequence 14, Appl
59	50	62.5	15	5	US-10-490-326-42	Sequence 42, Appl
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63	49	61.3	40	4	US-10-838-226-231	Sequence 231, App
64	49	61.3	93	4	US-10-058-053A-116	Sequence 116, App
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66	48	60.0	7	5	US-10-775-180-845	Sequence 845, App
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68	48	60.0	9	3	US-09-758-426-2	Sequence 2, Appl
69	48	60.0	9	3	US-09-758-198-2	Sequence 2, Appl
70	48	60.0	9	3	US-09-861-661-2	Sequence 2, Appl
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72	47	58.8	7	4	US-10-258-766A-10	Sequence 10, Appl
73	47	58.8	7	4	US-10-258-766A-12	Sequence 12, Appl
74	47	58.8	45	4	US-10-058-053A-280	Sequence 280, App
75	47	58.8	45	4	US-10-838-226-280	Sequence 280, App
76	47	58.8	95	4	US-10-058-053A-89	Sequence 89, Appl
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78	46	57.5	8	3	US-09-758-128-3	Sequence 3, Appl
79	46	57.5	8	3	US-09-758-426-3	Sequence 3, Appl
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81	46	57.5	8	3	US-09-861-661-3	Sequence 3, Appl
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86	45	56.2	7	3	US-09-758-198-1	Sequence 1, Appl
87	45	56.2	7	3	US-09-861-661-1	Sequence 1, Appl
88	45	56.2	8	5	US-10-399-542-5	Sequence 5, Appl
89	45	56.2	134	3	US-09-898-659-15	Sequence 15, Appl
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91	44	55.6	41	4	US-10-437-963-152616	Sequence 152616, A
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96	44	55.0	21	4	US-10-058-053A-233	Sequence 233, App
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103	44	55.0	93	4	US-10-058-053A-32	Sequence 32, Appl	176	42	52.5	539	4	US-10-137-872A-140	Sequence 140, App
104	44	55.0	93	4	US-10-058-053A-41	Sequence 41, Appl	177	42	52.5	539	4	US-10-147-500-140	Sequence 140, App
105	44	55.0	93	4	US-10-838-226-32	Sequence 32, Appl	178	42	52.5	539	4	US-10-147-502-140	Sequence 140, App
106	44	55.0	93	4	US-10-838-226-41	Sequence 41, Appl	179	42	52.5	539	4	US-10-147-515-140	Sequence 140, App
107	44	55.0	98	4	US-10-425-115-364147	Sequence 364147, A	180	42	52.5	539	4	US-10-147-517-140	Sequence 140, App
108	43	53.8	8	3	US-09-852-870A-2	Sequence 2, Appl	181	42	52.5	539	4	US-10-147-526-140	Sequence 140, App
109	43	53.8	34	4	US-10-252-734-6	Sequence 6, Appl	182	42	52.5	539	4	US-10-147-527-140	Sequence 140, App
110	43	53.8	36	4	US-10-437-963-170139	Sequence 70139, A	183	42	52.5	539	4	US-10-121-041-140	Sequence 140, App
111	43	53.8	39	5	US-10-808-187-784	Sequence 784, App	184	42	52.5	539	4	US-10-121-043-140	Sequence 140, App
112	43	53.8	39	5	US-10-807-807-784	Sequence 784, App	185	42	52.5	539	4	US-10-121-047-140	Sequence 140, App
113	43	53.8	44	4	US-10-424-599-244658	Sequence 244658, A	186	42	52.5	539	4	US-10-123-215-140	Sequence 140, App
114	43	53.8	83	4	US-10-424-599-255156	Sequence 255156, A	187	42	52.5	539	4	US-10-123-902-140	Sequence 140, App
115	43	53.8	231	4	US-10-424-599-226507	Sequence 226507, A	188	42	52.5	539	4	US-10-123-908-140	Sequence 140, App
116	43	53.8	241	5	US-10-450-763-36735	Sequence 36735, A	189	42	52.5	539	4	US-10-123-909-140	Sequence 140, App
117	43	53.8	686	4	US-10-437-963-184435	Sequence 184435, A	190	42	52.5	539	4	US-10-123-910-140	Sequence 140, App
118	42.5	53.1	262	6	US-11-097-143-19371	Sequence 19371, A	191	42	52.5	539	4	US-10-124-813-140	Sequence 140, App
119	42	52.5	7	6	US-11-066-697-640	Sequence 640, App	192	42	52.5	539	4	US-10-124-817-140	Sequence 140, App
120	42	52.5	8	5	US-10-399-542-9	Sequence 9, Appl	193	42	52.5	539	4	US-10-125-922-140	Sequence 140, App
121	42	52.5	40	4	US-10-280-066-174	Sequence 174, App	194	42	52.5	539	4	US-10-125-924-140	Sequence 140, App
122	42	52.5	65	4	US-10-424-599-186899	Sequence 186899, A	195	42	52.5	539	4	US-10-140-860-140	Sequence 140, App
123	42	52.5	103	4	US-10-437-963-193718	Sequence 193718, A	196	42	52.5	539	4	US-10-142-417-140	Sequence 140, App
124	42	52.5	116	4	US-10-424-599-257579	Sequence 257579, A	197	42	52.5	539	4	US-10-147-519-140	Sequence 140, App
125	42	52.5	182	4	US-10-425-115-208136	Sequence 208136, A	198	42	52.5	539	4	US-10-157-782-140	Sequence 140, App
126	42	52.5	200	4	US-10-437-963-115971	Sequence 115971, A	199	42	52.5	539	4	US-10-152-395-140	Sequence 140, App
127	42	52.5	258	3	US-09-965-529-25	Sequence 25, Appl	200	42	52.5	539	4	US-10-125-926A-140	Sequence 140, App
128	42	52.5	258	3	US-09-969-680A-25	Sequence 25, Appl	201	42	52.5	539	4	US-10-125-930A-140	Sequence 140, App
129	42	52.5	258	6	US-11-048-692-25	Sequence 25, Appl	202	42	52.5	539	4	US-10-127-831A-140	Sequence 140, App
130	42	52.5	331	4	US-10-296-115-1478	Sequence 1478, Ap	203	42	52.5	539	4	US-10-127-837A-140	Sequence 140, App
131	42	52.5	368	4	US-10-437-963-189927	Sequence 189927, A	204	42	52.5	539	4	US-10-127-838B-140	Sequence 140, App
132	42	52.5	539	4	US-10-028-072-140	Sequence 140, App	205	42	52.5	539	4	US-10-127-842A-140	Sequence 140, App
133	42	52.5	539	4	US-10-140-808-140	Sequence 140, App	206	42	52.5	539	4	US-10-127-843A-140	Sequence 140, App
134	42	52.5	539	4	US-10-121-049-140	Sequence 140, App	207	42	52.5	539	4	US-10-127-845A-140	Sequence 140, App
135	42	52.5	539	4	US-10-123-904-140	Sequence 140, App	208	42	52.5	539	4	US-10-127-846A-140	Sequence 140, App
136	42	52.5	539	4	US-10-140-470-140	Sequence 140, App	209	42	52.5	539	4	US-10-127-848A-140	Sequence 140, App
137	42	52.5	539	4	US-10-175-746-140	Sequence 140, App	210	42	52.5	539	4	US-10-127-849A-140	Sequence 140, App
138	42	52.5	539	4	US-10-176-918-140	Sequence 140, App	211	42	52.5	539	4	US-10-127-850A-140	Sequence 140, App
139	42	52.5	539	4	US-10-176-921-140	Sequence 140, App	212	42	52.5	539	4	US-10-127-851A-140	Sequence 140, App
140	42	52.5	539	4	US-10-137-865-140	Sequence 140, App	213	42	52.5	539	4	US-10-128-684A-140	Sequence 140, App
141	42	52.5	539	4	US-10-140-474-140	Sequence 140, App	214	42	52.5	539	4	US-10-128-686A-140	Sequence 140, App
142	42	52.5	539	4	US-10-142-431-140	Sequence 140, App	215	42	52.5	539	4	US-10-128-690A-140	Sequence 140, App
143	42	52.5	539	4	US-10-143-114-140	Sequence 140, App	216	42	52.5	539	4	US-10-128-691A-140	Sequence 140, App
144	42	52.5	539	4	US-10-152-031-4	Sequence 4, Appl	217	42	52.5	539	4	US-10-131-819A-140	Sequence 140, App
145	42	52.5	539	4	US-10-142-419-140	Sequence 140, App	218	42	52.5	539	4	US-10-131-829A-140	Sequence 140, App
146	42	52.5	539	4	US-10-123-262-140	Sequence 140, App	219	42	52.5	539	4	US-10-131-836A-140	Sequence 140, App
147	42	52.5	539	4	US-10-142-423-140	Sequence 140, App	220	42	52.5	539	4	US-10-146-729-140	Sequence 140, App
148	42	52.5	539	4	US-10-121-050-140	Sequence 140, App	221	42	52.5	539	4	US-10-146-791-140	Sequence 140, App
149	42	52.5	539	4	US-10-141-755-140	Sequence 140, App	222	42	52.5	539	4	US-10-147-484-140	Sequence 140, App
150	42	52.5	539	4	US-10-143-032-140	Sequence 140, App	223	42	52.5	539	4	US-10-147-508-140	Sequence 140, App
151	42	52.5	539	4	US-10-123-108-140	Sequence 140, App	224	42	52.5	539	4	US-10-147-512-140	Sequence 140, App
152	42	52.5	539	4	US-10-123-236-140	Sequence 140, App	225	42	52.5	539	4	US-10-175-735-140	Sequence 140, App
153	42	52.5	539	4	US-10-123-261-140	Sequence 140, App	226	42	52.5	539	4	US-10-121-040-140	Sequence 140, App
154	42	52.5	539	4	US-10-140-921-140	Sequence 140, App	227	42	52.5	539	4	US-10-121-056-140	Sequence 140, App
155	42	52.5	539	4	US-10-140-928-140	Sequence 140, App	228	42	52.5	539	4	US-10-121-061-140	Sequence 140, App
156	42	52.5	539	4	US-10-121-045-140	Sequence 140, App	229	42	52.5	539	4	US-10-123-235-140	Sequence 140, App
157	42	52.5	539	4	US-10-123-232-140	Sequence 140, App	230	42	52.5	539	4	US-10-124-818-140	Sequence 140, App
158	42	52.5	539	4	US-10-123-903-140	Sequence 140, App	231	42	52.5	539	4	US-10-137-868-140	Sequence 140, App
159	42	52.5	539	4	US-10-124-819-140	Sequence 140, App	232	42	52.5	539	4	US-10-147-492-140	Sequence 140, App
160	42	52.5	539	4	US-10-124-822-140	Sequence 140, App	233	42	52.5	539	4	US-10-158-782-140	Sequence 140, App
161	42	52.5	539	4	US-10-140-925-140	Sequence 140, App	234	42	52.5	539	4	US-10-123-905-140	Sequence 140, App
162	42	52.5	539	4	US-10-160-498-140	Sequence 140, App	235	42	52.5	539	4	US-10-123-907-140	Sequence 140, App
163	42	52.5	539	4	US-10-124-824-140	Sequence 140, App	236	42	52.5	539	4	US-10-124-815-140	Sequence 140, App
164	42	52.5	539	4	US-10-127-825A-140	Sequence 140, App	237	42	52.5	539	4	US-10-125-921A-140	Sequence 140, App
165	42	52.5	539	4	US-10-127-829A-140	Sequence 140, App	238	42	52.5	539	4	US-10-125-928A-140	Sequence 140, App
166	42	52.5	539	4	US-10-127-835A-140	Sequence 140, App	239	42	52.5	539	4	US-10-127-821A-140	Sequence 140, App
167	42	52.5	539	4	US-10-137-839A-140	Sequence 140, App	240	42	52.5	539	4	US-10-127-822A-140	Sequence 140, App
168	42	52.5	539	4	US-10-127-901A-140	Sequence 140, App	241	42	52.5	539	4	US-10-127-824A-140	Sequence 140, App
169	42	52.5	539	4	US-10-128-693A-140	Sequence 140, App	242	42	52.5	539	4	US-10-127-826A-140	Sequence 140, App
170	42	52.5	539	4	US-10-131-813A-140	Sequence 140, App	243	42	52.5	539	4	US-10-127-827A-140	Sequence 140, App
171	42	52.5	539	4	US-10-131-818A-140	Sequence 140, App	244	42	52.5	539	4	US-10-127-828A-140	Sequence 140, App
172	42	52.5	539	4	US-10-131-823A-140	Sequence 140, App	245	42	52.5	539	4	US-10-127-830A-140	Sequence 140, App
173	42	52.5	539	4	US-10-131-824A-140	Sequence 140, App	246	42	52.5	539	4	US-10-127-832A-140	Sequence 140, App

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540	42	52.5	539	4	US-10-140-023-140	Sequence 140, App	613	40	50.0	26	4	US-10-838-226-303	Sequence 303, App
541	42	52.5	539	4	US-10-140-809-140	Sequence 140, App	614	40	50.0	30	4	US-10-058-053A-285	Sequence 285, App
542	42	52.5	539	4	US-10-140-865-140	Sequence 140, App	615	40	50.0	30	4	US-10-058-053A-286	Sequence 286, App
543	42	52.5	539	4	US-10-141-701-140	Sequence 140, App	616	40	50.0	30	4	US-10-838-226-285	Sequence 285, App
544	42	52.5	539	4	US-10-141-754-140	Sequence 140, App	617	40	50.0	30	4	US-10-838-226-286	Sequence 286, App
545	42	52.5	539	4	US-10-141-760-140	Sequence 140, App	618	40	50.0	30	5	US-10-456-375-28	Sequence 28, Appl
546	42	52.5	539	4	US-10-142-425-140	Sequence 140, App	619	40	50.0	30	5	US-10-456-375-29	Sequence 29, Appl
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548	42	52.5	539	4	US-10-143-113-140	Sequence 140, App	621	40	50.0	43	4	US-10-437-963-163013	Sequence 163013,
549	42	52.5	539	4	US-10-146-730-140	Sequence 140, App	622	40	50.0	60	4	US-10-424-599-151813	Sequence 151813,
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551	42	52.5	539	4	US-10-158-791-140	Sequence 140, App	624	40	50.0	71	4	US-10-058-053A-29	Sequence 29, Appl
552	42	52.5	539	4	US-10-156-843-140	Sequence 140, App	625	40	50.0	71	4	US-10-838-226-29	Sequence 29, Appl
553	42	52.5	539	4	US-10-157-786-140	Sequence 140, App	626	40	50.0	77	3	US-09-749-637A-294	Sequence 294, App
554	42	52.5	539	4	US-10-152-405-140	Sequence 140, App	627	40	50.0	77	3	US-09-749-637A-330	Sequence 330, App
555	42	52.5	539	4	US-10-147-528-140	Sequence 140, App	628	40	50.0	77	5	US-10-839-227-294	Sequence 294, App
556	42	52.5	539	4	US-10-128-692A-140	Sequence 140, App	629	40	50.0	77	5	US-10-839-227-330	Sequence 330, App
557	42	52.5	539	4	US-10-140-927-140	Sequence 140, App	630	40	50.0	78	3	US-09-749-637A-122	Sequence 122, App
558	42	52.5	539	4	US-10-147-493-140	Sequence 140, App	631	40	50.0	78	5	US-10-839-227-122	Sequence 122, App
559	42	52.5	539	4	US-10-145-127-140	Sequence 140, App	632	40	50.0	80	4	US-10-058-053A-110	Sequence 110, App
560	42	52.5	539	4	US-10-160-503-140	Sequence 140, App	633	40	50.0	80	4	US-10-838-226-110	Sequence 110, App
561	42	52.5	539	4	US-10-143-118-140	Sequence 140, App	634	40	50.0	81	4	US-10-058-053A-92	Sequence 92, Appl
562	42	52.5	539	4	US-10-144-593-140	Sequence 140, App	635	40	50.0	81	4	US-10-058-053A-95	Sequence 95, Appl
563	42	52.5	539	4	US-10-158-787-140	Sequence 140, App	636	40	50.0	81	4	US-10-838-226-92	Sequence 92, Appl
564	42	52.5	539	4	US-10-142-426-140	Sequence 140, App	637	40	50.0	81	4	US-10-838-226-95	Sequence 95, Appl
565	42	52.5	539	4	US-10-140-024-140	Sequence 140, App	638	40	50.0	80	4	US-10-425-115-340910	Sequence 340910,
566	42	52.5	539	4	US-10-147-536-140	Sequence 140, App	639	40	50.0	91	4	US-10-425-115-321043	Sequence 321043,
567	42	52.5	539	4	US-10-152-372-140	Sequence 140, App	640	40	50.0	102	4	US-10-425-115-344868	Sequence 344868,
568	42	52.5	539	4	US-10-125-795-140	Sequence 140, App	641	40	50.0	111	4	US-10-437-963-119691	Sequence 119691,
569	42	52.5	539	4	US-10-145-626-140	Sequence 140, App	642	40	50.0	140	5	US-10-450-763-57555	Sequence 57555, A
570	42	52.5	539	4	US-10-145-819-140	Sequence 140, App	643	40	50.0	160	4	US-10-112-944-849	Sequence 849, App
571	42	52.5	539	4	US-10-145-825-140	Sequence 140, App	644	40	50.0	160	5	US-10-450-763-53620	Sequence 53620, A
572	42	52.5	539	4	US-10-147-513-140	Sequence 140, App	645	40	50.0	163	3	US-09-791-279-132	Sequence 132, App
573	42	52.5	539	4	US-10-147-518-140	Sequence 140, App	646	40	50.0	178	5	US-10-758-846-85	Sequence 85, Appl
574	42	52.5	539	5	US-10-145-961-140	Sequence 140, App	647	40	50.0	214	4	US-10-017-161-1946	Sequence 1946, Ap
575	42	52.5	539	5	US-10-147-488-140	Sequence 140, App	648	40	50.0	214	4	US-10-292-798-1594	Sequence 1594, Ap
576	42	52.5	539	5	US-10-147-531-140	Sequence 140, App	649	40	50.0	222	4	US-10-424-599-149842	Sequence 149842,
577	42	52.5	539	5	US-10-931-886-140	Sequence 140, App	650	40	50.0	266	4	US-10-343-650A-432	Sequence 432, App
578	42	52.5	539	5	US-10-158-788-140	Sequence 140, App	651	40	50.0	291	4	US-10-072-012-66	Sequence 66, Appl
579	42	52.5	539	5	US-10-955-952-140	Sequence 140, App	652	40	50.0	304	4	US-10-017-161-466	Sequence 466, App
580	42	52.5	540	4	US-10-424-599-283794	Sequence 283794,	653	40	50.0	304	4	US-10-017-161-480	Sequence 480, App
581	41	51.2	9	4	US-10-058-053A-316	Sequence 316, App	654	40	50.0	304	4	US-10-292-798-416	Sequence 416, App
582	41	51.2	9	4	US-10-838-226-316	Sequence 316, App	655	40	50.0	304	4	US-10-292-798-428	Sequence 428, App
583	41	51.2	11	4	US-10-058-053A-313	Sequence 313, App	656	40	50.0	310	4	US-10-017-161-546	Sequence 546, App
584	41	51.2	11	4	US-10-838-226-313	Sequence 313, App	657	40	50.0	310	4	US-10-292-798-478	Sequence 478, App
585	41	51.2	15	4	US-10-058-053A-311	Sequence 311, App	658	40	50.0	311	4	US-10-024-212-8	Sequence 8, Appl
586	41	51.2	15	4	US-10-838-226-311	Sequence 311, App	659	40	50.0	311	4	US-10-024-212-10	Sequence 10, Appl
587	41	51.2	15	4	US-10-424-599-211279	Sequence 211279,	660	40	50.0	311	4	US-10-024-212-12	Sequence 12, Appl
588	41	51.2	47	4	US-10-424-599-243608	Sequence 243608,	661	40	50.0	311	4	US-10-024-212-14	Sequence 14, Appl
589	41	51.2	49	4	US-10-424-599-243744	Sequence 243744,	662	40	50.0	311	4	US-10-024-212-16	Sequence 16, Appl
590	41	51.2	52	4	US-10-424-599-155058	Sequence 155058,	663	40	50.0	347	4	US-10-046-938-13	Sequence 13, Appl
591	41	51.2	61	4	US-10-425-115-317505	Sequence 317505,	664	40	50.0	350	4	US-10-221-625-87	Sequence 87, Appl
592	41	51.2	61	4	US-10-425-115-368475	Sequence 368475,	665	40	50.0	353	4	US-10-381-898-14	Sequence 14, Appl
593	41	51.2	97	4	US-10-425-115-325285	Sequence 325285,	666	40	50.0	370	4	US-10-219-834-24	Sequence 24, Appl
594	41	51.2	102	4	US-10-424-599-262798	Sequence 262798,	667	40	50.0	370	4	US-10-182-822A-15	Sequence 15, Appl
595	41	51.2	114	5	US-10-644-765-173	Sequence 173, App	668	40	50.0	384	6	US-11-097-143-7461	Sequence 7461, Ap
596	41	51.2	188	4	US-10-017-161-1046	Sequence 1046, Ap	669	40	50.0	407	4	US-10-017-161-2354	Sequence 2354, Ap
597	41	51.2	188	4	US-10-292-798-888	Sequence 888, App	670	40	50.0	407	4	US-10-292-798-1998	Sequence 1998, Ap
598	41	51.2	399	4	US-10-369-493-7020	Sequence 7020, Ap	671	40	50.0	422	4	US-10-124-608C-4	Sequence 4, Appl
599	41	51.2	408	4	US-10-424-599-212014	Sequence 212014,	672	40	50.0	430	3	US-09-734-569-174	Sequence 174, App
600	41	51.2	463	4	US-10-424-599-148050	Sequence 148050,	673	40	50.0	444	5	US-10-491-183-45	Sequence 45, Appl
601	41	51.2	555	5	US-10-739-930-7395	Sequence 7395, Ap	674	40	50.0	496	4	US-10-002-720-50	Sequence 50, Appl
602	41	51.2	577	4	US-10-437-963-124414	Sequence 124414,	675	40	50.0	496	4	US-10-002-750-50	Sequence 50, Appl
603	41	51.2	740	4	US-10-437-963-124417	Sequence 124417,	676	40	50.0	496	5	US-10-857-137-6	Sequence 6, Appl
604	41	51.2	817	4	US-10-425-115-3266079	Sequence 266079,	677	40	50.0	496	5	US-10-613-106-6	Sequence 6, Appl
605	40	50.0	8	6	US-11-066-697-197	Sequence 197, App	678	40	50.0	524	4	US-10-205-522-40	Sequence 40, Appl
606	40	50.0	8	6	US-11-066-697-198	Sequence 198, App	679	40	50.0	527	4	US-10-307-817-118	Sequence 118, App
607	40	50.0	9	4	US-10-036-869-13	Sequence 13, Appl	680	40	50.0	529	3	US-09-981-353-194	Sequence 194, App
608	40	50.0	10	3	US-09-852-870A-3	Sequence 3, Appl	681	40	50.0	529	4	US-10-057-834A-2	Sequence 2, Appl
609	40	50.0	10	3	US-09-852-870A-4	Sequence 4, Appl	682	40	50.0	529	4	US-10-438-929-2	Sequence 2, Appl
610	40	50.0	21	4	US-10-058-053A-290	Sequence 290, App	683	40	50.0	529	4	US-10-042-865-144	Sequence 144, App
611	40	50.0	21	4	US-10-838-226-290	Sequence 290, App	684	40	50.0	529	4	US-10-042-865-148	Sequence 148, App

685	40	50.0	529	4	US-10-072-012-502	Sequence 502, App	758	38	47.5	12	6	US-11-066-697-99	Sequence 99, Appl
686	40	50.0	529	4	US-10-072-012-506	Sequence 506, App	759	38	47.5	13	6	US-11-066-697-100	Sequence 100, Appl
687	40	50.0	529	5	US-10-783-228-115	Sequence 115, App	760	38	47.5	14	4	US-10-344-381A-19	Sequence 19, Appl
688	40	50.0	532	5	US-10-450-763-35883	Sequence 35883, A	761	38	47.5	17	4	US-10-344-381A-18	Sequence 18, Appl
689	40	50.0	533	4	US-10-042-865-28	Sequence 28, Appl	762	38	47.5	17	4	US-10-344-381A-24	Sequence 24, Appl
690	40	50.0	533	4	US-10-072-012-152	Sequence 152, App	763	38	47.5	20	3	US-09-171-432A-17	Sequence 17, Appl
691	40	50.0	533	5	US-10-450-763-35882	Sequence 35882, A	764	38	47.5	20	4	US-10-344-381A-26	Sequence 26, Appl
692	40	50.0	593	4	US-10-072-012-390	Sequence 390, App	765	38	47.5	20	4	US-10-344-381A-28	Sequence 28, Appl
693	40	50.0	940	4	US-10-437-963-180919	Sequence 180919, A	766	38	47.5	21	5	US-10-738-443-17	Sequence 17, Appl
694	40	50.0	940	4	US-10-425-114-62836	Sequence 62836, A	767	38	47.5	22	4	US-10-058-053A-266	Sequence 266, App
695	40	50.0	1456	4	US-10-437-963-180908	Sequence 180908, A	768	38	47.5	22	4	US-10-838-226-266	Sequence 266, App
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704	39	48.8	58	4	US-10-424-599-222430	Sequence 222430, A	777	38	47.5	65	5	US-10-721-793-24	Sequence 24, Appli
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706	39	48.8	66	4	US-10-083-357-1175	Sequence 1175, App	779	38	47.5	65	5	US-10-721-793-32	Sequence 32, Appli
707	39	48.8	68	4	US-10-425-115-201763	Sequence 201763, A	780	38	47.5	65	5	US-10-721-793-36	Sequence 36, Appli
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987 38 47.5 124 4 US-10-238-196-26 Sequence 26, Appl
988 38 47.5 124 4 US-10-245-013-26 Sequence 26, Appl
989 38 47.5 124 4 US-10-219-538-266 Sequence 266, App
990 38 47.5 124 5 US-10-820-474A-96 Sequence 96, Appl
991 38 47.5 124 5 US-10-950-374-266 Sequence 266, App
992 38 47.5 125 3 US-09-854-105-2 Sequence 2, Appl
993 38 47.5 131 4 US-10-479-670-102 Sequence 102, App
994 38 47.5 135 4 US-10-322-696-9 Sequence 9, Appl
995 38 47.5 139 4 US-10-322-696-12 Sequence 12, Appl
996 38 47.5 149 4 US-10-767-701-61515 Sequence 61515, A
997 38 47.5 163 4 US-10-437-963-130591 Sequence 130591,
998 38 47.5 175 6 US-11-097-143-519 Sequence 519, App
999 38 47.5 181 4 US-10-445-115-270806 Sequence 270806,
1000 38 47.5 197 6 US-11-018-645-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-10-796-158-6
; Sequence 6, Application US/10796158
; Publication No. US2005011809A1
; GENERAL INFORMATION:
; APPLICANT: IDEC Pharmaceuticals
; APPLICANT: Braslawsky, Gary
; APPLICANT: Chinn, Paul
; APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: THIOL-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
; FILE REFERENCE: 037003-0308678
; CURRENT APPLICATION NUMBER: US/10/796,158
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic SST analog
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: D stereoisomer
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDE OR ALCOHOL
; FILE REFERENCE: 037003-0308678
; CURRENT APPLICATION NUMBER: US/10/796,158
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic SST analog
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: D stereoisomer
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: D stereoisomer
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (5)..(10)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDE OR ALCOHOL
US-10-796-158-6

Query Match 100.0%; Score 80; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CYYCFWKTC 11

Db 1 CYYCFWKTC 11
RESULT 2
US-10-796-158-5
; Sequence 5, Application US/10796158
; Publication No. US2005011809A1
; GENERAL INFORMATION:
; APPLICANT: IDEC Pharmaceuticals
; APPLICANT: Braslawsky, Gary
; APPLICANT: Chinn, Paul
; APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: THIOL-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
; FILE REFERENCE: 037003-0308678
; CURRENT APPLICATION NUMBER: US/10/796,158
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic SST analog
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: D stereoisomer
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDATION OR ALCOHOL
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDE OR ALCOHOL
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (5)..(10)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: D stereoisomer
US-10-796-158-5

Query Match 80.0%; Score 64; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YCFWKTC 11
Db 3 YCFWKTC 11

RESULT 3
US-10-490-326-25
; Sequence 25, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851

; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 25
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-490-326-25

Query Match 80.0%; Score 64; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
 |||||
 Db 7 YYCFWKTKCT 15

RESULT 4
 US-10-490-326-27
 ; Sequence 27, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; FILE REFERENCE: Bombesin Analog Conjugates and Uses Thereof
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; NAME/KEY: MOD_RES
 ; LOCATION: 9, 14
 ; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
 US-10-490-326-27

Query Match 80.0%; Score 64; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
 |||||
 Db 7 YYCFWKTKCT 15

RESULT 5
 US-10-490-326-37
 ; Sequence 37, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; FILE REFERENCE: Bombesin Analog Conjugates and Uses Thereof
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 37
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; NAME/KEY: MOD_RES
 ; LOCATION: 9, 14
 ; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
 US-10-490-326-37

; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 37
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-490-326-37

Query Match 80.0%; Score 64; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
 |||||
 Db 12 YYCFWKTKCT 20

RESULT 6
 US-10-490-326-38
 ; Sequence 38, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; FILE REFERENCE: Bombesin Analog Conjugates and Uses Thereof
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: 14, 19
 ; OTHER INFORMATION: Cys at positions 14 and 19 are circularized
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-490-326-38

Query Match 80.0%; Score 64; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYCFWKTKCT 11
 |||||
 Db 12 YYCFWKTKCT 20

RESULT 7
 US-10-490-326-45
 ; Sequence 45, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.

; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 14..19
; OTHER INFORMATION: Cys at positions 14 and 19 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-45

Query Match 80.0%; Score 64; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 3 YYCFWKTC 11
| | | | | | | |
Db 12 YYCFWKTC 20

RESULT 8
US-10-490-326-22
; Sequence 22, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 16..21
; OTHER INFORMATION: Cys at positions 16 and 21 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-22

Query Match 80.0%; Score 64; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 3 YYCFWKTC 11
| | | | | | | |
Db 14 YYCFWKTC 22

RESULT 9
US-10-490-326-43
; Sequence 43, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 19..24
; OTHER INFORMATION: Cys at positions 19 and 24 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-43

Query Match 80.0%; Score 64; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 3 YYCFWKTC 11
| | | | | | | |
Db 17 YYCFWKTC 25

RESULT 10
US-10-490-326-46
; Sequence 46, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 19..24
; OTHER INFORMATION: Cys at positions 19 and 24 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-46

US-10-490-326-46

Query Match 80.0%; Score 64; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
| | | | | | | | | |
Db 17 YYCFWKTCCT 25

RESULT 11

US-10-490-326-44
; Sequence 44, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 24_29
; OTHER INFORMATION: Cys at positions 24 and 29 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-44

Query Match 80.0%; Score 64; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
| | | | | | | | | |
Db 22 YYCFWKTCCT 30

RESULT 12

US-10-796-158-7
; Sequence 7, Application US/10796158
; Publication No. US20050118099A1
; GENERAL INFORMATION:
; APPLICANT: IDEC Pharmaceuticals
; APPLICANT: Braslawsky, Gary
; APPLICANT: Chinn, Paul
; APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: THIOL-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
; FILE REFERENCE: 037003-0308678
; CURRENT APPLICATION NUMBER: US/10/796,158
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic SST analog

; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: D stereoisomer
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: D stereoisomer
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (5)..(10)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDE OR ALCOHOL
US-10-796-158-7

Query Match 77.5%; Score 62; DB 5; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YYCFWKTCCT 11
| | | | | | | | | |
Db 2 YYCFWKTCCT 11

RESULT 13

US-10-490-326-24
; Sequence 24, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-24

Query Match 68.8%; Score 55; DB 5; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
| | | | | | | | | |
Db 4 YYCFWKTCCT 12

RESULT 14

US-10-490-326-30
; Sequence 30, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun

; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa = Sar
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 6, 11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-490-326-30

Query Match 68.8%; Score 55; DB 5; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKT 11
| | | | | | | |
Db 4 YSCFWKTKT 12

RESULT 15
US-10-490-326-31
; Sequence 31, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 6, 11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-490-326-31

Query Match 68.8%; Score 55; DB 5; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 YYCFWKTKT 11
| | | | | | | |
Db 4 YSCFWKTKT 12
RESULT 16
US-10-490-326-32
; Sequence 32, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa = OH-Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 6, 11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-490-326-32

Query Match 68.8%; Score 55; DB 5; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKT 11
| | | | | | | |
Db 4 YSCFWKTKT 12

RESULT 17
US-10-490-326-41
; Sequence 41, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143

RESULT 19
US-10-490-326-23
; Sequence 23, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002 US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-41

Query Match 68.8%; Score 55; DB 5; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 4 YSCFWKTKCT 12

RESULT 18
US-10-490-326-21
; Sequence 21, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-21

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 7 YSCFWKTKCT 15

RESULT 20
US-10-490-326-35
; Sequence 35, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002 US/10/490,326
; CURRENT APPLICATION NUMBER: PCT/US02/30143
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-35

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 7 YSCFWKTKCT 15

RESULT 20
US-10-490-326-35
; Sequence 35, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002 US/10/490,326
; CURRENT APPLICATION NUMBER: PCT/US02/30143
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa = Nle
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-35

Query Match 68.8%; Score 55; DB 5; Length 15;
 Best Local Similarity 88.9%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 Db 7 YSCFWKTCCT 15

RESULT 21

US-10-490-326-36
 ; Sequence 36, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fusellier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 36
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 6
 ; OTHER INFORMATION: Xaa = Nle
 ; NAME/KEY: MOD.RES
 ; LOCATION: 9, 14
 ; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; US-10-490-326-36

Query Match 68.8%; Score 55; DB 5; Length 15;
 Best Local Similarity 88.9%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 Db 7 YSCFWKTCCT 15

RESULT 22

US-10-490-326-47
 ; Sequence 47, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fusellier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 47
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 6
 ; OTHER INFORMATION: Xaa = 4Pal
 ; NAME/KEY: MOD.RES
 ; LOCATION: 9, 14
 ; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; US-10-490-326-47

Query Match 68.8%; Score 55; DB 5; Length 15;
 Best Local Similarity 88.9%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 Db 7 YSCFWKTCCT 15

RESULT 23

US-10-490-326-48
 ; Sequence 48, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fusellier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 48
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MOD.RES
 ; LOCATION: 9, 14
 ; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; US-10-490-326-48

Query Match 68.8%; Score 55; DB 5; Length 15;
 Best Local Similarity 88.9%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTCCT 11
 Db 7 YSCFWKTCCT 15

RESULT 24

US-10-490-326-49
 ; Sequence 49, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fusellier, Joseph A.
 ; APPLICANT: Murphy, William A.

```

; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-49

```

```

Query Match      68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      3 YYCFWKTKCT 11
      | |||||
Db      7 YSCFWKTKCT 15

```

```

RESULT 25
US-10-490-326-51
; Sequence 51, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fueselner, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-51

```

```

Query Match      68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      3 YYCFWKTKCT 11
      | |||||
Db      7 YSCFWKTKCT 15

```

```

RESULT 26
US-10-490-326-52
; Sequence 52, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fueselner, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa = Abu
; NAME/KEY: MOD_RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-52

```

```

Query Match      68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      3 YYCFWKTKCT 11
      | |||||
Db      7 YSCFWKTKCT 15

```

```

RESULT 27
US-10-490-326-53
; Sequence 53, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fueselner, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized

```

; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-53

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 7 YSCFWKTKCT 15

RESULT 28
US-10-490-326-55
; Sequence 55, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa = hSer
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at position 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-55

Query Match 68.8%; Score 55; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 7 YSCFWKTKCT 15

RESULT 29
US-10-490-326-50
; Sequence 50, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 10, 15
; OTHER INFORMATION: Cys at positions 10 and 15 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-50

Query Match 68.8%; Score 55; DB 5; Length 16;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 8 YSCFWKTKCT 16

RESULT 30
US-10-490-326-54
; Sequence 54, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 10, 15
; OTHER INFORMATION: Cys at positions 10 and 15 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-54

Query Match 68.8%; Score 55; DB 5; Length 16;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTKCT 11
| | | | |
Db 8 YSCFWKTKCT 16

RESULT 31
US-10-490-326-56
; Sequence 56, Application US/10490326
; Publication No. US20050070470A1

; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; PRIOR FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 56
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 9
 ; OTHER INFORMATION: Xaa = 4Pal
 ; NAME/KEY: MOD_RES
 ; LOCATION: 12, 17
 ; OTHER INFORMATION: Cys at positions 12 and 17 are circularized
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ;
 ; US-10-490-326-56

Query Match 68.8%; Score 55; DB 5; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSCFWKTCT 11
 Db 10 YSCFWKTCT 18

RESULT 32
 US-10-490-326-26
 ; Sequence 26, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ;
 ; US-10-490-326-26

Query Match 68.8%; Score 55; DB 5; Length 19;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSCFWKTCT 11

Db 11 YSCFWKTCT 19
 RESULT 33
 US-10-490-326-58
 ; Sequence 58, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 58
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 10
 ; OTHER INFORMATION: Xaa = Abu
 ; NAME/KEY: MOD_RES
 ; LOCATION: 13, 18
 ; OTHER INFORMATION: Cys at positions 13 and 18 are circularized
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ;
 ; US-10-490-326-58

Query Match 68.8%; Score 55; DB 5; Length 19;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YSCFWKTCT 11
 Db 11 YSCFWKTCT 19

RESULT 34
 US-10-490-326-40
 ; Sequence 40, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 40
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ;
 ; US-10-490-326-40

```
; NAME/KEY: VARIANT
; LOCATION: 11
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD_RES
; LOCATION: 14, 19
; OTHER INFORMATION: Cys at positions 14 and 19 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-40
```

```
Query Match      68.8%; Score 55; DB 5; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      3 YYCFWKTCT 11
      | |||||
Db      12 YSCFWKTCT 20
```

```
RESULT 35
US-10-490-326-29
; Sequence 29, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 12
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD_RES
; LOCATION: 15, 20
; OTHER INFORMATION: Cys at positions 15 and 20 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-29
```

```
Query Match      68.8%; Score 55; DB 5; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      3 YYCFWKTCT 11
      | |||||
Db      13 YSCFWKTCT 21
```

```
RESULT 36
US-10-490-326-39
; Sequence 39, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
```

```
; TITLE OF INVENTION: Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 12
; OTHER INFORMATION: Xaa = Nle
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-39
```

```
Query Match      68.8%; Score 55; DB 5; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      3 YYCFWKTCT 11
      | |||||
Db      13 YSCFWKTCT 21
```

```
RESULT 37
US-10-490-326-57
; Sequence 57, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 13
; OTHER INFORMATION: Xaa = Nva
; NAME/KEY: MOD_RES
; LOCATION: 16, 21
; OTHER INFORMATION: Cys at positions 16 and 21 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-57
```

```
Query Match      68.8%; Score 55; DB 5; Length 22;
Best Local Similarity 88.9%; Pred. No. 2;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      3 YYCFWKTCT 11
      | |||||
Db      14 YSCFWKTCT 22
```

RESULT 38
US-09-781-980-5
; Sequence 5, Application US/09781980
; Publication No. US20010029035A1
; GENERAL INFORMATION:
; APPLICANT: EISENHUT, MICHAEL
; APPLICANT: MIER, WALTER
; APPLICANT: BRITJA, RAMON
; APPLICANT: HABERKORN, UWE
; TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
; FILE REFERENCE: 2502498.991110
; CURRENT APPLICATION NUMBER: US/09/781.980
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: DE 100 06 572
; PRIOR FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-781-980-5

Query Match 66.2%; Score 53; DB 3; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
:|||||
Db 1 FCFWKTKCT 8

RESULT 39
US-10-818-246-1
; Sequence 1, Application US/10818246
; Publication No. US20040249121A1
; GENERAL INFORMATION:
; APPLICANT: Novetide, Ltd.
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF CYCLIC PEPTIDES
; FILE REFERENCE: 12647/46002
; CURRENT APPLICATION NUMBER: US/10/818.246
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: 60/461,222
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-818-246-1

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
:|||||
Db 1 FCFWKTKCT 8

RESULT 40
US-10-473-721A-15
; Sequence 15, Application US/10473721A
; Publication No. US20050004000A1
; GENERAL INFORMATION:

; APPLICANT: SHECHTER, Yoram
; APPLICANT: GOLDWASER, Itzhak
; APPLICANT: LAVON, Iris
; APPLICANT: BRODIE, David
; APPLICANT: EVAL, Nurit
; APPLICANT: FASS, Stanley
; APPLICANT: FRIDKIN, Matityahu
; TITLE OF INVENTION: ORAL ABSORBED DRUGS
; FILE REFERENCE: SHECTERS
; CURRENT APPLICATION NUMBER: US/10/473.721A
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/IL02/00252
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: IL 142353
; PRIOR FILING DATE: 2001-04-01
; PRIOR APPLICATION NUMBER: IL 146383
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(8)
; OTHER INFORMATION: Cyclic eight-amino acid peptide. Phe (residue 1) is D-Phe. Trp (residue 4) is D-Trp. Thr (residue 8) is Thr-O-acetate.
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; OTHER INFORMATION: Disulfide bond between the two Cys amino acid residues.
US-10-473-721A-15

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
:|||||
Db 1 FCFWKTKCT 8

RESULT 41
US-10-473-721A-16
; Sequence 16, Application US/10473721A
; Publication No. US20050004000A1
; GENERAL INFORMATION:
; APPLICANT: SHECHTER, Yoram
; APPLICANT: GOLDWASER, Itzhak
; APPLICANT: LAVON, Iris
; APPLICANT: BRODIE, David
; APPLICANT: EVAL, Nurit
; APPLICANT: FASS, Stanley
; APPLICANT: FRIDKIN, Matityahu
; TITLE OF INVENTION: ORAL ABSORBED DRUGS
; FILE REFERENCE: SHECTERS
; CURRENT APPLICATION NUMBER: US/10/473.721A
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/IL02/00252
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: IL 142353
; PRIOR FILING DATE: 2001-04-01
; PRIOR APPLICATION NUMBER: IL 146383
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial

```
;
;
; OTHER INFORMATION: Synthetic
;
; FEATURE:
;
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(8)
; OTHER INFORMATION: Cyclic eight-amino acid peptide. Phe (residue 1) is D-Phe. Trp
; OTHER INFORMATION: (residue 4) is D-Trp. Lys (residue 5) is N-Fmoc-Lys or N-Fms-Lys.
; OTHER INFORMATION: Thr (residue 8) is Thr-O-acetate.
;
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; OTHER INFORMATION: Disulfide bond between the two Cys amino acid groups.
US-10-473-721A-16

Query Match          66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
Db 1 FCFWKTKCT 8

RESULT 42
US-10-916-522A-4
; Sequence 4, Application US/10916522A
; Publication No. US20050043226A1
; GENERAL INFORMATION:
; APPLICANT: Hotnik, Vered
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOG
; FILE REFERENCE: 87534-3099
; CURRENT APPLICATION NUMBER: US/10/916.522A
; CURRENT FILING DATE: 2004-08-12
; PRIOR FILING DATE: 2004-08-12
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Phe residue is a D isomer
;
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: The Thr residue ends with CH2OH
;
; NAME/KEY: DISULFIDE BRIDGE
; LOCATION: (2)..(2)
; OTHER INFORMATION: A disulfide bridge is formed between Cys residues 2 and 7
;
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: The Trp residue is a D isomer
;
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-916-522A-4

Query Match          66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
Db 1 FCFWKTKCT 8

RESULT 43
US-10-505-239-12
; Sequence 12, Application US/10505239
```

```
;
;
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505.239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
;
; NAME/KEY: misc.feature
; LOCATION: (1)..(8)
; OTHER INFORMATION: wherein the peptide is carboxylated at either the N-or C-
; OTHER INFORMATION: terminus
US-10-505-239-12

Query Match          66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKCT 11
Db 1 FCFWKTKCT 8

RESULT 44
US-11-006-071-7
; Sequence 7, Application US/11006071
; Publication No. US20050229275A1
; GENERAL INFORMATION:
; APPLICANT: Koprowski, Hilary
; APPLICANT: Yusibov, Vidadi
; TITLE OF INVENTION: Production Of Biomedical Peptides And Proteins In
; TITLE OF INVENTION: Plants Using Plant Virus Vectors
; FILE REFERENCE: JEFF-KOPO1.P0001
; CURRENT APPLICATION NUMBER: US/11/006,071
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US/09/673,174
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/118,867
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: PCT/US99/25566
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A peptide to
; OTHER INFORMATION: suppress the synthesis of human growth hormone
US-11-006-071-7

Query Match          66.2%; Score 53; DB 6; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 4 YCFWKTCCT 11
:|||||
Db 2 FCFWKTCCT 9

RESULT 45
US-10-490-326-34
; Sequence 34, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fueselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1, 6
; OTHER INFORMATION: Cys at positions 1 and 6 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-34

Query Match 62.5%; Score 50; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CFWKTCCT 11
:|||||
Db 1 CFWKTCCT 7

RESULT 46
US-10-796-158-4
; Sequence 4, Application US/10796158
; Publication No. US20050118099A1
; GENERAL INFORMATION:
; APPLICANT: IDEC Pharmaceuticals
; APPLICANT: Braslawsky, Gary
; APPLICANT: Chinn, Paul
; APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: THIOLE-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
; FILE REFERENCE: 037003-0308678
; CURRENT APPLICATION NUMBER: US/10/796,158
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic SSFR binding domain
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (1)..(6)
; OTHER INFORMATION:
; FEATURE:

Oy 5 CFWKTCCT 11
:|||||
Db 1 CFWKTCCT 7

RESULT 47
US-09-781-980-6
; Sequence 6, Application US/09781980
; Publication No. US20010029035A1
; GENERAL INFORMATION:
; APPLICANT: EISENHUT, MICHAEL
; APPLICANT: MIER, WALTER
; APPLICANT: ERITJA, RAMON
; APPLICANT: HABERKORN, UWE
; TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
; FILE REFERENCE: 2502498.991110
; CURRENT APPLICATION NUMBER: US/09/781,980
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: DE 100 06 572
; PRIOR FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-781-980-6

Query Match 62.5%; Score 50; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YCFWKTCCT 11
:|||||
Db 1 FCFWKTCCT 8

RESULT 48
US-10-427-160A-22
; Sequence 22, Application US/10427160A
; Publication No. US20040110296A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Vargeese, Chandra
; APPLICANT: Haeblerli, Peter
; APPLICANT: Wang, Weimin
; APPLICANT: Chen, Tongqian
; TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery
; FILE REFERENCE: 600/032 (MBHH02-312-A)
; CURRENT APPLICATION NUMBER: US/10/427,160A
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: PCT/US 02/15876
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
```

; PRIOR APPLICATION NUMBER: US 60/306,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Ser stands for optional Serine for coupling
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Phe stands for optional D isomer for stability
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Trp stands for optional D isomer for stability
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic peptide
US-10-427-160A-22

Query Match 62.5%; Score 50; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|:|||||
Db 2 FCYWKTCCT 9

RESULT 49
US-10-444-853A-515
; Sequence 515, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fossnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBH03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 515
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Somatostatin (tyr-3-octreotate)
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Ser at position 1 is optionally present for coupling.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)..(2)
; OTHER INFORMATION: Phe at position 2 is optionally the D-isomer.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (5)..(5)
; OTHER INFORMATION: Trp at position 5 is optionally the D-isomer.
US-10-444-853A-515

Query Match 62.5%; Score 50; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|:|||||
Db 2 FCYWKTCCT 9

RESULT 50
US-10-780-447-22
; Sequence 22, Application US/10780447
; Publication No. US20040249178A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Vargeese, Chandra
; APPLICANT: Haerberli, Peter
; APPLICANT: Wang, Weimin
; APPLICANT: Chen, Tongqian
; TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery
; FILE REFERENCE: 600/032 (MBH02-312-A)
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242	34	42.5	32	11	US-11-198-847-256	Sequence 256, App	315	34	42.5	354	9	US-10-152-370-400	Sequence 400, App
243	34	42.5	33	11	US-11-198-847-238	Sequence 238, App	316	34	42.5	354	11	US-11-290-153-400	Sequence 400, App
244	34	42.5	33	11	US-11-198-847-239	Sequence 239, App	317	34	42.5	356	9	US-10-517-939-234	Sequence 234, App
245	34	42.5	34	11	US-11-198-847-253	Sequence 253, App	318	34	42.5	356	11	US-11-096-568A-31112	Sequence 31112, A
246	34	42.5	37	11	US-11-198-847-254	Sequence 254, App	319	34	42.5	358	9	US-10-517-939-370	Sequence 370, App
247	34	42.5	37	11	US-11-198-847-289	Sequence 289, App	320	34	42.5	387	9	US-10-467-657-5522	Sequence 5522, App
248	34	42.5	38	11	US-11-198-847-250	Sequence 250, App	321	34	42.5	452	11	US-11-096-568A-27763	Sequence 27763, A
249	34	42.5	38	11	US-11-198-847-251	Sequence 251, App	322	34	42.5	467	11	US-11-096-568A-31111	Sequence 31111, A
250	34	42.5	45	11	US-11-123-896-129	Sequence 123, App	323	34	42.5	500	10	US-11-254-195-6	Sequence 6, Appli
251	34	42.5	45	11	US-11-123-896-132	Sequence 132, App	324	34	42.5	503	10	US-11-317-983-9	Sequence 9, Appli
252	34	42.5	45	11	US-11-198-847-90	Sequence 90, Appl	325	34	42.5	520	10	US-11-317-983-2	Sequence 2, Appli
253	34	42.5	66	9	US-10-948-571-104	Sequence 104, App	326	34	42.5	542	9	US-10-517-939-262	Sequence 262, App
254	34	42.5	71	11	US-11-198-847-71	Sequence 71, Appl	327	34	42.5	547	10	US-11-317-983-25	Sequence 25, Appl
255	34	42.5	71	11	US-11-198-847-74	Sequence 74, Appl	328	34	42.5	635	9	US-10-821-234-1673	Sequence 1673, App
256	34	42.5	72	11	US-11-198-847-20	Sequence 20, Appl	329	34	42.5	672	9	US-10-499-290-2	Sequence 2, Appli
257	34	42.5	72	11	US-11-198-847-77	Sequence 77, Appl	330	34	42.5	740	9	US-10-455-772-170	Sequence 170, App
258	34	42.5	72	11	US-11-198-847-113	Sequence 113, App	331	34	42.5	816	11	US-11-087-099-10395	Sequence 10395, A
259	34	42.5	74	11	US-11-198-847-26	Sequence 26, Appl	332	34	42.5	818	11	US-11-144-985-13	Sequence 13, Appl
260	34	42.5	74	11	US-11-198-847-59	Sequence 59, Appl	333	34	42.5	847	11	US-11-087-099-3302	Sequence 3302, App
261	34	42.5	74	11	US-11-198-847-104	Sequence 104, App	334	34	42.5	1014	11	US-11-204-187-20	Sequence 20, Appl
262	34	42.5	74	11	US-11-198-847-107	Sequence 107, App	335	34	42.5	1020	11	US-11-144-985-3	Sequence 3, Appli
263	34	42.5	74	11	US-11-198-847-140	Sequence 140, App	336	34	42.5	2011	11	US-11-080-991-56	Sequence 56, Appl
264	34	42.5	74	11	US-11-198-847-170	Sequence 170, App	337	34	42.5	2281	9	US-10-455-772-166	Sequence 166, App
265	34	42.5	76	11	US-11-123-896-128	Sequence 128, App	338	34	42.5	2281	9	US-10-455-772-172	Sequence 172, App
266	34	42.5	76	11	US-11-123-896-131	Sequence 131, App	339	34	42.5	2299	9	US-10-455-772-168	Sequence 168, App
267	34	42.5	80	11	US-11-198-847-131	Sequence 47, Appl	340	34	42.5	2300	9	US-10-455-772-178	Sequence 178, App
268	34	42.5	80	11	US-11-198-847-47	Sequence 47, Appl	341	34	42.5	16	11	US-11-198-847-309	Sequence 309, App
269	34	42.5	80	11	US-11-198-847-65	Sequence 65, Appl	342	34	42.5	56	11	US-11-207-078-127	Sequence 127, App
270	34	42.5	80	11	US-11-198-847-200	Sequence 200, App	343	34	42.5	99	11	US-11-050-857-1080	Sequence 1080, App
271	34	42.5	80	11	US-11-198-847-203	Sequence 203, App	344	34	42.5	142	9	US-10-793-626-2342	Sequence 2342, App
272	34	42.5	81	11	US-11-198-847-101	Sequence 101, App	345	34	42.5	201	11	US-11-098-686-10983	Sequence 10983, A
273	34	42.5	82	11	US-11-198-847-185	Sequence 185, App	346	34	42.5	215	11	US-11-050-857-651	Sequence 651, App
274	34	42.5	82	11	US-11-198-847-188	Sequence 188, App	347	34	42.5	276	11	US-11-054-281-85	Sequence 85, Appl
275	34	42.5	83	11	US-11-198-847-191	Sequence 191, App	348	34	42.5	277	11	US-11-054-281-84	Sequence 84, Appl
276	34	42.5	83	11	US-11-198-847-194	Sequence 44, Appl	349	34	42.5	305	11	US-11-098-686-11298	Sequence 11298, A
277	34	42.5	83	11	US-11-198-847-33	Sequence 53, Appl	350	34	42.5	306	9	US-10-793-626-574	Sequence 574, App
278	34	42.5	83	11	US-11-198-847-56	Sequence 56, Appl	351	34	42.5	306	9	US-10-793-626-2490	Sequence 2490, App
279	34	42.5	89	11	US-11-198-847-62	Sequence 62, Appl	352	34	42.5	306	9	US-10-793-626-2640	Sequence 2640, App
280	34	42.5	89	11	US-11-198-847-197	Sequence 197, App	353	34	42.5	367	9	US-10-455-772-500	Sequence 500, App
281	34	42.5	89	11	US-11-198-847-209	Sequence 209, App	354	34	42.5	2613	9	US-10-455-772-530	Sequence 530, App
282	34	42.5	93	11	US-11-079-463-5874	Sequence 5874, App	355	34	42.5	2628	9	US-10-455-772-502	Sequence 502, App
283	34	42.5	107	11	US-11-040-159-17	Sequence 17, Appl	356	34	42.5	2715	11	US-11-096-051-2	Sequence 2, Appli
284	34	42.5	108	11	US-11-040-159-13	Sequence 13, Appl	357	34	42.5	2721	9	US-10-455-772-522	Sequence 522, App
285	34	42.5	108	11	US-11-054-669-94	Sequence 94, Appl	358	34	42.5	2721	11	US-11-096-051-10	Sequence 10, Appl
286	34	42.5	108	11	US-11-054-669-111	Sequence 111, App	359	34	42.5	2725	9	US-10-455-772-486	Sequence 486, App
287	34	42.5	109	11	US-11-040-159-7	Sequence 7, Appli	360	34	42.5	2725	9	US-10-455-772-526	Sequence 526, App
288	34	42.5	109	11	US-11-040-159-9	Sequence 9, Appli	361	34	42.5	2725	9	US-10-455-772-546	Sequence 546, App
289	34	42.5	109	11	US-11-040-159-11	Sequence 11, Appl	362	34	42.5	2725	9	US-10-455-772-546	Sequence 546, App
290	34	42.5	109	11	US-11-040-159-13	Sequence 13, Appl	363	34	42.5	2725	9	US-10-455-772-548	Sequence 548, App
291	34	42.5	109	11	US-11-040-159-13	Sequence 143, App	364	34	42.5	2725	9	US-10-455-772-550	Sequence 550, App
292	34	42.5	116	11	US-11-264-096-1934	Sequence 1934, Ap	365	34	42.5	2725	9	US-10-455-772-552	Sequence 552, App
293	34	42.5	124	11	US-11-072-512-3002	Sequence 3002, App	366	34	42.5	2725	11	US-11-096-051-8	Sequence 8, Appli
294	34	42.5	159	11	US-11-087-099-10505	Sequence 10505, A	367	34	42.5	7	11	US-11-129-741-3979	Sequence 3979, App
295	34	42.5	169	11	US-11-186-284-53	Sequence 53, Appl	368	34	42.5	13	11	US-11-198-847-306	Sequence 306, App
296	34	42.5	190	11	US-11-170-653-33	Sequence 33, Appl	369	34	42.5	21	11	US-11-198-847-291	Sequence 291, App
297	34	42.5	223	11	US-11-170-653-34	Sequence 34, Appl	370	34	42.5	26	11	US-11-264-096-823	Sequence 823, App
298	34	42.5	223	11	US-11-198-298-6926	Sequence 6926, Ap	371	34	42.5	26	11	US-11-153-260-1	Sequence 1, Appli
299	34	42.5	224	11	US-11-096-568A-29718	Sequence 29718, A	372	34	42.5	28	11	US-11-198-847-240	Sequence 240, App
300	34	42.5	225	9	US-10-517-939-172	Sequence 172, App	373	34	42.5	28	11	US-11-198-847-242	Sequence 241, App
301	34	42.5	228	11	US-11-096-568A-29717	Sequence 29717, A	374	34	42.5	28	11	US-11-198-847-242	Sequence 242, App
302	34	42.5	234	11	US-11-096-568A-29716	Sequence 29716, A	375	34	42.5	28	11	US-11-198-847-243	Sequence 243, App
303	34	42.5	237	11	US-11-054-669-109	Sequence 109, App	376	34	42.5	29	11	US-11-198-847-283	Sequence 283, App
304	34	42.5	292	11	US-11-096-568A-27765	Sequence 27765, A	377	34	42.5	29	11	US-11-198-847-305	Sequence 305, App
305	34	42.5	307	11	US-11-096-568A-31113	Sequence 31113, A	378	34	42.5	29	11	US-11-264-096-801	Sequence 801, App
306	34	42.5	341	10	US-11-317-983-8	Sequence 8, Appli	379	34	42.5	33	11	US-11-198-847-298	Sequence 298, App
307	34	42.5	341	10	US-11-096-568A-27764	Sequence 27764, A	380	34	42.5	32	11	US-11-198-847-267	Sequence 267, App
308	34	42.5	341	9	US-10-517-939-220	Sequence 220, App	381	34	42.5	32	11	US-11-198-847-268	Sequence 268, App
309	34	42.5	353	10	US-11-254-195-4	Sequence 4, Appli	382	34	42.5	37	11	US-11-233-798-26	Sequence 26, Appl
310	34	42.5	354	9	US-10-131-826A-400	Sequence 400, App	383	34	42.5	37	11	US-11-198-847-287	Sequence 287, App
311	34	42.5	354	9	US-10-838-616-16	Sequence 16, Appl	384	34	42.5	37	11	US-11-198-847-288	Sequence 288, App
312	34	42.5	354	9	US-10-973-115B-400	Sequence 400, App	385	34	42.5	37	11	US-11-096-568A-2740	Sequence 2740, App
313	34	42.5	354	9	US-10-216-161A-178	Sequence 178, App	386	34	42.5	38	11	US-11-198-847-293	Sequence 293, App

387	33	41.2	38	11	US-11-198-847-294	Sequence 294, App	460	33	41.2	344	11	US-11-108-163B-10	Sequence 10, Appl
388	33	41.2	50	11	US-11-198-847-302	Sequence 302, App	461	33	41.2	348	9	US-10-055-877-174	Sequence 174, App
389	33	41.2	55	11	US-11-004-399-3433	Sequence 3433, App	462	33	41.2	348	9	US-10-517-939-166	Sequence 166, App
390	33	41.2	63	9	US-10-467-657-7520	Sequence 7520, App	463	33	41.2	348	11	US-11-127-877-48	Sequence 48, Appl
391	33	41.2	64	11	US-11-096-568A-8330	Sequence 8330, App	464	33	41.2	348	11	US-11-174-816-20	Sequence 20, Appl
392	33	41.2	68	11	US-11-096-568A-83329	Sequence 8329, App	465	33	41.2	348	11	US-11-174-816-48	Sequence 48, Appl
393	33	41.2	70	7	US-09-978-360A-502	Sequence 502, App	466	33	41.2	348	11	US-11-174-819-34	Sequence 34, Appl
394	33	41.2	70	11	US-11-198-847-17	Sequence 17, Appl	467	33	41.2	348	11	US-11-174-819-72	Sequence 72, Appl
395	33	41.2	71	11	US-11-198-847-68	Sequence 68, Appl	468	33	41.2	349	11	US-11-174-751-22	Sequence 22, Appl
396	33	41.2	75	11	US-11-198-847-164	Sequence 164, App	469	33	41.2	400	11	US-11-079-463-8323	Sequence 8323, App
397	33	41.2	78	11	US-11-198-847-125	Sequence 125, App	470	33	41.2	408	11	US-11-079-463-8323	Sequence 8323, App
398	33	41.2	78	11	US-11-198-847-128	Sequence 128, App	471	33	41.2	425	11	US-11-037-243-92	Sequence 92, Appl
399	33	41.2	78	11	US-11-198-847-215	Sequence 215, App	472	33	41.2	467	11	US-11-087-099-11202	Sequence 11202, A
400	33	41.2	78	11	US-11-198-847-218	Sequence 218, App	473	33	41.2	513	11	US-11-000-463-458	Sequence 458, App
401	33	41.2	79	11	US-11-198-847-149	Sequence 149, App	474	33	41.2	549	11	US-11-188-298-3355	Sequence 3355, App
402	33	41.2	79	11	US-11-198-847-224	Sequence 224, App	475	33	41.2	612	11	US-11-087-099-264	Sequence 264, App
403	33	41.2	80	11	US-11-198-847-83	Sequence 83, Appl	476	33	41.2	614	11	US-11-110-748-2	Sequence 2, Appl
404	33	41.2	82	11	US-11-198-847-119	Sequence 119, App	477	33	41.2	620	11	US-11-072-512-2045	Sequence 2045, App
405	33	41.2	82	11	US-11-198-847-122	Sequence 122, App	478	33	41.2	657	11	US-11-227-543-15	Sequence 15, Appl
406	33	41.2	84	11	US-11-153-260-9	Sequence 9, Appl	479	33	41.2	664	11	US-11-045-004-224	Sequence 224, App
407	33	41.2	85	11	US-11-004-399-104	Sequence 104, App	480	33	41.2	666	11	US-11-188-298-3594	Sequence 3594, App
408	33	41.2	85	11	US-11-004-399-474	Sequence 474, App	481	33	41.2	666	11	US-11-188-298-7174	Sequence 7174, App
409	33	41.2	85	11	US-11-004-399-3907	Sequence 3907, App	482	33	41.2	702	11	US-11-188-298-2417	Sequence 2417, App
410	33	41.2	92	9	US-10-467-657-328	Sequence 328, App	483	33	41.2	796	11	US-11-188-298-10947	Sequence 10947, A
411	33	41.2	93	9	US-10-467-657-3640	Sequence 3640, App	484	33	41.2	798	11	US-11-079-463-10034	Sequence 10034, A
412	33	41.2	93	11	US-11-198-847-131	Sequence 131, App	485	33	41.2	849	11	US-11-188-298-3853	Sequence 3853, App
413	33	41.2	110	11	US-11-198-847-167	Sequence 167, App	486	33	41.2	990	11	US-11-188-298-2875	Sequence 2875, App
414	33	41.2	110	11	US-11-198-847-173	Sequence 173, App	487	33	41.2	1042	11	US-11-067-811-1	Sequence 1, Appl
415	33	41.2	118	9	US-10-467-657-4296	Sequence 4296, App	488	33	41.2	1115	9	US-10-055-877-160	Sequence 160, App
416	33	41.2	133	9	US-10-644-807-295	Sequence 295, App	489	33	41.2	1274	11	US-11-096-568A-29137	Sequence 29137, A
417	33	41.2	137	9	US-09-978-360A-765	Sequence 765, App	490	33	41.2	1283	11	US-11-096-568A-29136	Sequence 29136, A
418	33	41.2	172	9	US-10-644-807-208	Sequence 208, App	491	33	41.2	1286	11	US-11-096-568A-29135	Sequence 29135, A
419	33	41.2	172	11	US-11-072-512-3472	Sequence 3472, App	492	33	41.2	1440	11	US-11-096-568A-28130	Sequence 28130, A
420	33	41.2	173	11	US-11-096-568A-20604	Sequence 20604, A	493	33	41.2	1441	11	US-11-096-568A-28129	Sequence 28129, A
421	33	41.2	191	11	US-11-096-568A-20603	Sequence 20603, A	494	33	41.2	1490	10	US-11-096-568A-28128	Sequence 28128, A
422	33	41.2	193	11	US-11-108-163B-11	Sequence 14, Appl	495	33	41.2	1980	10	US-11-263-326-128	Sequence 128, App
423	33	41.2	196	9	US-10-467-657-4914	Sequence 4914, App	496	33	41.2	1980	10	US-11-363-326-134	Sequence 134, App
424	33	41.2	208	11	US-11-188-298-2274	Sequence 5274, App	497	32.5	40.6	9	11	US-11-041-676A-5	Sequence 5, Appl
425	33	41.2	217	11	US-11-108-163B-13	Sequence 13, Appl	498	32.5	40.6	9	11	US-11-041-676A-8	Sequence 8, Appl
426	33	41.2	217	11	US-11-153-260-11	Sequence 11, Appl	499	32.5	40.6	107	11	US-11-188-298-20880	Sequence 20880, A
427	33	41.2	219	11	US-11-170-653-29	Sequence 29, Appl	500	32.5	40.6	464	11	US-11-096-568A-16302	Sequence 16302, A
428	33	41.2	219	11	US-11-096-568A-20602	Sequence 20602, A	501	32.5	40.6	494	11	US-11-096-568A-16301	Sequence 16301, A
429	33	41.2	220	11	US-11-108-163B-12	Sequence 12, Appl	502	32.5	40.6	514	11	US-11-096-568A-16300	Sequence 16300, A
430	33	41.2	225	11	US-11-170-653-36	Sequence 36, Appl	503	32.5	40.6	530	11	US-11-054-281-94	Sequence 94, Appl
431	33	41.2	226	11	US-11-170-653-63	Sequence 63, Appl	504	32.5	40.6	586	11	US-11-054-281-93	Sequence 93, Appl
432	33	41.2	227	9	US-10-948-429A-6	Sequence 6, Appl	505	32.5	40.6	603	11	US-11-024-359-484	Sequence 484, App
433	33	41.2	232	11	US-11-170-653-64	Sequence 64, Appl	506	32	40.0	8	11	US-11-007-772A-35	Sequence 35, Appl
434	33	41.2	234	11	US-11-098-686-10787	Sequence 10787, A	507	32	40.0	33	11	US-11-121-301-65	Sequence 65, Appl
435	33	41.2	239	11	US-11-170-653-40	Sequence 40, Appl	508	32	40.0	36	11	US-11-198-847-301	Sequence 301, App
436	33	41.2	240	11	US-11-170-653-42	Sequence 42, Appl	509	32	40.0	40	11	US-11-198-847-264	Sequence 264, App
437	33	41.2	240	11	US-11-264-096-1157	Sequence 1157, App	510	32	40.0	49	11	US-11-198-847-270	Sequence 270, App
438	33	41.2	240	11	US-11-264-096-1158	Sequence 1158, App	511	32	40.0	49	11	US-11-198-847-271	Sequence 271, App
439	33	41.2	241	11	US-11-170-653-43	Sequence 43, Appl	512	32	40.0	80	11	US-11-198-847-152	Sequence 152, App
440	33	41.2	249	11	US-11-087-099-261	Sequence 261, App	513	32	40.0	80	11	US-11-198-847-161	Sequence 161, App
441	33	41.2	254	7	US-09-810-501-69	Sequence 69, Appl	514	32	40.0	81	11	US-11-198-847-158	Sequence 158, App
442	33	41.2	254	11	US-11-167-831-16	Sequence 16, Appl	515	32	40.0	85	11	US-11-198-847-134	Sequence 134, App
443	33	41.2	254	11	US-11-167-831-17	Sequence 17, Appl	516	32	40.0	90	11	US-11-198-847-80	Sequence 80, Appl
444	33	41.2	254	11	US-11-167-831-18	Sequence 18, Appl	517	32	40.0	103	11	US-11-072-512-2826	Sequence 2826, App
445	33	41.2	254	11	US-11-167-831-19	Sequence 19, Appl	518	32	40.0	107	11	US-11-072-512-2260	Sequence 2260, App
446	33	41.2	254	11	US-11-167-831-22	Sequence 22, Appl	519	32	40.0	109	9	US-10-941-717A-17	Sequence 17, Appl
447	33	41.2	259	9	US-10-993-143-20	Sequence 20, Appl	520	32	40.0	113	9	US-10-941-717A-8	Sequence 8, Appl
448	33	41.2	299	11	US-11-045-004-2757	Sequence 2757, App	521	32	40.0	113	11	US-11-072-512-3738	Sequence 3738, App
449	33	41.2	301	11	US-11-108-163B-11	Sequence 11, Appl	522	32	40.0	125	11	US-11-264-096-1463	Sequence 1463, App
450	33	41.2	327	11	US-11-096-568A-30702	Sequence 30702, A	523	32	40.0	125	11	US-11-264-096-1464	Sequence 1464, App
451	33	41.2	327	11	US-11-233-798-2	Sequence 2, Appl	524	32	40.0	140	11	US-11-072-512-3489	Sequence 3489, App
452	33	41.2	332	11	US-11-241-956-9	Sequence 9, Appl	525	32	40.0	148	11	US-11-153-071-24	Sequence 24, Appl
453	33	41.2	335	11	US-11-188-298-18806	Sequence 18806, A	526	32	40.0	165	11	US-11-239-769-281	Sequence 281, App
454	33	41.2	338	9	US-10-055-877-175	Sequence 175, App	527	32	40.0	175	11	US-11-096-568A-2290	Sequence 2290, App
455	33	41.2	338	11	US-11-174-816-63	Sequence 63, Appl	528	32	40.0	181	11	US-11-153-071-4	Sequence 4, Appl
456	33	41.2	338	11	US-11-174-819-82	Sequence 82, Appl	529	32	40.0	181	11	US-11-153-071-27	Sequence 27, Appl
457	33	41.2	339	9	US-10-055-877-28	Sequence 28, Appl	530	32	40.0	183	11	US-11-229-769-136	Sequence 136, App
458	33	41.2	339	9	US-10-517-939-154	Sequence 154, App	531	32	40.0	201	11	US-11-170-653-23	Sequence 23, Appl
459	33	41.2	343	11	US-11-174-751-9	Sequence 9, Appl	532	32	40.0				

533	32	40.0	203	11	US-11-096-568A-30022	Sequence 30022, A	606	32	40.0	593	11	US-11-096-568A-25705	Sequence 25705, A
534	32	40.0	214	11	US-11-096-568A-30021	Sequence 30021, A	607	32	40.0	626	11	US-11-188-298-22376	Sequence 22376, A
535	32	40.0	219	11	US-11-098-686-11237	Sequence 11237, A	608	32	40.0	645	11	US-11-072-512-3418	Sequence 3418, Ap
536	32	40.0	225	11	US-11-170-653-24	Sequence 24, Appl	609	32	40.0	648	11	US-11-096-568A-25704	Sequence 25704, A
537	32	40.0	228	11	US-11-188-298-22426	Sequence 22426, A	610	32	40.0	659	8	US-10-511-937-2593	Sequence 2593, Ap
538	32	40.0	233	11	US-11-170-653-28	Sequence 28, Appl	611	32	40.0	887	11	US-11-079-463-6663	Sequence 6663, Ap
539	32	40.0	235	11	US-11-159-597-2	Sequence 2, Appl	612	32	40.0	992	11	US-11-072-512-2473	Sequence 2473, Ap
540	32	40.0	235	11	US-11-219-359-5	Sequence 5, Appl	613	32	40.0	1076	11	US-11-096-568A-29101	Sequence 29101, A
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542	32	40.0	247	9	US-10-533-811-9	Sequence 9, Appl	615	32	40.0	1113	11	US-11-067-811-4	Sequence 4, Appl
543	32	40.0	249	11	US-11-054-515-550	Sequence 550, App	616	32	40.0	1238	11	US-11-078-735-21	Sequence 21, Appl
544	32	40.0	249	11	US-11-266-444-550	Sequence 550, App	617	32	40.0	1238	11	US-11-050-346-66	Sequence 66, Appl
545	32	40.0	251	9	US-10-527-500-3	Sequence 3, Appl	618	32	40.0	1238	11	US-11-103-077-21	Sequence 21, Appl
546	32	40.0	252	9	US-10-527-500-19	Sequence 19, Appl	619	32	40.0	1238	11	US-11-058-066-21	Sequence 6, Appl
547	32	40.0	260	11	US-11-106-399-9	Sequence 9, Appl	620	32	40.0	1257	11	US-11-022-478-6	Sequence 6, Appl
548	32	40.0	267	11	US-11-096-568A-17567	Sequence 17567, A	621	32	40.0	1327	11	US-11-096-568A-29099	Sequence 29099, A
549	32	40.0	271	11	US-11-091-100-17	Sequence 17, Appl	622	32	40.0	1493	9	US-10-330-773-502	Sequence 502, App
550	32	40.0	271	11	US-11-172-740-336	Sequence 336, App	623	32	40.0	1625	9	US-10-757-832-2	Sequence 2, Appl
551	32	40.0	280	11	US-11-096-568A-21591	Sequence 21591, A	624	32	40.0	1826	9	US-10-330-773-499	Sequence 499, App
552	32	40.0	281	9	US-10-055-877-125	Sequence 125, App	625	32	40.0	8746	11	US-11-098-686-10232	Sequence 10232, A
553	32	40.0	281	9	US-10-055-877-125	Sequence 262, App	626	31.5	39.4	198	9	US-10-523-038-3	Sequence 3, Appl
554	32	40.0	281	11	US-11-087-177-15	Sequence 15, Appl	627	31.5	39.4	198	9	US-10-459-469-200	Sequence 200, App
555	32	40.0	281	11	US-11-087-177-17	Sequence 17, Appl	628	31.5	39.4	198	9	US-10-459-469-202	Sequence 202, App
556	32	40.0	288	8	US-10-511-937-2409	Sequence 2409, Ap	629	31.5	39.4	198	9	US-10-459-469-204	Sequence 204, App
557	32	40.0	288	11	US-11-029-188-2	Sequence 2, Appl	630	31.5	39.4	299	11	US-11-058-924-10	Sequence 10, Appl
558	32	40.0	295	11	US-11-091-100-2	Sequence 2, Appl	631	31.5	39.4	425	11	US-11-096-568A-25564	Sequence 25564, A
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563	32	40.0	355	11	US-11-182-946-14	Sequence 14, Appl	636	31.5	39.4	564	11	US-11-096-568A-29681	Sequence 29681, A
564	32	40.0	368	11	US-11-188-298-19698	Sequence 19698, A	637	31.5	39.4	572	11	US-11-096-568A-29680	Sequence 29680, A
565	32	40.0	369	11	US-11-188-298-714	Sequence 714, App	638	31.5	39.4	738	9	US-10-523-038-39	Sequence 39, Appl
566	32	40.0	369	11	US-11-188-298-5459	Sequence 5459, App	639	31.5	39.4	1285	11	US-11-079-463-9072	Sequence 9072, Ap
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568	32	40.0	369	11	US-11-188-298-16415	Sequence 16415, A	641	31	38.8	7	9	US-10-895-064-983	Sequence 983, App
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570	32	40.0	369	11	US-11-188-298-19492	Sequence 19492, A	643	31	38.8	9	11	US-11-198-847-317	Sequence 317, App
571	32	40.0	369	11	US-11-188-298-19804	Sequence 19804, A	644	31	38.8	10	11	US-11-198-847-319	Sequence 319, App
572	32	40.0	370	11	US-11-188-298-5711	Sequence 5711, Ap	645	31	38.8	11	11	US-11-198-847-314	Sequence 314, App
573	32	40.0	370	11	US-11-188-298-17120	Sequence 17120, A	646	31	38.8	14	9	US-10-939-890-23	Sequence 23, Appl
574	32	40.0	370	11	US-11-188-298-20348	Sequence 20348, A	647	31	38.8	14	9	US-10-939-890-31	Sequence 31, Appl
575	32	40.0	371	11	US-11-188-298-498	Sequence 498, App	648	31	38.8	14	9	US-10-939-890-64	Sequence 64, Appl
576	32	40.0	372	11	US-11-188-298-5199	Sequence 5199, App	649	31	38.8	14	11	US-11-232-439-52	Sequence 52, Appl
577	32	40.0	373	11	US-11-040-218-59	Sequence 59, Appl	650	31	38.8	16	11	US-11-198-847-310	Sequence 310, App
578	32	40.0	378	9	US-10-793-626-1428	Sequence 1428, App	651	31	38.8	17	9	US-10-895-064-2137	Sequence 2137, Ap
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581	32	40.0	378	11	US-11-183-599A-12	Sequence 12, Appl	654	31	38.8	20	11	US-11-106-415-19	Sequence 19, Appl
582	32	40.0	380	9	US-10-989-313-4	Sequence 4, Appl	655	31	38.8	20	11	US-11-233-256-19	Sequence 271, App
583	32	40.0	380	11	US-11-185-230-2	Sequence 2, Appl	656	31	38.8	22	9	US-10-939-890-271	Sequence 279, App
584	32	40.0	380	11	US-11-182-384A-2	Sequence 2, Appl	657	31	38.8	22	9	US-10-939-890-279	Sequence 36, Appl
585	32	40.0	380	11	US-11-183-599A-2	Sequence 2, Appl	658	31	38.8	24	11	US-11-120-501-36	Sequence 394, App
586	32	40.0	383	9	US-10-989-313-2	Sequence 2, Appl	659	31	38.8	25	9	US-10-644-807-394	Sequence 248, App
587	32	40.0	387	11	US-11-040-218-61	Sequence 61, Appl	660	31	38.8	26	11	US-11-198-847-248	Sequence 33, Appl
588	32	40.0	388	11	US-11-040-218-63	Sequence 63, Appl	661	31	38.8	27	11	US-11-120-501-33	Sequence 33, Appl
589	32	40.0	402	11	US-11-040-218-65	Sequence 65, Appl	662	31	38.8	28	11	US-11-120-501-31	Sequence 31, Appl
590	32	40.0	414	11	US-11-188-298-1168	Sequence 1168, Ap	663	31	38.8	28	11	US-11-120-501-34	Sequence 34, Appl
591	32	40.0	479	11	US-11-087-099-6677	Sequence 6677, Ap	664	31	38.8	29	11	US-11-120-501-18	Sequence 18, Appl
592	32	40.0	479	11	US-11-188-298-17131	Sequence 17131, A	665	31	38.8	29	11	US-11-120-501-21	Sequence 21, Appl
593	32	40.0	500	11	US-11-188-298-8362	Sequence 8362, Ap	666	31	38.8	29	11	US-11-120-501-22	Sequence 22, Appl
594	32	40.0	501	11	US-11-079-463-6749	Sequence 6749, Ap	667	31	38.8	29	11	US-11-120-501-24	Sequence 24, Appl
595	32	40.0	502	11	US-11-188-298-9832	Sequence 9832, Ap	668	31	38.8	29	11	US-11-120-501-25	Sequence 25, Appl
596	32	40.0	513	11	US-11-096-568A-28076	Sequence 28076, A	669	31	38.8	29	11	US-11-120-501-26	Sequence 26, Appl
597	32	40.0	523	9	US-10-453-372-1006	Sequence 1006, Ap	670	31	38.8	29	11	US-11-120-501-27	Sequence 27, Appl
598	32	40.0	523	9	US-10-453-372-1008	Sequence 1008, Ap	671	31	38.8	29	11	US-11-120-501-30	Sequence 30, Appl
599	32	40.0	523	9	US-10-204-639-24	Sequence 24, Appl	672	31	38.8	29	11	US-11-120-501-32	Sequence 32, Appl
600	32	40.0	531	11	US-11-096-568A-28075	Sequence 28075, A	673	31	38.8	29	11	US-11-120-501-37	Sequence 37, Appl
601	32	40.0	535	11	US-11-087-099-2008	Sequence 2008, Ap	674	31	38.8	30	11	US-11-120-501-7	Sequence 7, Appl
602	32	40.0	547	11	US-11-096-568A-8409	Sequence 8409, Ap	675	31	38.8	32	11	US-11-120-501-40	Sequence 40, Appl
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604	32	40.0	566	11	US-11-096-568A-8408	Sequence 8408, Ap	677	31	38.8	40	11	US-11-198-847-33	Sequence 33, Appl
605	32	40.0	566	11	US-11-096-568A-25706	Sequence 25706, A	678	31	38.8	40	11	US-11-198-847-42	Sequence 42, Appl

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683	31	38.8	53	11	US-11-096-568A-3534	Sequence 3534, App	756	31	38.8	310	11	US-11-096-568A-12784	Sequence 12784, A
684	31	38.8	68	11	US-11-096-568A-3533	Sequence 3533, App	757	31	38.8	313	11	US-11-098-686-10326	Sequence 10326, A
685	31	38.8	65	11	US-11-096-568A-1604	Sequence 1604, App	758	31	38.8	317	11	US-11-096-568A-21817	Sequence 21817, A
686	31	38.8	69	11	US-11-198-847-50	Sequence 50, Appl	759	31	38.8	318	11	US-11-127-877-38	Sequence 38, Appl
687	31	38.8	72	11	US-11-198-847-155	Sequence 155, App	760	31	38.8	322	9	US-10-194-487-172	Sequence 172, App
688	31	38.8	79	11	US-11-198-847-206	Sequence 206, App	761	31	38.8	322	9	US-10-195-883-172	Sequence 172, App
689	31	38.8	83	11	US-11-096-568A-4111	Sequence 4111, App	762	31	38.8	322	9	US-10-195-888-172	Sequence 172, App
690	31	38.8	85	9	US-10-999-866-13	Sequence 13, Appl	763	31	38.8	322	9	US-10-195-889-172	Sequence 172, App
691	31	38.8	85	9	US-10-935-005B-43	Sequence 43, Appl	764	31	38.8	322	11	US-11-045-004-260	Sequence 260, App
692	31	38.8	85	10	US-11-091-234A-13	Sequence 13, Appl	765	31	38.8	324	11	US-11-087-099-8410	Sequence 8410, App
693	31	38.8	85	11	US-11-061-821-13	Sequence 13, Appl	766	31	38.8	328	11	US-11-096-568A-1749	Sequence 1749, App
694	31	38.8	94	11	US-11-264-096-1552	Sequence 1552, App	767	31	38.8	328	11	US-11-096-568A-34102	Sequence 34102, A
695	31	38.8	98	9	US-10-467-657-7082	Sequence 7082, App	768	31	38.8	329	11	US-11-096-568A-1748	Sequence 1748, App
696	31	38.8	107	9	US-10-982-357-8	Sequence 8, Appl	769	31	38.8	332	11	US-11-096-568A-34101	Sequence 34101, A
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698	31	38.8	110	9	US-10-644-807-423	Sequence 423, App	771	31	38.8	336	11	US-11-079-463-5860	Sequence 5860, App
699	31	38.8	143	11	US-11-096-568A-30279	Sequence 30279, A	772	31	38.8	346	9	US-10-517-939-170	Sequence 170, App
700	31	38.8	146	11	US-11-087-099-4208	Sequence 4208, App	773	31	38.8	346	9	US-10-131-826A-18	Sequence 18, Appl
701	31	38.8	151	11	US-11-087-099-5350	Sequence 5350, App	774	31	38.8	347	9	US-10-517-939-222	Sequence 222, App
702	31	38.8	168	11	US-11-200-389-3	Sequence 3, Appl	775	31	38.8	347	9	US-10-517-939-254	Sequence 254, App
703	31	38.8	169	11	US-11-200-389-9	Sequence 9, Appl	776	31	38.8	347	9	US-10-517-939-218	Sequence 218, App
704	31	38.8	169	11	US-11-200-389-11	Sequence 11, Appl	777	31	38.8	347	9	US-10-973-115B-18	Sequence 18, Appl
705	31	38.8	173	9	US-10-644-807-339	Sequence 339, App	778	31	38.8	347	9	US-10-137-873A-18	Sequence 18, Appl
706	31	38.8	177	11	US-11-087-099-4172	Sequence 4172, App	779	31	38.8	347	9	US-10-152-370-18	Sequence 18, Appl
707	31	38.8	178	9	US-10-784-004-729	Sequence 729, App	780	31	38.8	347	11	US-11-079-463-6856	Sequence 6856, App
708	31	38.8	180	11	US-11-079-463-5368	Sequence 5368, App	781	31	38.8	347	11	US-11-290-153-18	Sequence 18, Appl
709	31	38.8	181	11	US-11-000-463-890	Sequence 890, App	782	31	38.8	350	9	US-10-517-939-200	Sequence 200, App
710	31	38.8	182	11	US-11-000-463-418	Sequence 418, App	783	31	38.8	354	9	US-10-517-939-218	Sequence 218, App
711	31	38.8	186	9	US-10-644-807-245	Sequence 245, App	784	31	38.8	362	8	US-10-511-937-2466	Sequence 2466, App
712	31	38.8	193	11	US-11-200-389-2	Sequence 2, Appl	785	31	38.8	364	11	US-11-140-284-36	Sequence 36, Appl
713	31	38.8	193	11	US-11-079-463-6622	Sequence 6622, App	786	31	38.8	370	11	US-11-140-284-36	Sequence 36, Appl
714	31	38.8	208	9	US-10-467-657-228	Sequence 228, App	787	31	38.8	376	11	US-11-096-568A-16238	Sequence 16238, A
715	31	38.8	208	9	US-10-467-657-600	Sequence 600, App	788	31	38.8	378	9	US-10-517-939-256	Sequence 256, App
716	31	38.8	209	11	US-11-096-568A-3423	Sequence 3423, App	789	31	38.8	390	11	US-11-096-568A-25267	Sequence 25267, A
717	31	38.8	219	11	US-11-188-298-13534	Sequence 13534, A	790	31	38.8	397	11	US-11-096-568A-1747	Sequence 1747, App
718	31	38.8	227	11	US-11-087-099-2505	Sequence 2505, App	791	31	38.8	397	11	US-11-096-568A-34100	Sequence 34100, A
719	31	38.8	227	11	US-11-087-099-5875	Sequence 5875, App	792	31	38.8	397	11	US-11-096-568A-34100	Sequence 34100, A
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722	31	38.8	233	11	US-11-087-099-3052	Sequence 3052, App	795	31	38.8	406	11	US-11-188-298-4500	Sequence 4500, App
723	31	38.8	233	11	US-11-087-099-6395	Sequence 6395, App	796	31	38.8	407	11	US-11-096-568A-5204	Sequence 5204, App
724	31	38.8	233	11	US-11-087-099-6579	Sequence 6579, App	797	31	38.8	420	11	US-11-096-568A-31929	Sequence 31929, A
725	31	38.8	233	11	US-11-087-099-7318	Sequence 7318, App	798	31	38.8	420	11	US-11-087-099-1471	Sequence 1471, App
726	31	38.8	235	11	US-11-087-099-3077	Sequence 3077, App	799	31	38.8	424	9	US-10-243-586-12	Sequence 12, Appl
727	31	38.8	235	11	US-11-087-099-3482	Sequence 3482, App	800	31	38.8	424	9	US-10-243-902-12	Sequence 12, Appl
728	31	38.8	235	11	US-11-087-099-4175	Sequence 4175, App	801	31	38.8	424	9	US-10-243-116-12	Sequence 12, Appl
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732	31	38.8	236	11	US-11-087-099-7684	Sequence 7684, App	805	31	38.8	424	9	US-10-243-236-12	Sequence 12, Appl
733	31	38.8	236	11	US-11-087-099-8761	Sequence 8761, App	806	31	38.8	424	9	US-10-243-298-12	Sequence 12, Appl
734	31	38.8	236	11	US-11-087-099-11734	Sequence 11734, A	807	31	38.8	424	9	US-10-243-304-12	Sequence 12, Appl
735	31	38.8	240	11	US-11-000-463-448	Sequence 248, App	808	31	38.8	424	9	US-10-243-338-12	Sequence 12, Appl
736	31	38.8	252	11	US-10-512-184-28	Sequence 28, Appl	809	31	38.8	424	9	US-10-243-345-12	Sequence 12, Appl
737	31	38.8	252	11	US-11-087-099-10413	Sequence 10413, A	810	31	38.8	424	9	US-10-243-357-12	Sequence 12, Appl
738	31	38.8	252	11	US-11-087-099-11103	Sequence 11103, A	811	31	38.8	424	9	US-10-243-083-12	Sequence 12, Appl
739	31	38.8	252	11	US-11-045-004-2648	Sequence 2648, App	812	31	38.8	424	11	US-11-096-568A-25265	Sequence 25265, A
740	31	38.8	256	11	US-11-054-515-1285	Sequence 1285, App	813	31	38.8	433	11	US-11-096-568A-5203	Sequence 5203, App
741	31	38.8	256	11	US-11-087-099-5474	Sequence 5474, App	814	31	38.8	436	9	US-10-455-772-914	Sequence 914, App
742	31	38.8	256	11	US-11-266-444-1285	Sequence 1285, App	815	31	38.8	441	11	US-11-045-004-297	Sequence 297, App
743	31	38.8	262	11	US-11-087-099-8793	Sequence 8793, App	816	31	38.8	446	11	US-11-096-568A-12783	Sequence 12783, A
744	31	38.8	263	11	US-11-087-099-5632	Sequence 5632, App	817	31	38.8	452	8	US-10-505-928-621	Sequence 621, App
745	31	38.8	263	11	US-11-087-099-10938	Sequence 10938, A	818	31	38.8	455	9	US-10-063-703-4	Sequence 4, Appl
746	31	38.8	264	11	US-11-096-568A-5205	Sequence 5205, App	819	31	38.8	455	9	US-10-194-487-14	Sequence 14, Appl
747	31	38.8	268	11	US-11-045-004-2466	Sequence 2466, App	820	31	38.8	455	9	US-10-195-883-14	Sequence 14, Appl
748	31	38.8	271	11	US-11-096-568A-30278	Sequence 30278, A	821	31	38.8	455	9	US-10-195-883-14	Sequence 14, Appl
749	31	38.8	273	11	US-11-096-568A-30277	Sequence 30277, A	822	31	38.8	455	9	US-10-195-889-14	Sequence 14, Appl
750	31	38.8	280	11	US-11-264-096-1818	Sequence 1818, App	823	31	38.8	455	9	US-10-216-161A-430	Sequence 430, Appl
751	31	38.8	289	11	US-11-096-568A-16240	Sequence 16240, App	824	31	38.8	455	11	US-11-102-240-4	Sequence 4, Appl

825	31	38.8	455	11	US-11-103-195-4	Sequence 4, Appli	898	31	38.8	1094	11	US-11-096-568A-27715	Sequence 27715, A
826	31	38.8	456	9	US-10-641-678-51	Sequence 51, Appli	899	31	38.8	1190	9	US-10-506-454-1349	Sequence 1349, Ap
827	31	38.8	458	11	US-11-087-099-11153	Sequence 11153, A	900	31	38.8	1244	11	US-11-052-554A-130	Sequence 130, App
828	31	38.8	459	11	US-11-087-099-8193	Sequence 8193, Ap	901	31	38.8	1341	11	US-11-096-568A-32147	Sequence 32147, A
829	31	38.8	465	9	US-10-490-824-1	Sequence 1, Appli	902	31	38.8	1372	11	US-11-096-568A-32146	Sequence 32146, A
830	31	38.8	466	11	US-11-087-099-3072	Sequence 3072, Ap	903	31	38.8	1393	11	US-11-096-568A-32145	Sequence 32145, A
831	31	38.8	469	9	US-10-516-635-8	Sequence 8, Appli	904	31	38.8	1463	11	US-11-096-568A-14692	Sequence 14692, A
832	31	38.8	469	9	US-10-784-004-784	Sequence 784, App	905	31	38.8	1473	11	US-11-096-568A-14691	Sequence 14691, A
833	31	38.8	476	11	US-10-784-004-1112	Sequence 1112, Ap	906	31	38.8	1529	11	US-11-096-568A-14690	Sequence 14690, A
834	31	38.8	476	11	US-11-087-099-10733	Sequence 10733, A	907	31	38.8	2531	11	US-11-124-367A-467	Sequence 467, App
835	31	38.8	476	11	US-11-096-568A-20043	Sequence 20043, A	908	31	38.8	2597	11	US-11-124-367A-466	Sequence 466, App
836	31	38.8	479	9	US-10-516-635-10	Sequence 10, Appli	909	31	38.8	2597	11	US-11-124-367A-468	Sequence 468, App
837	31	38.8	480	9	US-10-516-635-12	Sequence 12, Appli	910	31	38.8	2760	11	US-11-124-367A-444	Sequence 444, App
838	31	38.8	480	9	US-10-516-635-14	Sequence 14, Appli	911	31	38.8	2803	11	US-11-124-367A-442	Sequence 442, App
839	31	38.8	480	9	US-10-784-004-465	Sequence 465, App	912	31	38.8	2803	11	US-11-124-367A-445	Sequence 445, App
840	31	38.8	480	9	US-10-784-004-961	Sequence 961, App	913	31	38.8	2984	11	US-11-124-367A-443	Sequence 443, App
841	31	38.8	480	11	US-11-096-568A-12782	Sequence 12782, A	914	31	38.8	3012	11	US-11-124-367A-465	Sequence 465, App
842	31	38.8	489	11	US-11-087-099-8528	Sequence 8528, Ap	915	31	38.8	3027	11	US-11-124-367A-441	Sequence 441, App
843	31	38.8	490	11	US-11-079-463-3351	Sequence 5351, Ap	916	31	38.8	3144	11	US-11-055-035-1	Sequence 1, Appli
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846	31	38.8	504	11	US-11-087-099-1958	Sequence 1958, Ap	919	30.5	38.1	128	9	US-10-475-075-198	Sequence 198, App
847	31	38.8	504	11	US-11-087-099-2938	Sequence 2938, Ap	920	30.5	38.1	157	9	US-10-467-657-8756	Sequence 8756, Ap
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851	31	38.8	515	11	US-11-087-099-2320	Sequence 2320, Ap	924	30.5	38.1	417	11	US-11-264-096-102	Sequence 102, App
852	31	38.8	520	11	US-11-087-099-7910	Sequence 7910, Ap	925	30.5	38.1	484	11	US-11-146-428-108	Sequence 108, App
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854	31	38.8	536	9	US-10-131-826A-490	Sequence 490, App	927	30.5	38.1	522	11	US-11-096-568A-29963	Sequence 29963, A
855	31	38.8	536	9	US-10-641-678-61	Sequence 61, Appli	928	30.5	38.1	528	11	US-11-096-568A-29962	Sequence 29962, A
856	31	38.8	536	9	US-10-973-1158-490	Sequence 490, App	929	30.5	38.1	569	11	US-11-188-298-3937	Sequence 3937, Ap
857	31	38.8	536	9	US-10-137-873A-490	Sequence 490, App	930	30.5	38.1	653	11	US-11-098-686-10093	Sequence 10093, A
858	31	38.8	536	9	US-10-152-370-490	Sequence 490, App	931	30.5	38.1	838	11	US-11-087-099-829	Sequence 829, App
859	31	38.8	536	11	US-11-079-463-8209	Sequence 8209, Ap	932	30.5	38.1	2715	11	US-11-113-424-51	Sequence 51, Appli
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862	31	38.8	537	11	US-11-087-099-10695	Sequence 10695, A	935	30	37.5	12	9	US-10-626-719-154	Sequence 154, App
863	31	38.8	538	11	US-11-079-463-9342	Sequence 9342, Ap	936	30	37.5	13	11	US-11-152-974A-328	Sequence 328, App
864	31	38.8	548	9	US-10-055-877-320	Sequence 320, App	937	30	37.5	13	11	US-11-152-974A-352	Sequence 352, App
865	31	38.8	565	11	US-11-087-099-3971	Sequence 3971, Ap	938	30	37.5	13	11	US-11-152-974A-362	Sequence 362, App
866	31	38.8	567	11	US-11-127-817-16	Sequence 16, Appli	939	30	37.5	13	11	US-11-152-974A-328	Sequence 328, App
867	31	38.8	573	11	US-11-072-512-3669	Sequence 3669, Ap	940	30	37.5	13	11	US-11-153-143A-352	Sequence 352, App
868	31	38.8	585	11	US-11-241-347-15	Sequence 15, Appli	941	30	37.5	13	11	US-11-153-143A-362	Sequence 362, App
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870	31	38.8	608	11	US-11-226-701-8	Sequence 8, Appli	943	30	37.5	14	9	US-10-626-719-9	Sequence 9, Appli
871	31	38.8	608	11	US-11-241-347-8	Sequence 8, Appli	944	30	37.5	14	11	US-11-041-676A-1	Sequence 1, Appli
872	31	38.8	608	11	US-11-241-347-9	Sequence 9, Appli	945	30	37.5	14	11	US-11-123-895-1	Sequence 1, Appli
873	31	38.8	617	11	US-11-188-298-10512	Sequence 10512, A	946	30	37.5	14	11	US-11-175-690-294	Sequence 294, App
874	31	38.8	617	11	US-11-188-298-14495	Sequence 14495, A	947	30	37.5	14	11	US-11-138-705-2	Sequence 2, Appli
875	31	38.8	626	11	US-11-098-686-10124	Sequence 10124, A	948	30	37.5	18	11	US-11-106-415-236	Sequence 236, App
876	31	38.8	632	11	US-11-188-298-4558	Sequence 4558, Ap	949	30	37.5	18	11	US-11-152-974A-101	Sequence 101, App
877	31	38.8	637	9	US-10-455-772-916	Sequence 916, App	950	30	37.5	18	11	US-11-153-143A-101	Sequence 101, App
878	31	38.8	669	11	US-11-198-886-6	Sequence 6, Appli	951	30	37.5	18	11	US-11-233-256-236	Sequence 236, App
879	31	38.8	673	9	US-10-055-877-321	Sequence 321, App	952	30	37.5	25	11	US-11-004-399-54	Sequence 54, Appli
880	31	38.8	674	9	US-10-055-877-319	Sequence 319, App	953	30	37.5	25	11	US-11-004-399-424	Sequence 424, App
881	31	38.8	675	9	US-10-055-877-117	Sequence 117, App	954	30	37.5	25	11	US-11-004-399-3646	Sequence 3646, Ap
882	31	38.8	675	9	US-10-055-877-317	Sequence 317, App	955	30	37.5	25	11	US-11-004-399-3857	Sequence 3857, Ap
883	31	38.8	675	9	US-10-055-877-318	Sequence 318, App	956	30	37.5	28	11	US-11-123-895-2	Sequence 2, Appli
884	31	38.8	675	9	US-10-455-772-912	Sequence 912, App	957	30	37.5	29	11	US-11-120-501-19	Sequence 19, Appli
885	31	38.8	675	9	US-10-455-772-918	Sequence 918, App	958	30	37.5	29	11	US-11-004-399-1748	Sequence 1748, Ap
886	31	38.8	725	9	US-10-499-290-3	Sequence 3, Appli	959	30	37.5	42	9	US-10-948-571-85	Sequence 85, Appli
887	31	38.8	816	9	US-10-216-161A-375	Sequence 375, App	960	30	37.5	58	11	US-11-000-463-910	Sequence 910, App
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889	31	38.8	840	11	US-11-079-463-9922	Sequence 9922, Ap	962	30	37.5	67	11	US-11-004-399-1065	Sequence 1065, Ap
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891	31	38.8	854	11	US-11-087-099-11341	Sequence 11341, A	964	30	37.5	73	11	US-11-096-568A-17429	Sequence 17429, A
892	31	38.8	859	11	US-11-087-099-3325	Sequence 3325, Ap	965	30	37.5	76	11	US-11-188-298-20066	Sequence 20066, A
893	31	38.8	891	11	US-11-182-016-38	Sequence 38, Appli	966	30	37.5	77	11	US-11-188-298-9758	Sequence 9758, Ap
894	31	38.8	960	11	US-11-087-099-8676	Sequence 8676, Ap	967	30	37.5	79	11	US-11-079-463-5310	Sequence 5310, Ap
895	31	38.8	1014	9	US-10-491-468-7	Sequence 7, Appli	968	30	37.5	84	11	US-11-188-298-4813	Sequence 4813, Ap
896	31	38.8	1051	11	US-11-096-568A-27717	Sequence 27717, A	969	30	37.5	85	11	US-11-188-298-19214	Sequence 19214, A
897	31	38.8	1061	11	US-11-096-568A-27716	Sequence 27716, A	970	30	37.5	86	11	US-11-188-298-2781	Sequence 2781, Ap

971 30 37.5 86 11 US-11-188-298-8724 Sequence 8724, Ap
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973 30 37.5 91 9 US-10-821-234-1703 Sequence 1703, Ap
974 30 37.5 97 11 US-11-172-740-1554 Sequence 1554, Ap
975 30 37.5 98 11 US-11-188-298-1119 Sequence 1119, Ap
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978 30 37.5 101 11 US-11-172-740-1552 Sequence 1552, Ap
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980 30 37.5 102 11 US-11-096-568A-12132 Sequence 12132, A
981 30 37.5 106 11 US-11-096-568A-24286 Sequence 24286, A
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983 30 37.5 110 9 US-10-966-648-3 Sequence 3, Appl
984 30 37.5 110 9 US-10-986-405-239 Sequence 239, Appl
985 30 37.5 110 11 US-11-126-772-3 Sequence 3, Appl
986 30 37.5 110 11 US-11-172-740-1549 Sequence 1549, Ap
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988 30 37.5 110 11 US-11-188-298-353 Sequence 353, Appl
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997 30 37.5 110 11 US-11-188-298-17121 Sequence 17121, A
998 30 37.5 110 11 US-11-188-298-17288 Sequence 17288, A
999 30 37.5 110 11 US-11-188-298-17374 Sequence 17374, A
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ALIGNMENTS

RESULT 1
US-10-506-223-16
; Sequence 16, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa at position 3 is Nle
US-10-506-223-16
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Best Local Similarity 88.9%; Pred. No. 0.089;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 YYCFWKTC 11
DB 4 YSCFWKTC 12
US-10-506-223-17
; Sequence 17, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa at position 3 is Nle
US-10-506-223-17
Query Match 68.8%; Score 55; DB 9; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.089;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 YYCFWKTC 11
DB 4 YSCFWKTC 12
RESULT 3
US-10-506-223-39
; Sequence 39, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
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; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa at position 3 is Nle
US-10-506-223-39

Query Match 68.8%; Score 55; DB 9; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.089;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
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Db 4 YSCFWKTCCT 12

RESULT 4
US-10-506-223-40
; Sequence 40, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
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; SEQ ID NO 40
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa at position 3 is Nle
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 6, 11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
US-10-506-223-40

Query Match 68.8%; Score 55; DB 9; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.089;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | | | | |
Db 4 YSCFWKTCCT 12

RESULT 5
US-10-506-223-21
; Sequence 21, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 13

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa at position 4 is Nle
US-10-506-223-21

Query Match 68.8%; Score 55; DB 9; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.094;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | | | | |
Db 5 YSCFWKTCCT 13

RESULT 6
US-10-506-223-22
; Sequence 22, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa at position 4 is Nle
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 7, 12
; OTHER INFORMATION: Cys at positions 7 and 12 are circularized
US-10-506-223-22

Query Match 68.8%; Score 55; DB 9; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.094;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | | | | |
Db 5 YSCFWKTCCT 13

RESULT 7
US-10-506-223-23
; Sequence 23, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223

; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 5
; OTHER INFORMATION: Xaa at position 5 is Nle
US-10-506-223-23

Query Match 68.8%; Score 55; DB 9; Length 14;
Best Local Similarity 88.9%; Pred. No. 0.099;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
Db 6 YSCFWKTCCT 14

RESULT 8
US-10-506-223-24
; Sequence 24, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa at position 6 is Nle
US-10-506-223-24

Query Match 68.8%; Score 55; DB 9; Length 15;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
Db 7 YSCFWKTCCT 15

RESULT 9
US-10-506-223-25
; Sequence 25, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.

; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa at position 7 is Nle
US-10-506-223-25

Query Match 68.8%; Score 55; DB 9; Length 16;
Best Local Similarity 88.9%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
Db 8 YSCFWKTCCT 16

RESULT 10
US-10-506-223-26
; Sequence 26, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 8
; OTHER INFORMATION: Xaa at position 8 is Nle
US-10-506-223-26

Query Match 68.8%; Score 55; DB 9; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
Db 9 YSCFWKTCCT 17

RESULT 11

US-10-506-223-27
; Sequence 27, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 9
; OTHER INFORMATION: Xaa at position 9 is Nle
US-10-506-223-27

Query Match 68.8%; Score 55; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTC 11
| | | | |
Db 10 YSCFWKTC 18

RESULT 12
US-10-506-223-28
; Sequence 28, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa at position 10 is Nle
US-10-506-223-28

Query Match 68.8%; Score 55; DB 9; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTC 11

Db 11 YSCFWKTC 19
| | | | |
RESULT 13
US-10-506-223-29
; Sequence 29, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 11
; OTHER INFORMATION: Xaa at position 11 is Nle
US-10-506-223-29

Query Match 68.8%; Score 55; DB 9; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YYCFWKTC 11
| | | | |
Db 12 YSCFWKTC 20

RESULT 14
US-10-506-223-30
; Sequence 30, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 12
; OTHER INFORMATION: Xaa at position 12 is Nle
US-10-506-223-30

Query Match 68.8%; Score 55; DB 9; Length 21;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
Db 13 YSCFWKTCCT 21

RESULT 15
US-10-506-223-31
; Sequence 31, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 13
; OTHER INFORMATION: Xaa at position 13 is Nle
US-10-506-223-31

Query Match 68.8%; Score 55; DB 9; Length 22;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
Db 14 YSCFWKTCCT 22

RESULT 16
US-10-506-223-32
; Sequence 32, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:

; NAME/KEY: VARIANT
; LOCATION: 14
; OTHER INFORMATION: Xaa at position 14 is Nle
US-10-506-223-32

Query Match 68.8%; Score 55; DB 9; Length 23;
Best Local Similarity 88.9%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
Db 15 YSCFWKTCCT 23

RESULT 17
US-10-506-223-33
; Sequence 33, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 15
; OTHER INFORMATION: Xaa at position 15 is Nle
US-10-506-223-33

Query Match 68.8%; Score 55; DB 9; Length 24;
Best Local Similarity 88.9%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
Db 16 YSCFWKTCCT 24

RESULT 18
US-10-506-223-34
; Sequence 34, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 25

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 16
; OTHER INFORMATION: Xaa at position 16 is Nle
US-10-506-223-34

Query Match 68.8%; Score 55; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
DB 17 YSCFWKTCCT 25

RESULT 19
US-10-506-223-35
; Sequence 35, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 17
; OTHER INFORMATION: Xaa at position 17 is Nle
US-10-506-223-35

Query Match 68.8%; Score 55; DB 9; Length 26;
Best Local Similarity 88.9%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
DB 18 YSCFWKTCCT 26

RESULT 20
US-10-506-223-36
; Sequence 36, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831

; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 18
; OTHER INFORMATION: Xaa at position 18 is Nle
US-10-506-223-36

Query Match 68.8%; Score 55; DB 9; Length 27;
Best Local Similarity 88.9%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYCFWKTCCT 11
| | | | |
DB 19 YSCFWKTCCT 27

RESULT 21
US-10-626-719-158
; Sequence 158, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-626-719-158

Query Match 66.2%; Score 53; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
: | | | | |
DB 1 FCFWKTCCT 8

RESULT 22
US-10-626-719-159
; Sequence 159, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS

APPLICANT: SEMMLER, WOLFGANG
APPLICANT: WEIDENMANN, BERTRAM
APPLICANT: HESSNIUS, CARSTEN
APPLICANT: VOLKMER-ENGERT, RUDOLF
APPLICANT: SCHNEIDER-MERGENGER, JENS
APPLICANT: BHARGAVA, SARAH
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
FILE REFERENCE: SCH-1731
CURRENT APPLICATION NUMBER: US/10/626,719
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US/09/528,200
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: DE 199 17 713.9
PRIOR FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 159
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-10-626-719-159

Query Match 62.5%; Score 50; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
DB 1 FCFWKCT 8

RESULT 23
US-11-198-847-234
Sequence 234, Application US/11198847
Publication No. US20050271589A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Jones, Robert M.
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: B-Superfamily Conotoxins
FILE REFERENCE: 2314-296
CURRENT APPLICATION NUMBER: US/11/198,847
CURRENT FILING DATE: 2005-08-08
PRIOR APPLICATION NUMBER: US 10/838,226
PRIOR FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US 10/058,053
PRIOR FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US 60/264323
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.0
SEQ ID NO 234
LENGTH: 21
TYPE: PRT
ORGANISM: Conus geographus
US-11-198-847-234

Query Match 61.3%; Score 49; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 0.85;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
DB 2 FCFWKCT 9

RESULT 24
US-11-198-847-231
Sequence 231, Application US/11198847
Publication No. US20050271589A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Jones, Robert M.
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: B-Superfamily Conotoxins
FILE REFERENCE: 2314-296
CURRENT APPLICATION NUMBER: US/11/198,847
CURRENT FILING DATE: 2005-08-08
PRIOR APPLICATION NUMBER: US 10/838,226
PRIOR FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US 10/058,053
PRIOR FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US 60/264323
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.0
SEQ ID NO 231
LENGTH: 40
TYPE: PRT
ORGANISM: Conus geographus
US-11-198-847-231

Query Match 61.3%; Score 49; DB 11; Length 40;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
DB 21 FCFWKCT 28

RESULT 25
US-11-198-847-116
Sequence 116, Application US/11198847
Publication No. US20050271589A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Jones, Robert M.
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: B-Superfamily Conotoxins
FILE REFERENCE: 2314-296
CURRENT APPLICATION NUMBER: US/11/198,847
CURRENT FILING DATE: 2005-08-08
PRIOR APPLICATION NUMBER: US 10/838,226
PRIOR FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US 10/058,053
PRIOR FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US 60/264323
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.0
SEQ ID NO 116
LENGTH: 93
TYPE: PRT
ORGANISM: Conus geographus
US-11-198-847-116

Query Match 61.3%; Score 49; DB 11; Length 93;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
DB 21 FCFWKCT 28

```
Db          71 PCFWKST 78

RESULT 26
US-10-626-719-156
; Sequence 156, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-626-719-156

Query Match          60.0%; Score 48; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy          4 YCFWKTCCT 11
          :|||||
Db          1 PCFWKST 8

RESULT 27
US-11-188-298-2272
; Sequence 2272, Application US/11188298
; Publication No. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 2272
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(361)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-188-298-2272

Query Match          60.0%; Score 48; DB 11; Length 361;
Best Local Similarity 71.4%; Pred. No. 7.7;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CYYFCFW 7

Db          71 PCFWKST 78

RESULT 28
US-11-198-847-280
; Sequence 280, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Conus cinereus
US-11-198-847-280

Query Match          58.8%; Score 47; DB 11; Length 45;
Best Local Similarity 66.7%; Pred. No. 2.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy          3 YCFWKTCCT 11
          :|||||
Db          10 FKCFWKST 18

RESULT 29
US-11-198-847-89
; Sequence 89, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Conus cinereus
US-11-198-847-89

Query Match          58.8%; Score 47; DB 11; Length 95;
Best Local Similarity 66.7%; Pred. No. 4.4;
```

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 3 YCFWKTC 11
: |||||:
Db 60 FCFWKSCT 68

RESULT 30

US-10-506-223-37
; Sequence 37, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-506-223-37

Query Match 56.2%; Score 45; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 CFWKTC 10
: |||||:
Db 1 CFWKTC 6

RESULT 31

US-10-506-223-38
; Sequence 38, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MOD RES
; LOCATION: 1, 6
; OTHER INFORMATION: Cys at positions 1 and 6 are circularized
US-10-506-223-38
Query Match 56.2%; Score 45; DB 9; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 CFWKTC 10
: |||||:
Db 1 CFWKTC 6

RESULT 32

US-10-626-719-157
; Sequence 157, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARTSEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-626-719-157

Query Match 56.2%; Score 45; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.9e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 4 YCFWKTC 11
: |||||:
Db 1 FCFWKTC 8

RESULT 33

US-11-198-847-322
; Sequence 322, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0


```
; SEQ ID NO 322
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-322

Query Match      55.0%; Score 44; DB 11; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.5;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTC 10
Db      1 FCFWKSC 7

RESULT 34
US-11-198-847-232
; Sequence 232, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 232
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Conus tulipa
US-11-198-847-232

Query Match      55.0%; Score 44; DB 11; Length 21;
Best Local Similarity 71.4%; Pred. No. 4.1;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTC 10
Db      2 FCFWKSC 8

RESULT 35
US-11-198-847-233
; Sequence 233, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
```

```
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 233
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-233

Query Match      55.0%; Score 44; DB 11; Length 21;
Best Local Similarity 71.4%; Pred. No. 4.1;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTC 10
Db      2 FCFWKSC 8

RESULT 36
US-11-198-847-229
; Sequence 229, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 229
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus tulipa
US-11-198-847-229

Query Match      55.0%; Score 44; DB 11; Length 40;
Best Local Similarity 71.4%; Pred. No. 6.3;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTC 10
Db      21 FCFWKSC 27

RESULT 37
US-11-198-847-230
; Sequence 230, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
```

; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 230
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-230

Query Match 55.0%; Score 44; DB 11; Length 93;
Best Local Similarity 71.4%; Pred. No. 6.3;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:|
Db 21 FCFWKSC 27

RESULT 38

US-11-198-847-32
; Sequence 32, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Oliveira, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Conus tulipa
US-11-198-847-32

Query Match 55.0%; Score 44; DB 11; Length 93;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:|
Db 71 FCFWKSC 77

RESULT 39

US-11-198-847-41
; Sequence 41, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Oliveira, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847

; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-41

Query Match 55.0%; Score 44; DB 11; Length 93;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:|
Db 71 FCFWKSC 77

RESULT 40

US-11-121-301-6
; Sequence 6, Application US/11121301
; Publication No. US2005027176A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY, JR., PAUL B.
; APPLICANT: SCHUTTE, BRIAN C.
; APPLICANT: JIA, HONG PENG
; APPLICANT: CASAVANT, THOMAS L.
; TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: IOWA:041USD1
; CURRENT APPLICATION NUMBER: US/11/121,301
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/323,991
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 10/252,734
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-121-301-6

Query Match 53.8%; Score 43; DB 11; Length 34;
Best Local Similarity 33.8%; Pred. No. 7.7;
Matches 7; Conservative 1; Mismatches 2; Indels 12; Gaps 1;

Qy 1 CYYYCF-----WKTC 10
|||:|
Db 10 CYFYCFSSHKKIGSCFPEWPC 31

RESULT 41

US-11-004-399-1477
; Sequence 1477, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; FILE REFERENCE: Sequences and Methods of Use Thereof For Immunization Against SARS
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03

; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1477
; LENGTH: 39
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399-1477

Query Match 53.8%; Score 43; DB 11; Length 39;
Best Local Similarity 53.8%; Pred. No. 8.5;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Qy 1 CYYG-CFWKTCT 11
|:|:| | |:
Db 20 CHYIGCNWWSCT 32

RESULT 42
US-11-087-099-11435
; Sequence 11435, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11435
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Chenopodium rubrum
US-11-087-099-11435

Query Match 52.5%; Score 42; DB 11; Length 144;
Best Local Similarity 45.5%; Pred. No. 28;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CYYG-CFWKTCT 11
|:|:| | |:
Db 116 CHYCHGRCCS 126

RESULT 43
US-11-098-686-10572
; Sequence 10572, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10572
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10572

Query Match 52.5%; Score 42; DB 11; Length 308;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YYGFWKTCT 11

Db 89 YQYIFWVTCs 98
| | | | |:
| | | | |:

RESULT 44
US-10-517-939-176
; Sequence 176, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(27)
US-10-517-939-176

Query Match 52.5%; Score 42; DB 9; Length 350;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YYGFWK 8
| | | | |:
Db 41 YYTFWK 47

RESULT 45
US-10-517-939-216
; Sequence 216, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216
; LENGTH: 354
; TYPE: PRT

; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
US-10-517-939-216

Query Match 52.5%; Score 42; DB 9; Length 354;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YYCFWK 8
||| |||
Db 46 YYSFWK 52

RESULT 46
US-10-517-939-182
; Sequence 182, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(25)
US-10-517-939-182

Query Match 52.5%; Score 42; DB 9; Length 358;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YYCFWK 8
||| |||
Db 40 YYSFWK 46

RESULT 47
US-10-517-939-178
; Sequence 178, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM

; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(26)
US-10-517-939-178

Query Match 52.5%; Score 42; DB 9; Length 432;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YYCFWK 8
||| |||
Db 40 YYSFWK 46

RESULT 48
US-10-131-826A-140
; Sequence 140, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 140
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-140

Query Match 52.5%; Score 42; DB 9; Length 539;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CYYCFWKTC 10
| | | | |
Db 17 CLYSCHWRKC 26

RESULT 49

US-10-973-115B-140
; Sequence 140, Application US/10973115B
; Publication No. US2006040351A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING

; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT APPLICATION NUMBER: US/10/973,115B
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 140
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-115B-140

Query Match 52.5%; Score 42; DB 9; Length 539;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CYYCFWKTC 10
| | | | |
Db 17 CLYSCHWRKC 26

RESULT 50

US-10-137-873A-140
; Sequence 140, Application US/10137873A
; Publication No. US20060084138A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C149

; CURRENT APPLICATION NUMBER: US/10/137,873A
; CURRENT FILING DATE: 2002-04-23

; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 140
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-873A-140

Query Match 52.5%; Score 42; DB 9; Length 539;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CYYCFWKTC 10
| | | | |
Db 17 CLYSCHWRKC 26

Search completed: May 9, 2006, 12:16:17
Job time : 14 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:04:09 ; Search time 49.6667 Seconds
(without alignments)
97.312 Million cell updates/sec

Title: us-10-796-158-7
Perfect score: 80
Sequence: 1 YYCYCFWKTCT 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	11	8	ADS74379 Somatosta
2	69	86.2	11	2	AAW48645 Somatosta
3	69	86.2	11	8	ADM35520 Somatosta
4	69	86.2	11	9	ADW95422 Somatosta
5	62.5	78.1	11	8	ADS74377 Somatosta
6	62	77.5	11	8	ADS74378 Somatosta
7	62	77.5	13	7	ADC68595 Somatosta
8	57	71.2	8	6	AAO26828 Somatosta
9	57	71.2	8	6	AAO26832 Somatosta
10	57	71.2	8	6	AAO26830 Somatosta
11	57	71.2	8	6	AAO26825 Somatosta
12	57	71.2	8	6	AAO26827 Somatosta
13	57	71.2	8	6	AAO26826 Somatosta
14	57	71.2	8	6	AAO26829 Somatosta
15	57	71.2	8	6	AAO26831 Somatosta
16	57	71.2	9	2	AAW48642 Somatosta
17	57	71.2	9	6	ABG71792 Somatosta
18	57	71.2	10	7	ADU14934 Somatosta
19	57	71.2	10	8	ADU05247 Somatosta
20	57	71.2	11	7	ADU14956 Somatosta
21	57	71.2	11	7	ADU14951 Somatosta
22	57	71.2	11	7	ADU14959 Somatosta
23	57	71.2	11	7	ADU14954 Somatosta
24	57	71.2	11	8	ADU05246 Cyclic so

25	71.2	7	ADU14894	Adi14894 Somatosta
26	71.2	13	ADU14957	Adi14957 Somatosta
27	71.2	7	ADU14895	Adi14895 Somatosta
28	71.2	14	ADU14952	Adi14952 Somatosta
29	71.2	15	ABR42184	AbR42184 Somatosta
30	71.2	15	ADU14935	Adi14935 Somatosta
31	71.2	15	ADU14898	Adi14898 Somatosta
32	71.2	20	ABR42192	AbR42192 Peptide a
33	71.2	20	ABR42198	AbR42198 Somatosta
34	71.2	20	ADU14936	Adi14936 Somatosta
35	71.2	20	ADU14897	Adi14897 Somatosta
36	71.2	22	ABR42181	AbR42181 Somatosta
37	71.2	23	ABR42199	AbR42199 Somatosta
38	71.2	30	ABR42197	AbR42197 Somatosta
39	70.0	10	AAW48643	AAW48643 Somatosta
40	67.5	10	ADU05266	ADU05266 Cyclic so
41	67.5	11	ADU05270	ADU05270 Cyclic so
42	67.5	11	ADU05281	ADU05281 Cyclic so
43	66.2	8	AAPI0586	AAPI0586 GH, Gastr
44	66.2	8	AAPI0593	AAPI0593 GH, Gastr
45	66.2	8	AAPI0593	AAPI0593 GH, Gastr
46	66.2	8	AAPI0593	AAPI0593 GH, Gastr
47	66.2	8	AAPI0593	AAPI0593 GH, Gastr
48	66.2	8	AAPI0593	AAPI0593 GH, Gastr
49	66.2	8	AAPI0593	AAPI0593 GH, Gastr
50	66.2	8	AAPI0593	AAPI0593 GH, Gastr
51	66.2	8	AAPI0593	AAPI0593 GH, Gastr
52	66.2	8	AAPI0593	AAPI0593 GH, Gastr
53	66.2	8	AAPI0593	AAPI0593 GH, Gastr
54	66.2	8	AAPI0593	AAPI0593 GH, Gastr
55	66.2	8	AAPI0593	AAPI0593 GH, Gastr
56	66.2	8	AAPI0593	AAPI0593 GH, Gastr
57	66.2	8	AAPI0593	AAPI0593 GH, Gastr
58	66.2	8	AAPI0593	AAPI0593 GH, Gastr
59	66.2	8	AAPI0593	AAPI0593 GH, Gastr
60	66.2	8	AAPI0593	AAPI0593 GH, Gastr
61	66.2	8	AAPI0593	AAPI0593 GH, Gastr
62	66.2	8	AAPI0593	AAPI0593 GH, Gastr
63	66.2	8	AAPI0593	AAPI0593 GH, Gastr
64	66.2	8	AAPI0593	AAPI0593 GH, Gastr
65	66.2	8	AAPI0593	AAPI0593 GH, Gastr
66	66.2	8	AAPI0593	AAPI0593 GH, Gastr
67	66.2	8	AAPI0593	AAPI0593 GH, Gastr
68	66.2	8	AAPI0593	AAPI0593 GH, Gastr
69	66.2	8	AAPI0593	AAPI0593 GH, Gastr
70	66.2	8	AAPI0593	AAPI0593 GH, Gastr
71	66.2	8	AAPI0593	AAPI0593 GH, Gastr
72	66.2	8	AAPI0593	AAPI0593 GH, Gastr
73	66.2	8	AAPI0593	AAPI0593 GH, Gastr
74	66.2	8	AAPI0593	AAPI0593 GH, Gastr
75	66.2	8	AAPI0593	AAPI0593 GH, Gastr
76	66.2	8	AAPI0593	AAPI0593 GH, Gastr
77	66.2	8	AAPI0593	AAPI0593 GH, Gastr
78	66.2	8	AAPI0593	AAPI0593 GH, Gastr
79	66.2	8	AAPI0593	AAPI0593 GH, Gastr
80	66.2	8	AAPI0593	AAPI0593 GH, Gastr
81	66.2	8	AAPI0593	AAPI0593 GH, Gastr
82	66.2	8	AAPI0593	AAPI0593 GH, Gastr
83	66.2	8	AAPI0593	AAPI0593 GH, Gastr
84	66.2	8	AAPI0593	AAPI0593 GH, Gastr
85	66.2	8	AAPI0593	AAPI0593 GH, Gastr
86	66.2	8	AAPI0593	AAPI0593 GH, Gastr
87	66.2	8	AAPI0593	AAPI0593 GH, Gastr
88	66.2	8	AAPI0593	AAPI0593 GH, Gastr
89	66.2	8	AAPI0593	AAPI0593 GH, Gastr
90	66.2	8	AAPI0593	AAPI0593 GH, Gastr
91	66.2	8	AAPI0593	AAPI0593 GH, Gastr
92	66.2	8	AAPI0593	AAPI0593 GH, Gastr
93	66.2	8	AAPI0593	AAPI0593 GH, Gastr
94	66.2	8	AAPI0593	AAPI0593 GH, Gastr
95	66.2	8	AAPI0593	AAPI0593 GH, Gastr
96	66.2	8	AAPI0593	AAPI0593 GH, Gastr
97	66.2	8	AAPI0593	AAPI0593 GH, Gastr

98	53	66.2	8	3	AAy82555	AAy82555 Somatosta	171	53	66.2	9	7	AD114962	AD114962 Somatosta
99	53	66.2	8	3	AA06244	AA06244 Somatosta	172	53	66.2	9	7	AD114937	AD114937 Somatosta
100	53	66.2	8	3	AAy81017	AAy81017 Somatosta	173	53	66.2	9	8	ADU05262	ADU05262 Cyclic so
101	53	66.2	8	3	AAy81016	AAy81016 Somatosta	174	53	66.2	9	8	ADU05244	ADU05244 Cyclic so
102	53	66.2	8	3	AAy83802	AAy83802 Somatosta	175	53	66.2	10	7	AD114931	AD114931 Somatosta
103	53	66.2	8	3	AAAB24186	AAAB24186 Somatosta	176	53	66.2	11	7	AD114900	AD114900 Somatosta
104	53	66.2	8	3	AAAB24182	AAAB24182 Somatosta	177	53	66.2	12	2	AAW48646	AAW48646
105	53	66.2	8	3	AAAB19026	AAAB19026 Amino aci	178	53	66.2	12	3	AAy98159	AAy98159 Thiol con
106	53	66.2	8	4	ABW77167	ABW77167 Octreotid	179	53	66.2	12	3	AAy94484	AAy94484 Human som
107	53	66.2	8	4	AAU05146	AAU05146 Receptor-	180	53	66.2	12	3	AAy94487	AAy94487 Human som
108	53	66.2	8	4	AAW51439	AAW51439 Somatosta	181	53	66.2	12	7	AD114932	AD114932 Somatosta
109	53	66.2	8	4	AAy97708	AAy97708 Rat Urothe	182	52	65.0	8	1	AAp61467	AAp61467 Cyclic oc
110	53	66.2	8	4	AAAB45664	AAAB45664 Somatosta	183	52	65.0	8	2	AAr14238	AAr14238 Somatosta
111	53	66.2	8	4	AAU08826	AAU08826 Somatosta	184	52	65.0	8	2	AAr10503	AAr10503 Pamocate o
112	53	66.2	8	4	AAU08827	AAU08827 Somatosta	185	52	65.0	8	2	AAr23950	AAr23950 LH-RH, so
113	53	66.2	8	4	AAU08925	AAU08925 Somatosta	186	52	65.0	8	2	AAr41503	AAr41503 Somatosta
114	53	66.2	8	5	AAE17934	AAE17934 Somatosta	187	52	65.0	8	2	AAr31509	AAr31509 Somatosta
115	53	66.2	8	5	ABW09976	ABW09976 Octreotid	188	52	65.0	8	2	AAr42654	AAr42654 Somatosta
116	53	66.2	8	5	ABW09974	ABW09974 Straight	189	52	65.0	8	2	AAr56779	AAr56779 Somatosta
117	53	66.2	8	5	ABP53367	ABP53367 Somatosta	190	52	65.0	8	2	AAr76203	AAr76203 Somatosta
118	53	66.2	8	5	AAE15400	AAE15400 Somatosta	191	52	65.0	8	2	AAr85571	AAr85571 Somatosta
119	53	66.2	8	5	AAE19360	AAE19360 Somatosta	192	52	65.0	8	2	AAW51863	AAW51863 Somatosta
120	53	66.2	8	5	AAE19364	AAE19364 Somatosta	193	52	65.0	8	2	AAy22042	AAy22042 Somatosta
121	53	66.2	8	5	ADH68884	ADH68884 Synthetic	194	52	65.0	8	2	AAy18227	AAy18227 Somatosta
122	53	66.2	8	5	ADH68893	ADH68893 Synthetic	195	52	65.0	8	2	AAW45741	AAW45741 Somatosta
123	53	66.2	8	6	ABG99249	ABG99249 Somatosta	196	52	65.0	8	2	AAW97186	AAW97186 Somatosta
124	53	66.2	8	6	ABG99248	ABG99248 Somatosta	197	52	65.0	8	2	ADH35405	ADH35405 Human som
125	53	66.2	8	6	AAO26852	AAO26852 Somatosta	198	52	65.0	8	2	ADH68006	ADH68006 Somatosta
126	53	66.2	8	6	AAO26824	AAO26824 Somatosta	199	52	65.0	8	2	ADK11158	ADK11158 Somatosta
127	53	66.2	8	6	AAO26818	AAO26818 Somatosta	200	52	65.0	8	3	AAAB06247	AAAB06247 Somatosta
128	53	66.2	8	6	AAO26822	AAO26822 Somatosta	201	52	65.0	8	3	AAy81019	AAy81019 Somatosta
129	53	66.2	8	6	AAO26851	AAO26851 Somatosta	202	52	65.0	8	3	AAy24185	AAy24185 Somatosta
130	53	66.2	8	6	AAO26819	AAO26819 Somatosta	203	52	65.0	8	3	AAAB19025	AAAB19025 Amino aci
131	53	66.2	8	6	AAO26820	AAO26820 Somatosta	204	52	65.0	8	4	AAAB74612	AAAB74612 Somatosta
132	53	66.2	8	6	AAO26821	AAO26821 Somatosta	205	52	65.0	8	4	AAU08829	AAU08829 Somatosta
133	53	66.2	8	6	AAO26823	AAO26823 Somatosta	206	52	65.0	8	5	AAE19363	AAE19363 Somatosta
134	53	66.2	8	6	ABP55049	ABP55049 Octreotid	207	52	65.0	8	6	ABG99251	ABG99251 Somatosta
135	53	66.2	8	6	ABP55050	ABP55050 Octreotid	208	52	65.0	8	6	AAO26854	AAO26854 Somatosta
136	53	66.2	8	6	ADA41667	ADA41667 Cyclic te	209	52	65.0	8	9	ADZ99638	ADZ99638 Somatosta
137	53	66.2	8	7	ADB88527	ADB88527 Somatosta	210	52	65.0	9	1	AAp40513	AAp40513 Sequence
138	53	66.2	8	7	ABR83029	ABR83029 Somatosta	211	52	65.0	9	2	AAr14232	AAr14232 Somatosta
139	53	66.2	8	7	ADP61742	ADP61742 Somatosta	212	52	65.0	10	7	AD114944	AD114944 Somatosta
140	53	66.2	8	7	AD114899	AD114899 Somatosta	213	52	65.0	11	7	AD114943	AD114943 Somatosta
141	53	66.2	8	7	ADL16034	ADL16034 Octreotid	214	52	65.0	11	7	AD114945	AD114945 Somatosta
142	53	66.2	8	8	ADH63166	ADH63166 Octreotid	215	51	63.7	10	2	AAr14235	AAr14235 Somatosta
143	53	66.2	8	8	ADJ56707	ADJ56707 Cyclic pe	216	51	63.7	12	3	AAy94481	AAy94481 Human som
144	53	66.2	8	8	ADM35518	ADM35518 Somatosta	217	51	63.7	12	3	AAy94489	AAy94489 Human som
145	53	66.2	8	8	ADR87508	ADR87508 Backbone	218	51	63.7	12	3	AAy94485	AAy94485 Human som
146	53	66.2	8	8	ADr7485	ADr7485 Somatosta	219	51	63.7	12	3	AAy94490	AAy94490 Human som
147	53	66.2	8	8	ADS12361	ADS12361 Octreotate	220	51	63.7	12	3	AAy94480	AAy94480 Human som
148	53	66.2	8	8	ADU05219	ADU05219 Cyclic so	221	51	63.7	12	6	ABR42183	ABR42183 Somatosta
149	53	66.2	8	8	ADU95227	ADU95227 Novel cyt	222	51	63.7	14	3	AAy94482	AAy94482 Human som
150	53	66.2	8	8	ADU07144	ADU07144 Octreotid	223	51	63.7	14	3	AAy94483	AAy94483 Human som
151	53	66.2	8	9	ADW95415	ADW95415 Peptide #	224	51	63.7	14	5	ABW04754	ABW04754 Arg-Gly-A
152	53	66.2	8	9	ADW95416	ADW95416 Peptide #	225	50	62.5	7	2	AAW48639	AAW48639 Somatosta
153	53	66.2	8	9	ADW95412	ADW95412 Peptide #	226	50	62.5	7	2	AAW97196	AAW97196 Somatosta
154	53	66.2	8	9	ADW95413	ADW95413 Peptide #	227	50	62.5	7	8	ADS74376	ADS74376 Somatosta
155	53	66.2	8	9	ADW95411	ADW95411 Peptide #	228	50	62.5	7	8	ADU05220	ADU05220 Cyclic so
156	53	66.2	8	9	ADW95418	ADW95418 Peptide #	229	50	62.5	8	1	AAp40369	AAp40369 Sequence
157	53	66.2	8	9	ADW95419	ADW95419 Peptide #	230	50	62.5	8	2	AAr12865	AAr12865 Somatosta
158	53	66.2	8	9	ADW95414	ADW95414 Peptide #	231	50	62.5	8	2	AAr28861	AAr28861 Somatosta
159	53	66.2	8	9	ADW95417	ADW95417 Peptide #	232	50	62.5	8	2	AAr42660	AAr42660 Somatosta
160	53	66.2	8	9	ADW95420	ADW95420 Peptide #	233	50	62.5	8	2	AAr56785	AAr56785 Somatosta
161	53	66.2	8	9	ADY51780	ADY51780 Cyclic pe	234	50	62.5	8	2	AAr56784	AAr56784 Somatosta
162	53	66.2	8	9	ADZ99635	ADZ99635 Somatosta	235	50	62.5	8	2	AAr50279	AAr50279 Tyrosinat
163	53	66.2	8	9	ADZ99636	ADZ99636 Somatosta	236	50	62.5	8	2	AAW01511	AAW01511 [Tyr3]-oc
164	53	66.2	9	1	AAp92299	AAp92299 Peptide s	237	50	62.5	8	2	AAr99320	AAr99320 Cyclic so
165	53	66.2	9	2	AAr14231	AAr14231 Somatosta	238	50	62.5	8	2	AAW12316	AAW12316 Site-spec
166	53	66.2	9	2	AAr28860	AAr28860 Somatosta	239	50	62.5	8	2	AAW6232	AAW6232 Somatosta
167	53	66.2	9	3	AAr81662	AAr81662 Somatosta	240	50	62.5	8	2	AAy22034	AAy22034 Somatosta
168	53	66.2	9	3	AAy95247	AAy95247 Sandostat	241	50	62.5	8	2	AAy22048	AAy22048 Somatosta
169	53	66.2	9	3	AAAB15191	AAAB15191 Sandostat	242	50	62.5	8	2	AAy18219	AAy18219 Somatosta
170	53	66.2	9	7	AD114930	AD114930 Somatosta	243	50	62.5	8	2	AAy18232	AAy18232 Somatosta

244 50 62.5 8 2 AAW52877 Tyr-3-Oct 317
245 50 62.5 8 2 ADH35415 Human som 318
246 50 62.5 8 2 ADH35414 Human som 319
247 50 62.5 8 2 ADH35413 Human som 320
248 50 62.5 8 2 ADH35394 Human som 321
249 50 62.5 8 2 ADH68016 Somatosta 322
250 50 62.5 8 2 ADH68014 Somatosta 323
251 50 62.5 8 2 ADH67995 Somatosta 324
252 50 62.5 8 2 ADH68015 Somatosta 325
253 50 62.5 8 2 ADK11147 Somatosta 326
254 50 62.5 8 2 ADK11166 Somatosta 327
255 50 62.5 8 2 ADK11168 Somatosta 328
256 50 62.5 8 2 ADK11167 Somatosta 329
257 50 62.5 8 3 AAB12843 Tyr-3-Oct 330
258 50 62.5 8 3 AAB06920 Somatosta 331
259 50 62.5 8 3 AAB06252 Somatosta 332
260 50 62.5 8 3 AAB06236 Somatosta 333
261 50 62.5 8 3 AAB061027 Somatosta 334
262 50 62.5 8 3 AAY81028 Somatosta 335
263 50 62.5 8 3 AAY81008 Somatosta 336
264 50 62.5 8 3 AAY81029 Somatosta 337
265 50 62.5 8 4 AAB19952 Octreotid 338
266 50 62.5 8 4 AAB19951 Octreotat 339
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268 50 62.5 8 4 AAB71696 Octreotat 341
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271 50 62.5 8 4 AAB70510 Octreotid 344
272 50 62.5 8 4 AAB73421 Octreotat 345
273 50 62.5 8 4 AAU07319 Octreotid 346
274 50 62.5 8 4 AAU07318 Octreotat 347
275 50 62.5 8 4 AAM51429 Somatosta 348
276 50 62.5 8 4 AAG67680 Amino aci 349
277 50 62.5 8 4 AAB60182 DTPA-Tyr- 350
278 50 62.5 8 4 AAE07132 Octreotat 351
279 50 62.5 8 4 AAE07133 Octreotid 352
280 50 62.5 8 4 AAB73427 Octreotat 353
281 50 62.5 8 4 AAB45665 Somatosta 354
282 50 62.5 8 4 AAG65283 Octreotid 355
283 50 62.5 8 4 AAG65290 Peptide s 356
284 50 62.5 8 4 AAU08837 Somatosta 357
285 50 62.5 8 4 AAU08839 Somatosta 358
286 50 62.5 8 4 AAU08838 Somatosta 359
287 50 62.5 8 4 AAU08818 Somatosta 360
288 50 62.5 8 5 ABB09975 Straight 361
289 50 62.5 8 5 ABB09977 Tyr-3-Oct 362
290 50 62.5 8 5 AAE23234 Yttrium 1 363
291 50 62.5 8 5 AAU97453 Synthetic 364
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293 50 62.5 8 5 ADH68885 Synthetic 366
294 50 62.5 8 5 ADH68894 Synthetic 367
295 50 62.5 8 6 ABU09466 Octreotat 368
296 50 62.5 8 6 ABG99259 Somatosta 369
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300 50 62.5 8 6 ABR42462 Octreotat 373
301 50 62.5 8 6 AAO26862 Somatosta 374
302 50 62.5 8 6 AAO26843 Somatosta 375
303 50 62.5 8 6 AAO26864 Somatosta 376
304 50 62.5 8 6 AAO26863 Somatosta 377
305 50 62.5 8 6 ABR55702 Amino aci 378
306 50 62.5 8 6 ABR55701 Amino aci 379
307 50 62.5 8 6 ABR44097 Amino aci 380
308 50 62.5 8 6 ABR44096 Amino aci 381
309 50 62.5 8 7 ABR82870 Amino aci 382
310 50 62.5 8 7 ABR82869 Amino aci 383
311 50 62.5 8 7 ADF61744 Somatosta 384
312 50 62.5 8 7 ADI14890 Somatosta 385
313 50 62.5 8 8 ADU05245 Cyclic so 386
314 50 62.5 8 8 ADU05223 Cyclic so 387
315 50 62.5 8 8 ADU05263 Cyclic so 388
316 50 62.5 8 9 ADV11333 Octreotid 389

ADV11332 Octreotat 317
ADX18052 Human som 318
ADZ99646 Somatosta 319
ADZ99627 Somatosta 320
ADZ99647 Somatosta 321
ADZ99648 Somatosta 322
AAP10594 GH, Gastr 323
AAR56792 Somatosta 324
AAR56797 Somatosta 325
AAR56791 Somatosta 326
AAR56793 Somatosta 327
AAR56786 Somatosta 328
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AAR56790 Somatosta 331
AAR56789 Somatosta 332
AAW01512 Octreotid 333
AAY22047 Somatosta 334
AAY22051 Somatosta 335
AAY18235 Somatosta 336
AAY18231 Somatosta 337
ADH35419 Human som 338
ADH35410 Human som 339
ADH35416 Human som 340
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ADH35424 Human som 350
ADH68017 Somatosta 351
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ADH68019 Somatosta 354
ADH68029 Somatosta 355
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ADH68025 Somatosta 357
ADH68012 Somatosta 358
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ADK11177 Somatosta 375
AAB06935 Somatosta 376
AAB06936 Somatosta 377
AAY81036 Somatosta 378
AAY81025 Somatosta 379
AAY81045 Somatosta 380
AAY81032 Somatosta 381
AAY81040 Somatosta 382
AAY81042 Somatosta 383
AAY81024 Somatosta 384
AAY81035 Somatosta 385
AAY81034 Somatosta 386
AAY81037 Somatosta 387
AAY81030 Somatosta 388
AAY81033 Somatosta 389

390	50	62.5	9	3	AAy81026	Adk11184	Somatosta	463	50	62.5	10	2	ADK11184	Adk11184	Somatosta
391	50	62.5	9	4	AAAB60181	Ab60936	Somatosta	464	50	62.5	10	3	AAAB6936	Ab60936	Somatosta
392	50	62.5	9	4	AAAB60076	Ab60076	Somatosta	465	50	62.5	10	3	AAAY94488	Human som	
393	50	62.5	9	4	AAU08834	Aau08834	Somatosta	466	50	62.5	10	3	AAAY81043	Somatosta	
394	50	62.5	9	4	AAU08846	Aau08846	Somatosta	467	50	62.5	10	4	AAU08853	Somatosta	
395	50	62.5	9	4	AAU08852	Aau08852	Somatosta	468	50	62.5	10	4	AAU08855	Somatosta	
396	50	62.5	9	4	AAU08844	Aau08844	Somatosta	469	50	62.5	10	6	ABG99277	Somatosta	
397	50	62.5	9	4	AAU08847	Aau08847	Somatosta	470	50	62.5	10	6	ABG99275	Somatosta	
398	50	62.5	9	4	AAU08835	Aau08835	Somatosta	471	50	62.5	10	6	AAO26880	Somatosta	
399	50	62.5	9	4	AAU08843	Aau08843	Somatosta	472	50	62.5	10	6	AAO26878	Somatosta	
400	50	62.5	9	4	AAU08845	Aau08845	Somatosta	473	50	62.5	10	7	AD114955	Somatosta	
401	50	62.5	9	4	AAU08848	Aau08848	Somatosta	474	50	62.5	10	8	ADU05268	Cyclic so	
402	50	62.5	9	4	AAU08842	Aau08842	Somatosta	475	50	62.5	10	9	ADZ99664	Somatosta	
403	50	62.5	9	4	AAU08836	Aau08836	Somatosta	476	50	62.5	10	9	ADZ99662	Somatosta	
404	50	62.5	9	4	AAU08840	Aau08840	Somatosta	477	50	62.5	11	7	AD114933	Somatosta	
405	50	62.5	9	6	AAE35393	Aae35393	Somatosta	478	50	62.5	11	7	AD114893	Somatosta	
406	50	62.5	9	6	ABG99268	Abg99268	Somatosta	479	50	62.5	11	7	AD114958	Somatosta	
407	50	62.5	9	6	ABG99256	Abg99256	Somatosta	480	50	62.5	11	7	AD114958	Somatosta	
408	50	62.5	9	6	ABG99257	Abg99257	Somatosta	481	50	62.5	12	1	AAAP40570	Sequence	
409	50	62.5	9	6	ABG99264	Abg99264	Somatosta	482	50	62.5	12	1	AAAP40571	Sequence	
410	50	62.5	9	6	ABG99266	Abg99266	Somatosta	483	50	62.5	12	3	AAAY94486	Human som	
411	50	62.5	9	6	ABG99267	Abg99267	Somatosta	484	50	62.5	12	3	AAAY94486	Human som	
412	50	62.5	9	6	ABG99270	Abg99270	Somatosta	485	50	62.5	12	6	ABR42188	Peptide a	
413	50	62.5	9	6	ABG99265	Abg99265	Somatosta	486	50	62.5	12	6	ABR42189	Peptide a	
414	50	62.5	9	6	ABG99258	Abg99258	Somatosta	487	50	62.5	12	7	ADE28588	Cytotoxic	
415	50	62.5	9	6	ABG99269	Abg99269	Somatosta	488	50	62.5	12	7	ADE28589	Cytotoxic	
416	50	62.5	9	6	ABG99274	Abg99274	Somatosta	489	50	62.5	12	7	ADE28611	Cytotoxic	
417	50	62.5	9	6	ABG99262	Abg99262	Somatosta	490	50	62.5	12	7	ADE28612	Cyclic cy	
418	50	62.5	9	6	ABG99272	Abg99272	Somatosta	491	50	62.5	13	2	AAW01513	Ocreotid	
419	50	62.5	9	6	AAO26877	Aao26877	Somatosta	492	50	62.5	13	7	ADE28593	Cytotoxic	
420	50	62.5	9	6	AAO26868	Aao26868	Somatosta	493	50	62.5	13	7	ADE28594	Cyclic cy	
421	50	62.5	9	6	AAO26860	Aao26860	Somatosta	494	50	62.5	14	7	ADE28595	Cytotoxic	
422	50	62.5	9	6	AAO26871	Aao26871	Somatosta	495	50	62.5	14	8	ADU97615	Novel cyt	
423	50	62.5	9	6	AAO26875	Aao26875	Somatosta	496	50	62.5	14	8	ADU97600	Novel cyt	
424	50	62.5	9	6	AAO26870	Aao26870	Somatosta	497	50	62.5	14	8	ADU97630	Novel cyt	
425	50	62.5	9	6	AAO26865	Aao26865	Somatosta	498	50	62.5	15	6	ABR42182	Somatosta	
426	50	62.5	9	6	AAO26869	Aao26869	Somatosta	499	50	62.5	15	6	ABR42206	Somatosta	
427	50	62.5	9	6	AAO26861	Aao26861	Somatosta	500	50	62.5	15	6	ABR42207	Somatosta	
428	50	62.5	9	6	AAO26859	Aao26859	Somatosta	501	50	62.5	15	6	ABR42202	Somatosta	
429	50	62.5	9	6	AAO26872	Aao26872	Somatosta	502	50	62.5	15	6	ABR42200	Somatosta	
430	50	62.5	9	6	AAO26873	Aao26873	Somatosta	503	50	62.5	15	6	ABR42191	Peptide a	
431	50	62.5	9	6	AAO26867	Aao26867	Somatosta	504	50	62.5	15	6	ABR42209	Somatosta	
432	50	62.5	9	8	ADO43346	Ado43346	Somatosta	505	50	62.5	15	6	ABR42205	Somatosta	
433	50	62.5	9	8	ADO08043	Ado08043	Synthetic	506	50	62.5	15	6	ABR42180	Control p	
434	50	62.5	9	8	ADU05267	Adu05267	Cyclic so	507	50	62.5	15	6	ABR42203	Somatosta	
435	50	62.5	9	8	ADU05224	Adu05224	Cyclic so	508	50	62.5	15	6	ABR42201	Somatosta	
436	50	62.5	9	8	ADU05213	Adu05213	Cyclic so	509	50	62.5	15	7	ADE28596	Cytotoxic	
437	50	62.5	9	9	ADV68518	Adv68518	Somatosta	510	50	62.5	15	7	AD114896	Somatosta	
438	50	62.5	9	9	ADV99688	Adv99688	Cyclic Cy	511	50	62.5	15	8	ADU97599	Novel cyt	
439	50	62.5	9	9	ADZ99644	Adz99644	Somatosta	512	50	62.5	15	8	ADU97629	Novel cyt	
440	50	62.5	9	9	ADZ99659	Adz99659	Somatosta	513	50	62.5	15	8	ADU97614	Novel cyt	
441	50	62.5	9	9	ADZ99661	Adz99661	Somatosta	514	50	62.5	16	6	ABR42208	Somatosta	
442	50	62.5	9	9	ADZ99654	Adz99654	Somatosta	515	50	62.5	16	6	ABR42204	Somatosta	
443	50	62.5	9	9	ADZ99652	Adz99652	Somatosta	516	50	62.5	16	6	ABR42204	Somatosta	
444	50	62.5	9	9	ADZ99656	Adz99656	Somatosta	517	50	62.5	16	8	ADU97616	Novel cyt	
445	50	62.5	9	9	ADZ99643	Adz99643	Somatosta	518	50	62.5	16	8	ADU97631	Novel cyt	
446	50	62.5	9	9	ADZ99657	Adz99657	Somatosta	519	50	62.5	16	8	ADU97601	Novel cyt	
447	50	62.5	9	9	ADZ99645	Adz99645	Somatosta	520	50	62.5	17	7	ADE28598	Cytotoxic	
448	50	62.5	9	9	ADZ99655	Adz99655	Somatosta	521	50	62.5	18	6	ABR42210	Somatosta	
449	50	62.5	9	9	ADZ99649	Adz99649	Somatosta	522	50	62.5	18	7	ADE28599	Cytotoxic	
450	50	62.5	9	9	ADZ99653	Adz99653	Somatosta	523	50	62.5	19	6	ABR42212	Somatosta	
451	50	62.5	9	9	ADZ99651	Adz99651	Somatosta	524	50	62.5	19	7	ADE28600	Cytotoxic	
452	50	62.5	9	9	AEA01716	Aea01716	Somatosta	525	50	62.5	20	7	ADE28601	Cytotoxic	
453	50	62.5	9	9	ADZ87448	Adz87448	Somatosta	526	50	62.5	21	6	ABR42187	Peptide a	
454	50	62.5	10	2	AAK56798	Aar56798	Somatosta	527	50	62.5	21	7	ADE28602	Cytotoxic	
455	50	62.5	10	2	AAK56800	Aar56800	Somatosta	528	50	62.5	22	6	ABR42211	Somatosta	
456	50	62.5	10	2	AAV22052	Aay22052	Somatosta	529	50	62.5	22	7	ADE28603	Cytotoxic	
457	50	62.5	10	2	AAV18236	Aay18236	Somatosta	530	50	62.5	23	4	AAW51433	Peptide K	
458	50	62.5	10	2	ADH35429	Adh35429	Human som	531	50	62.5	23	7	ADC33481	Peptide K	
459	50	62.5	10	2	ADH35431	Adh35431	Human som	532	50	62.5	23	7	ADE28604	Cytotoxic	
460	50	62.5	10	2	ADH68032	Adh68032	Somatosta	533	50	62.5	24	7	ADE28605	Cytotoxic	
461	50	62.5	10	2	ADH68030	Adh68030	Somatosta	534	50	62.5	25	7	ADE28606	Cytotoxic	
462	50	62.5	10	2	ADK11182	Adk11182	Somatosta	535	50	62.5	26	7	ADE28607	Cytotoxic	

536	50	62.5	27	7	ADE28608	Ade28608	Cytotoxic	609	49	61.3	12	7	AD114991	Ad114991	Somatosta
537	49	61.3	8	1	AAp10587	Asp10587	GH, gastr	610	49	61.3	12	7	AD115003	Ad115003	Somatosta
538	49	61.3	8	2	AAW48641	Asw48641	Somatosta	611	49	61.3	12	7	ADU95760	Adu95760	Novel cyt
539	49	61.3	9	2	AAW48644	Asw48644	Somatosta	612	49	61.3	12	8	ADU96514	Adu96514	Novel cyt
540	49	61.3	10	7	AD114971	Adi14971	Somatosta	613	49	61.3	12	8	ADU97110	Adu97110	Novel cyt
541	49	61.3	10	8	ADU05212	Adu05212	Cyclic so	614	49	61.3	12	8	ADU96506	Adu96506	Novel cyt
542	49	61.3	10	8	ADU05243	Adu05243	Cyclic so	615	49	61.3	12	8	ADU96509	Adu96509	Novel cyt
543	49	61.3	10	8	ADU05276	Adu05276	Cyclic so	616	49	61.3	12	8	ADU96456	Adu96456	Novel cyt
544	49	61.3	10	8	ADU05235	Adu05235	Cyclic so	617	49	61.3	12	8	ADU96529	Adu96529	Novel cyt
545	49	61.3	10	8	ADU05239	Adu05239	Cyclic so	618	49	61.3	12	8	ADU97104	Adu97104	Novel cyt
546	49	61.3	10	8	ADU05271	Adu05271	Cyclic so	619	49	61.3	12	8	ADU95838	Adu95838	Novel cyt
547	49	61.3	10	8	ADU95289	Adu95289	Novel cyt	620	49	61.3	12	8	ADU96469	Adu96469	Novel cyt
548	49	61.3	10	8	ADU96133	Adu96133	Novel cyt	621	49	61.3	12	8	ADU96521	Adu96521	Novel cyt
549	49	61.3	10	8	ADU96505	Adu96505	Novel cyt	622	49	61.3	12	8	ADU97532	Adu97532	Novel cyt
550	49	61.3	10	8	ADU95827	Adu95827	Novel cyt	623	49	61.3	12	8	ADU95296	Adu95296	Novel cyt
551	49	61.3	10	8	ADU95290	Adu95290	Novel cyt	624	49	61.3	12	8	ADU95851	Adu95851	Novel cyt
552	49	61.3	10	8	ADU96194	Adu96194	Novel cyt	625	49	61.3	12	8	ADU96462	Adu96462	Novel cyt
553	49	61.3	10	8	ADU97505	Adu97505	Novel cyt	626	49	61.3	12	8	ADU96599	Adu96599	Novel cyt
554	49	61.3	10	8	ADU97103	Adu97103	Novel cyt	627	49	61.3	12	8	ADU96534	Adu96534	Novel cyt
555	49	61.3	10	8	ADU95224	Adu95224	Novel cyt	628	49	61.3	12	8	ADU97043	Adu97043	Novel cyt
556	49	61.3	10	8	ADU96455	Adu96455	Novel cyt	629	49	61.3	12	8	ADU96581	Adu96581	Novel cyt
557	49	61.3	10	8	ADU95758	Adu95758	Novel cyt	630	49	61.3	12	8	ADU97545	Adu97545	Novel cyt
558	49	61.3	10	8	ADU95848	Adu95848	Novel cyt	631	49	61.3	12	8	ADU95757	Adu95757	Novel cyt
559	49	61.3	10	8	ADU96537	Adu96537	Novel cyt	632	49	61.3	12	8	ADU95843	Adu95843	Novel cyt
560	49	61.3	10	8	ADU95335	Adu95335	Novel cyt	633	49	61.3	12	8	ADU96153	Adu96153	Novel cyt
561	49	61.3	10	8	ADU97531	Adu97531	Novel cyt	634	49	61.3	12	8	ADU97117	Adu97117	Novel cyt
562	49	61.3	10	8	ADU97068	Adu97068	Novel cyt	635	49	61.3	12	8	ADU97540	Adu97540	Novel cyt
563	49	61.3	10	8	ADU97050	Adu97050	Novel cyt	636	49	61.3	12	8	ADU96126	Adu96126	Novel cyt
564	49	61.3	10	8	ADU95318	Adu95318	Novel cyt	637	49	61.3	12	8	ADU96162	Adu96162	Novel cyt
565	49	61.3	11	7	AD114990	Adi14990	Somatosta	638	49	61.3	12	8	ADU96464	Adu96464	Novel cyt
566	49	61.3	11	7	AD114972	Adi14972	Somatosta	639	49	61.3	12	8	ADU96586	Adu96586	Novel cyt
567	49	61.3	11	8	ADU05242	Adu05242	Cyclic so	640	49	61.3	12	8	ADU97112	Adu97112	Novel cyt
568	49	61.3	11	8	ADU05238	Adu05238	Cyclic so	641	49	61.3	12	8	ADU97538	Adu97538	Novel cyt
569	49	61.3	11	8	ADU05252	Adu05252	Cyclic so	642	49	61.3	12	8	ADU95292	Adu95292	Novel cyt
570	49	61.3	11	8	ADU05234	Adu05234	Cyclic so	643	49	61.3	12	8	ADU95772	Adu95772	Novel cyt
571	49	61.3	11	8	ADU05280	Adu05280	Cyclic so	644	49	61.3	12	8	ADU96132	Adu96132	Novel cyt
572	49	61.3	11	8	ADU05275	Adu05275	Cyclic so	645	49	61.3	12	8	ADU96593	Adu96593	Novel cyt
573	49	61.3	11	8	ADU95644	Adu95644	Novel cyt	646	49	61.3	13	7	AD114974	Adi14974	Somatosta
574	49	61.3	11	8	ADU96193	Adu96193	Novel cyt	647	49	61.3	13	7	AD114992	Adi14992	Somatosta
575	49	61.3	11	8	ADU97111	Adu97111	Novel cyt	648	49	61.3	13	8	ADU95756	Adu95756	Novel cyt
576	49	61.3	11	8	ADU97483	Adu97483	Novel cyt	649	49	61.3	13	8	ADU96587	Adu96587	Novel cyt
577	49	61.3	11	8	ADU95271	Adu95271	Novel cyt	650	49	61.3	13	8	ADU96595	Adu96595	Novel cyt
578	49	61.3	11	8	ADU95847	Adu95847	Novel cyt	651	49	61.3	13	8	ADU95761	Adu95761	Novel cyt
579	49	61.3	11	8	ADU96463	Adu96463	Novel cyt	652	49	61.3	13	8	ADU96585	Adu96585	Novel cyt
580	49	61.3	11	8	ADU95297	Adu95297	Novel cyt	653	49	61.3	13	8	ADU95846	Adu95846	Novel cyt
581	49	61.3	11	8	ADU96507	Adu96507	Novel cyt	654	49	61.3	13	8	ADU96465	Adu96465	Novel cyt
582	49	61.3	11	8	ADU96594	Adu96594	Novel cyt	655	49	61.3	13	8	ADU95771	Adu95771	Novel cyt
583	49	61.3	11	8	ADU97083	Adu97083	Novel cyt	656	49	61.3	13	8	ADU96533	Adu96533	Novel cyt
584	49	61.3	11	8	ADU97539	Adu97539	Novel cyt	657	49	61.3	13	8	ADU97044	Adu97044	Novel cyt
585	49	61.3	11	8	ADU95281	Adu95281	Novel cyt	658	49	61.3	13	8	ADU96518	Adu96518	Novel cyt
586	49	61.3	11	8	ADU97069	Adu97069	Novel cyt	659	49	61.3	13	8	ADU96602	Adu96602	Novel cyt
587	49	61.3	11	8	ADU97477	Adu97477	Novel cyt	660	49	61.3	13	8	ADU97113	Adu97113	Novel cyt
588	49	61.3	11	8	ADU97506	Adu97506	Novel cyt	661	49	61.3	13	8	ADU96524	Adu96524	Novel cyt
589	49	61.3	11	8	ADU95338	Adu95338	Novel cyt	662	49	61.3	13	8	ADU96513	Adu96513	Novel cyt
590	49	61.3	11	8	ADU95759	Adu95759	Novel cyt	663	49	61.3	13	8	ADU97105	Adu97105	Novel cyt
591	49	61.3	11	8	ADU96535	Adu96535	Novel cyt	664	49	61.3	13	8	ADU97546	Adu97546	Novel cyt
592	49	61.3	11	8	ADU96154	Adu96154	Novel cyt	665	49	61.3	13	8	ADU96470	Adu96470	Novel cyt
593	49	61.3	11	8	ADU97056	Adu97056	Novel cyt	666	49	61.3	13	8	ADU96530	Adu96530	Novel cyt
594	49	61.3	11	8	ADU95300	Adu95300	Novel cyt	667	49	61.3	13	8	ADU97533	Adu97533	Novel cyt
595	49	61.3	11	8	ADU97042	Adu97042	Novel cyt	668	49	61.3	13	8	ADU96131	Adu96131	Novel cyt
596	49	61.3	11	8	ADU95826	Adu95826	Novel cyt	669	49	61.3	13	8	ADU96515	Adu96515	Novel cyt
597	49	61.3	11	8	ADU97085	Adu97085	Novel cyt	670	49	61.3	13	8	ADU96590	Adu96590	Novel cyt
598	49	61.3	11	8	ADU97150	Adu97150	Novel cyt	671	49	61.3	13	8	ADU97541	Adu97541	Novel cyt
599	49	61.3	11	8	ADU96523	Adu96523	Novel cyt	672	49	61.3	13	8	ADU96152	Adu96152	Novel cyt
600	49	61.3	11	8	ADU95279	Adu95279	Novel cyt	673	49	61.3	13	8	ADU96161	Adu96161	Novel cyt
601	49	61.3	11	8	ADU97051	Adu97051	Novel cyt	674	49	61.3	13	8	ADU97118	Adu97118	Novel cyt
602	49	61.3	11	8	ADU97074	Adu97074	Novel cyt	675	49	61.3	13	8	ADU96457	Adu96457	Novel cyt
603	49	61.3	11	8	ADU97513	Adu97513	Novel cyt	676	49	61.3	13	8	ADU96598	Adu96598	Novel cyt
604	49	61.3	11	8	ADU97076	Adu97076	Novel cyt	677	49	61.3	14	7	AD114975	Adi14975	Somatosta
605	49	61.3	11	8	ADU97511	Adu97511	Novel cyt	678	49	61.3	14	7	AD114979	Adi14979	Somatosta
606	49	61.3	11	8	ADU97586	Adu97586	Novel cyt	679	49	61.3	14	7	AD114993	Adi14993	Somatosta
607	49	61.3	11	8	ADU97479	Adu97479	Novel cyt	680	49	61.3	14	8	ADU96151	Adu96151	Novel cyt
608	49	61.3	12	7	AD114973	Adi14973	Somatosta	681	49	61.3	14	8	ADU96160	Adu96160	Novel cyt

682	49	61.3	14	8	ADU96525	Novel	cyt	ADu96525	Novel	cyt	755	49	61.3	15	8	ADU96129	Novel	cyt	Adu96129	Novel	cyt
683	49	61.3	14	8	ADU97045	Novel	cyt	ADu97045	Novel	cyt	756	49	61.3	15	8	ADU96532	Novel	cyt	Adu96532	Novel	cyt
684	49	61.3	14	8	ADU97049	Novel	cyt	ADu97049	Novel	cyt	757	49	61.3	15	8	ADU96601	Novel	cyt	Adu96601	Novel	cyt
685	49	61.3	14	8	ADU97106	Novel	cyt	ADu97106	Novel	cyt	758	49	61.3	15	8	ADU97151	Novel	cyt	Adu97151	Novel	cyt
686	49	61.3	14	8	ADU95762	Novel	cyt	ADu95762	Novel	cyt	759	49	61.3	15	8	ADU96591	Novel	cyt	Adu96591	Novel	cyt
687	49	61.3	14	8	ADU96471	Novel	cyt	ADu96471	Novel	cyt	760	49	61.3	15	8	ADU97608	Novel	cyt	Adu97608	Novel	cyt
688	49	61.3	14	8	ADU95674	Novel	cyt	ADu95674	Novel	cyt	761	49	61.3	15	8	ADU97070	Novel	cyt	Adu97070	Novel	cyt
689	49	61.3	14	8	ADU97067	Novel	cyt	ADu97067	Novel	cyt	762	49	61.3	15	8	ADU97512	Novel	cyt	Adu97512	Novel	cyt
690	49	61.3	14	8	ADU95295	Novel	cyt	ADu95295	Novel	cyt	763	49	61.3	15	8	ADU97587	Novel	cyt	Adu97587	Novel	cyt
691	49	61.3	14	8	ADU95828	Novel	cyt	ADu95828	Novel	cyt	764	49	61.3	15	8	ADU97052	Novel	cyt	Adu97052	Novel	cyt
692	49	61.3	14	8	ADU96528	Novel	cyt	ADu96528	Novel	cyt	765	49	61.3	15	8	ADU95532	Novel	cyt	Adu95532	Novel	cyt
693	49	61.3	14	8	ADU95302	Novel	cyt	ADu95302	Novel	cyt	766	49	61.3	16	7	AD114977	Somatosta		Ad114977	Somatosta	
694	49	61.3	14	8	ADU95755	Novel	cyt	ADu95755	Novel	cyt	767	49	61.3	16	7	AD114995	Somatosta		Ad114995	Somatosta	
695	49	61.3	14	8	ADU96458	Novel	cyt	ADu96458	Novel	cyt	768	49	61.3	16	8	ADU95337	Novel	cyt	Adu95337	Novel	cyt
696	49	61.3	14	8	ADU96458	Novel	cyt	ADu96458	Novel	cyt	769	49	61.3	16	8	ADU96468	Novel	cyt	Adu96468	Novel	cyt
697	49	61.3	14	8	ADU96596	Novel	cyt	ADu96596	Novel	cyt	770	49	61.3	16	8	ADU95764	Novel	cyt	Adu95764	Novel	cyt
698	49	61.3	14	8	ADU97534	Novel	cyt	ADu97534	Novel	cyt	771	49	61.3	16	8	ADU96583	Novel	cyt	Adu96583	Novel	cyt
699	49	61.3	14	8	ADU96536	Novel	cyt	ADu96536	Novel	cyt	772	49	61.3	16	8	ADU96128	Novel	cyt	Adu96128	Novel	cyt
700	49	61.3	14	8	ADU96600	Novel	cyt	ADu96600	Novel	cyt	773	49	61.3	16	8	ADU95765	Novel	cyt	Adu95765	Novel	cyt
701	49	61.3	14	8	ADU97114	Novel	cyt	ADu97114	Novel	cyt	774	49	61.3	16	8	ADU96149	Novel	cyt	Adu96149	Novel	cyt
702	49	61.3	14	8	ADU97609	Novel	cyt	ADu97609	Novel	cyt	775	49	61.3	16	8	ADU96460	Novel	cyt	Adu96460	Novel	cyt
703	49	61.3	14	8	ADU95268	Novel	cyt	ADu95268	Novel	cyt	776	49	61.3	16	8	ADU96196	Novel	cyt	Adu96196	Novel	cyt
704	49	61.3	14	8	ADU96130	Novel	cyt	ADu96130	Novel	cyt	777	49	61.3	16	8	ADU97048	Novel	cyt	Adu97048	Novel	cyt
705	49	61.3	14	8	ADU96195	Novel	cyt	ADu96195	Novel	cyt	778	49	61.3	16	8	ADU95829	Novel	cyt	Adu95829	Novel	cyt
706	49	61.3	14	8	ADU97119	Novel	cyt	ADu97119	Novel	cyt	779	49	61.3	16	8	ADU97536	Novel	cyt	Adu97536	Novel	cyt
707	49	61.3	14	8	ADU97594	Novel	cyt	ADu97594	Novel	cyt	780	49	61.3	16	8	ADU95753	Novel	cyt	Adu95753	Novel	cyt
708	49	61.3	14	8	ADU95333	Novel	cyt	ADu95333	Novel	cyt	781	49	61.3	16	8	ADU97108	Novel	cyt	Adu97108	Novel	cyt
709	49	61.3	14	8	ADU96510	Novel	cyt	ADu96510	Novel	cyt	782	49	61.3	16	8	ADU97595	Novel	cyt	Adu97595	Novel	cyt
710	49	61.3	14	8	ADU97547	Novel	cyt	ADu97547	Novel	cyt	783	49	61.3	16	8	ADU97116	Novel	cyt	Adu97116	Novel	cyt
711	49	61.3	14	8	ADU96531	Novel	cyt	ADu96531	Novel	cyt	784	49	61.3	16	8	ADU97610	Novel	cyt	Adu97610	Novel	cyt
712	49	61.3	14	8	ADU97542	Novel	cyt	ADu97542	Novel	cyt	785	49	61.3	16	8	ADU95267	Novel	cyt	Adu95267	Novel	cyt
713	49	61.3	14	8	ADU97624	Novel	cyt	ADu97624	Novel	cyt	786	49	61.3	16	8	ADU97047	Novel	cyt	Adu97047	Novel	cyt
714	49	61.3	14	8	ADU95336	Novel	cyt	ADu95336	Novel	cyt	787	49	61.3	16	8	ADU97544	Novel	cyt	Adu97544	Novel	cyt
715	49	61.3	14	8	ADU95303	Novel	cyt	ADu95303	Novel	cyt	788	49	61.3	16	8	ADU96511	Novel	cyt	Adu96511	Novel	cyt
716	49	61.3	14	8	ADU95770	Novel	cyt	ADu95770	Novel	cyt	789	49	61.3	16	8	ADU97066	Novel	cyt	Adu97066	Novel	cyt
717	49	61.3	14	8	ADU95582	Novel	cyt	ADu95582	Novel	cyt	790	49	61.3	16	8	ADU97503	Novel	cyt	Adu97503	Novel	cyt
718	49	61.3	14	8	ADU95325	Novel	cyt	ADu95325	Novel	cyt	791	49	61.3	16	8	ADU97625	Novel	cyt	Adu97625	Novel	cyt
719	49	61.3	14	8	ADU96466	Novel	cyt	ADu96466	Novel	cyt	792	49	61.3	17	7	AD114978	Somatosta		Ad114978	Somatosta	
720	49	61.3	14	8	ADU97504	Novel	cyt	ADu97504	Novel	cyt	793	49	61.3	17	8	ADU95844	Novel	cyt	Adu95844	Novel	cyt
721	49	61.3	15	7	AD114994	Somatosta		Ad114994	Somatosta		794	49	61.3	17	8	ADU95752	Novel	cyt	Adu95752	Novel	cyt
722	49	61.3	15	7	AD114976	Somatosta		Ad114976	Somatosta		795	49	61.3	17	8	ADU96127	Novel	cyt	Adu96127	Novel	cyt
723	49	61.3	15	8	ADU95845	Novel	cyt	ADu95845	Novel	cyt	796	49	61.3	17	8	ADU96520	Novel	cyt	Adu96520	Novel	cyt
724	49	61.3	15	8	ADU96150	Novel	cyt	ADu96150	Novel	cyt	797	49	61.3	17	8	ADU96592	Novel	cyt	Adu96592	Novel	cyt
725	49	61.3	15	8	ADU97107	Novel	cyt	ADu97107	Novel	cyt	798	49	61.3	17	8	ADU95849	Novel	cyt	Adu95849	Novel	cyt
726	49	61.3	15	8	ADU95763	Novel	cyt	ADu95763	Novel	cyt	799	49	61.3	17	8	ADU96597	Novel	cyt	Adu96597	Novel	cyt
727	49	61.3	15	8	ADU96048	Novel	cyt	ADu96048	Novel	cyt	800	49	61.3	17	8	ADU95793	Novel	cyt	Adu95793	Novel	cyt
728	49	61.3	15	8	ADU96459	Novel	cyt	ADu96459	Novel	cyt	801	49	61.3	17	8	ADU96526	Novel	cyt	Adu96526	Novel	cyt
729	49	61.3	15	8	ADU95850	Novel	cyt	ADu95850	Novel	cyt	802	49	61.3	17	8	ADU96589	Novel	cyt	Adu96589	Novel	cyt
730	49	61.3	15	8	ADU96159	Novel	cyt	ADu96159	Novel	cyt	803	49	61.3	17	8	ADU96517	Novel	cyt	Adu96517	Novel	cyt
731	49	61.3	15	8	ADU96472	Novel	cyt	ADu96472	Novel	cyt	804	49	61.3	17	8	ADU97537	Novel	cyt	Adu97537	Novel	cyt
732	49	61.3	15	8	ADU95588	Novel	cyt	ADu95588	Novel	cyt	805	49	61.3	17	8	ADU96461	Novel	cyt	Adu96461	Novel	cyt
733	49	61.3	15	8	ADU95339	Novel	cyt	ADu95339	Novel	cyt	806	49	61.3	17	8	ADU97109	Novel	cyt	Adu97109	Novel	cyt
734	49	61.3	15	8	ADU96519	Novel	cyt	ADu96519	Novel	cyt	807	49	61.3	18	8	ADU96584	Novel	cyt	Adu96584	Novel	cyt
735	49	61.3	15	8	ADU95794	Novel	cyt	ADu95794	Novel	cyt	808	49	61.3	18	8	ADU96512	Novel	cyt	Adu96512	Novel	cyt
736	49	61.3	15	8	ADU95754	Novel	cyt	ADu95754	Novel	cyt	809	49	61.3	21	5	ABP68795	Marine sn		ABp68795	Marine sn	
737	49	61.3	15	8	ADU96580	Novel	cyt	ADu96580	Novel	cyt	810	49	61.3	21	5	ABP68792	Marine sn		ABp68792	Marine sn	
738	49	61.3	15	8	ADU97075	Novel	cyt	ADu97075	Novel	cyt	811	49	61.3	93	5	ABP68714	Marine sn		ABp68714	Marine sn	
739	49	61.3	15	8	ADU97084	Novel	cyt	ADu97084	Novel	cyt	812	49	61.3	7	1	AAPI0588	GH, gastr		AAp10588	GH, gastr	
740	49	61.3	15	8	ADU97507	Novel	cyt	ADu97507	Novel	cyt	813	48	60.0	7	2	AAR15361	Somatosta		AAr15361	Somatosta	
741	49	61.3	15	8	ADU97593	Novel	cyt	ADu97593	Novel	cyt	814	48	60.0	7	2	AAH04040	Heptapept		AAy04040	Heptapept	
742	49	61.3	15	8	ADU97623	Novel	cyt	ADu97623	Novel	cyt	815	48	60.0	7	2	ADH22048	Otreotid		Adh22048	Otreotid	
743	49	61.3	15	8	ADU95301	Novel	cyt	ADu95301	Novel	cyt	816	48	60.0	8	1	AAPI0585	GH, gastr		AAp10585	GH, gastr	
744	49	61.3	15	8	ADU95508	Novel	cyt	ADu95508	Novel	cyt	817	48	60.0	8	1	AAPI0589	GH, gastr		AAp10589	GH, gastr	
745	49	61.3	15	8	ADU97535	Novel	cyt	ADu97535	Novel	cyt	818	48	60.0	8	1	AAPI0589	GH, gastr		AAp10589	GH, gastr	
746	49	61.3	15	8	ADU96516	Novel	cyt	ADu96516	Novel	cyt	819	48	60.0	8	1	AAPI0589	GH, gastr		AAp10589	GH, gastr	
747	49	61.3	15	8	ADU97046	Novel	cyt	ADu97046	Novel	cyt	820	48	60.0	8	2	AAPI0589	GH, gastr		AAp10589	GH, gastr	
748	49	61.3	15	8	ADU97115	Novel	cyt	ADu97115	Novel	cyt	821	48	60.0	8	2	AAPI0589	GH, gastr		AAp10589	GH, gastr	
749	49	61.3	15	8	ADU97120	Novel	cyt	ADu97120	Novel	cyt	822	48	60.0	8	2	AAPI0589	GH, gastr		AAp10589	GH, gastr	
750	49																				

828	48	60.0	8	2	AAR85568	Aar85568	Somatosta	901	47	58.8	8	9	ADZ99624	Somatosta
829	48	60.0	8	2	AAW51862	AAW51862	Somatosta	902	46	57.5	8	1	AAPI0590	GH, Gastr
830	48	60.0	8	2	AAAY22032	AAAY22032	Somatosta	903	46	57.5	8	1	AAPI0592	GH, Gastr
831	48	60.0	8	2	RAY18217	Ray18217	Somatosta	904	46	57.5	8	2	AAR47605	Neuromedi
832	48	60.0	8	2	ADH35392	Adh35392	Human som	905	46	57.5	8	2	AAR91614	Chelator-
833	48	60.0	8	2	ADH67993	Adh67993	Somatosta	906	46	57.5	8	2	AAW33183	Mono-DTPA
834	48	60.0	8	2	ADK11145	Adk11145	Somatosta	907	46	57.5	8	2	AAW66233	Somatosta
835	48	60.0	8	2	ADK11267	Adk11267	Somatosta	908	46	57.5	8	2	AAW45985	Peptide #
836	48	60.0	8	3	AAAY77334	Aay77334	Synthetic	909	46	57.5	8	7	ADF61738	Somatosta
837	48	60.0	8	3	AAAB06234	Aab06234	Synthetic	910	46	57.5	8	7	ADF61741	Somatosta
838	48	60.0	8	3	RAY81006	Ray81006	Somatosta	911	46	57.5	8	8	ADJ87443	Somatosta
839	48	60.0	8	3	AAAB19022	Aab19022	Amino aci	912	46	57.5	8	8	ADU96403	Novel cys
840	48	60.0	8	4	AAU08278	Aau08278	Somastati	913	46	57.5	8	8	ADU96088	Novel cys
841	48	60.0	8	4	AAAB45662	Aab45662	Somatosta	914	46	57.5	8	8	ADU96085	Novel cys
842	48	60.0	8	4	AAAU08816	Aau08816	Somatosta	915	46	57.5	8	8	ADU97027	Novel cys
843	48	60.0	8	5	ABG73202	Abg73202	Somatosta	916	46	57.5	8	8	ADU95718	Novel cys
844	48	60.0	8	5	ABG73203	Abg73203	Somatosta	917	46	57.5	8	8	ADU95223	Novel cys
845	48	60.0	8	5	AAU76358	Aau76358	Synthetic	918	46	57.5	8	8	ADU96400	Novel cys
846	48	60.0	8	5	AAU76360	Aau76360	Synthetic	919	46	57.5	8	8	ADU97024	Novel cys
847	48	60.0	8	5	ADH68882	Adh68882	Synthetic	920	46	57.5	8	8	ADU97450	Novel cys
848	48	60.0	8	6	ADH68891	Adh68891	Synthetic	921	46	57.5	8	8	ADU95831	Novel cys
849	48	60.0	8	6	ABG71789	Abg71789	Somatosta	922	46	57.5	8	8	ADU97447	Novel cys
850	48	60.0	8	6	ABG99238	Abg99238	Somatosta	923	46	57.5	9	8	ADU97439	Novel cys
851	48	60.0	8	6	AAO26841	Aao26841	Somatosta	924	46	57.5	9	8	ADU96087	Novel cys
852	48	60.0	8	7	AD114938	Adi14938	Somatosta	925	46	57.5	9	8	ADU96404	Novel cys
853	48	60.0	8	8	ADR87510	Adr87510	Backbone	926	46	57.5	9	8	ADU97451	Novel cys
854	48	60.0	8	8	ADU07145	Adu07145	Basic for	927	46	57.5	9	8	ADU96388	Novel cys
855	48	60.0	8	8	ADU07146	Adu07146	Peptide u	928	46	57.5	9	8	ADU95717	Novel cys
856	48	60.0	8	9	ADZ99625	Adz99625	Somatosta	929	46	57.5	9	8	ADU95830	Novel cys
857	48	60.0	9	2	AAW45984	Aaw45984	Peptide #	930	46	57.5	9	8	ADU96073	Novel cys
858	48	60.0	9	3	AAAY76772	Aay76772	Somatosta	931	46	57.5	9	8	ADU96401	Novel cys
859	48	60.0	9	4	AAU08284	Aau08284	Assembly	932	46	57.5	9	8	ADU97028	Novel cys
860	48	60.0	9	5	ABG73217	Abg73217	Somatosta	933	46	57.5	9	8	ADU97448	Novel cys
861	48	60.0	9	5	ABG73216	Abg73216	Somatosta	934	46	57.5	9	8	ADU95705	Novel cys
862	48	60.0	9	5	ABG73215	Abg73215	Somatosta	935	46	57.5	9	8	ADU97016	Novel cys
863	48	60.0	9	5	ABG73214	Abg73214	Somatosta	936	46	57.5	9	8	ADU97025	Novel cys
864	48	60.0	9	5	ABG73218	Abg73218	Somatosta	937	46	57.5	9	8	ADU96084	Novel cys
865	48	60.0	9	5	ABG53362	Abg53362	Backbone	938	46	57.5	10	8	ADU05211	Cyclic so
866	48	60.0	9	6	ABG71793	Abg71793	Somatosta	939	46	57.5	10	8	ADU05265	Cyclic so
867	48	60.0	9	7	AD114939	Adi14939	Somatosta	940	46	57.5	10	8	ADU97017	Novel cys
868	48	60.0	9	7	AD114946	Adi14946	Somatosta	941	46	57.5	10	8	ADU95706	Novel cys
869	48	60.0	10	5	ABG73212	Abg73212	Somatosta	942	46	57.5	10	8	ADU96382	Novel cys
870	48	60.0	10	5	ABG73208	Abg73208	Somatosta	943	46	57.5	10	8	ADU97433	Novel cys
871	48	60.0	10	5	ABG73211	Abg73211	Somatosta	944	46	57.5	10	8	ADU96394	Novel cys
872	48	60.0	10	5	ABG73209	Abg73209	Somatosta	945	46	57.5	10	8	ADU96072	Novel cys
873	48	60.0	10	7	AD114940	Adi14940	Somatosta	946	46	57.5	10	8	ADU96074	Novel cys
874	48	60.0	11	3	AAAY77335	Aay77335	Synthetic	947	46	57.5	10	8	ADU97440	Novel cys
875	48	60.0	11	5	ABG73210	Abg73210	Somatosta	948	46	57.5	10	8	ADU96389	Novel cys
876	48	60.0	11	7	AD114941	Adi14941	Somatosta	949	46	57.5	10	8	ADU97438	Novel cys
877	48	60.0	12	7	AD114942	Adi14942	Somatosta	950	46	57.5	10	8	ADU96083	Novel cys
878	47.5	59.4	131	6	ABU97062	Abu97062	Recombina	951	46	57.5	10	8	ADU96387	Novel cys
879	47.5	59.4	260	6	ABU97146	Abu97146	Recombina	952	46	57.5	10	8	ADU95712	Novel cys
880	47	58.8	7	2	AAW48640	Aaw48640	Somatosta	953	46	57.5	10	8	ADU95704	Novel cys
881	47	58.8	7	8	ADU05225	Adu05225	Cyclic so	954	46	57.5	10	8	ADU95716	Novel cys
882	47	58.8	8	2	AAAR12866	Aar12866	Somatosta	955	46	57.5	10	8	ADU96079	Novel cys
883	47	58.8	8	2	AAAR40818	Aar40818	Octapepti	956	46	57.5	10	8	ADU97015	Novel cys
884	47	58.8	8	2	AAR99319	Aar99319	Cyclic so	957	46	57.5	10	8	ADU97010	Novel cys
885	47	58.8	8	2	AAW18455	Aaw18455	Somatosta	958	46	57.5	11	8	ADU96390	Novel cys
886	47	58.8	8	2	AAW66228	Aaw66228	Somatosta	959	46	57.5	11	8	ADU97441	Novel cys
887	47	58.8	8	2	AAAY22031	Aay22031	Somatosta	960	46	57.5	11	8	ADU96078	Novel cys
888	47	58.8	8	2	AAAY18285	Aay18285	Somatosta	961	46	57.5	11	8	ADU95715	Novel cys
889	47	58.8	8	2	ADH35391	Adh35391	Human som	962	46	57.5	11	8	ADU97018	Novel cys
890	47	58.8	8	2	ADH67992	Adh67992	Somatosta	963	46	57.5	11	8	ADU95711	Novel cys
891	47	58.8	8	2	ADK11294	Adk11294	Somatosta	964	46	57.5	11	8	ADU96082	Novel cys
892	47	58.8	8	2	ADK11144	Adk11144	Somatosta	965	46	57.5	11	8	ADU96395	Novel cys
893	47	58.8	8	3	AAAB06233	Aab06233	Somatosta	966	46	57.5	11	8	ADU97011	Novel cys
894	47	58.8	8	3	AAAY81002	Aay81002	Somatosta	967	46	57.5	11	8	ADU96071	Novel cys
895	47	58.8	8	3	AAAY81005	Aay81005	Somatosta	968	46	57.5	11	8	ADU95703	Novel cys
896	47	58.8	8	4	AAAB74613	Aab74613	Somatosta	969	46	57.5	11	8	ADU96383	Novel cys
897	47	58.8	8	4	AAU08921	Aau08921	Somatosta	970	46	57.5	11	8	ADU97434	Novel cys
898	47	58.8	8	6	ABG99237	Abg99237	Somatosta	971	46	57.5	12	7	ADZ86616	Cytotoxic
899	47	58.8	8	6	AAO26840	Aao26840	Somatosta	972	46	57.5	12	8	ADU96384	Novel cys
900	47	58.8	8	8	ADU05269	Adu05269	Cyclic so	973	46	57.5	12	8	ADU97446	Novel cys

974 46 57.5 12 8 ADU96399 Novel cyt
 975 46 57.5 12 8 ADU97627 Novel cyt
 976 46 57.5 12 8 ADU95702 Novel cyt
 977 46 57.5 12 8 ADU96089 Novel cyt
 978 46 57.5 12 8 ADU96391 Novel cyt
 979 46 57.5 12 8 ADU97023 Novel cyt
 980 46 57.5 12 8 ADU97435 Novel cyt
 981 46 57.5 12 8 ADU97597 Novel cyt
 982 46 57.5 12 8 ADU96077 Novel cyt
 983 46 57.5 12 8 ADU96396 Novel cyt
 984 46 57.5 12 8 ADU97442 Novel cyt
 985 46 57.5 12 8 ADU97012 Novel cyt
 986 46 57.5 12 8 ADU97612 Novel cyt
 987 46 57.5 12 8 ADU95714 Novel cyt
 988 46 57.5 12 8 ADU97019 Novel cyt
 989 46 57.5 12 8 ADU95710 Novel cyt
 990 46 57.5 12 8 ADU95832 Novel cyt
 991 46 57.5 12 8 ADU96070 Novel cyt
 992 46 57.5 12 8 ADU96081 Novel cyt
 993 46 57.5 13 8 ADU96069 Novel cyt
 994 46 57.5 13 8 ADU95719 Novel cyt
 995 46 57.5 13 8 ADU95701 Novel cyt
 996 46 57.5 13 8 ADU97626 Novel cyt
 997 46 57.5 13 8 ADU96397 Novel cyt
 998 46 57.5 13 8 ADU96402 Novel cyt
 999 46 57.5 13 8 ADU96086 Novel cyt
 1000 46 57.5 13 8 ADU96080 Novel cyt

ALIGNMENTS

RESULT 1
 ID AD874379 standard; peptide; 11 AA.
 XX
 AC AD874379;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Somatostatin analogue.
 XX
 KW Somatostatin analogue; cytostatic; gene therapy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..4 /note= "D-form residues"
 FT Disulfide-bond 5..10
 FT Misc-difference 7 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide or alcohol"
 FT
 PN WO2004081031-A2.
 XX
 XX 23-SEP-2004.
 XX
 PF 10-MAR-2004; 2004WO-US007143.
 XX
 PF 10-MAR-2003; 2003US-0452928P.
 XX
 XX (BIOG-) BIOGEN IDEC INC.
 XX
 PI Braslawsky GR, Chinn P;
 XX
 XX WPI; 2004-668933/65.
 XX

XX A composition comprising a somatostatin analog useful for thiol-specific
 FT drug attachment to somatostatin and other targeting peptides, or for
 PT diagnosing or treating somatostatin receptor-associated disorders, e.g.
 PT cancer.

XX Claim 4; SEQ ID NO 7; 43pp; English.
 PS
 XX
 CC The present sequence is that of a synthetic somatostatin analogue. The
 CC peptide can be used as component B in a claimed composition comprising a
 CC somatostatin analogue of formula (A-B), where A is Cys, or a peptide
 CC chain comprising one or more Cys residues, which is suitable for binding
 CC to a drug or chelator via a thiol linkage, and B is a naturally occurring
 CC or synthetic somatostatin peptide, or its fragment, that binds to the
 CC somatostatin receptor (SSTR). The drug or chelator is bound to the Cys
 CC residue(s) of component A by a thiol linkage. The drug is a therapeutic
 CC drug such as a radioisotope, a cytotoxic, an immunostimulant, an
 CC antiangiogenic agent, a therapeutic gene, or a chemotherapeutic agent.
 CC The somatostatin analogue preferably binds to SSTR-positive cells,
 CC especially human cancer cells. A claimed method for detecting SSTR-
 CC positive cells comprises administering the somatostatin analogue in which
 CC a detectable label is bound to the Cys residue(s) of component A, and
 CC detecting the label. A claimed method for treating an SSTR-associated
 CC disorder comprises administering a somatostatin analogue in which a
 CC therapeutic agent is bound to the Cys residue(s) of component A. The SSTR
 CC -associated disorder is especially cancer. Thiol-mediated drug attachment
 CC can also be used with other targeting peptides.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 80; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0043;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCPWKTC T 11
 |||||
 Db 1 YYCYCPWKTC T 11

RESULT 2

AAW48645
 ID AAW48645 standard; peptide; 11 AA.
 XX
 AC AAW48645;
 XX
 DT 04-AUG-1998 (first entry)
 XX
 DE Somatostatin peptide analog WOC-4.
 XX
 KW Somatostatin; acromegaly; radiolocalisation; blood-brain barrier; cancer;
 KW halogen.
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Disulfide-bond 5..10
 FT Misc-difference 7 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT
 PN WO9639161-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 03-JUN-1996; 96WO-US008437.
 XX
 XX 05-JUN-1995; 95US-00462223.
 PR
 XX (TULA) TULANE EDUCATIONAL FUND.
 PA (OHIS) UNIV OHIO STATE RES FOUND.
 PA (LOU) UNIV LOUISIANA STATE MEDICAL CENT FOUND.
 PA (CHIL-) CHILDRENS HOSPITAL INC.

XX FI Coy DH, Woltering EA, Odoriso MS, Odoriso TM, Murphy WA;
 XX DR WPI; 1997-042842/04.
 XX PI Multi-tyrosinated somatostatin analogues - useful for diagnosis and
 XX PT treatment of diseases related to altered somatostatin receptor
 XX FT expression.
 XX FS Claim 7; Page 60; 63pp; English.
 XX PS The invention provides for conventional somatostatin analogues (AAW48638-
 XX CC W48640 and AAW48664) and multi-tyrosinated analogues (AAW48641-W48645)
 XX CC such as the present one. The multi-tyrosinated somatostatin analogues
 XX CC bind to somatostatin receptors with practically the same affinity as
 XX CC native somatostatin. The somatostatin analogues are claimed to be useful
 XX CC for treating disease associated with increased production of factors
 XX CC which can be regulated by somatostatin, e.g. acromegaly. Also when
 XX CC radioactively labelled, the analogues are claimed to be useful for
 XX CC diagnosing cancer in vitro or in situ where aberrant expression of
 XX CC somatostatin receptors is involved. When halogenated, these analogues are
 XX CC found to bind somatostatin receptors with such high affinity that binding
 XX CC is nearly irreversible under physiological conditions. Therefore, by
 XX CC using radioactive halogenated analogues, the invention claims for
 XX CC improved sensitivity of radiolocalisation of the receptors. Multi-
 XX CC tyrosinated analogues have increased half-lives in vivo relative to
 XX CC conventional somatostatin analogues, are resistant to enzymatic
 XX CC degradation and have increased blood-brain barrier penetration
 XX CC

Sequence 11 AA;
 Query Match 86.2%; Score 69; DB 2; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.086;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYCYCFWKTCCT 11
 |||||
 Db 1 YYCYCFWKTCCT 11
 |||||

RESULT 3
 ADM35520
 ID ADM35520 standard; peptide; 11 AA.
 XX AC ADM35520;
 XX DT 03-JUN-2004 (first entry)
 XX DE Somatostatin analogue, Woc-4D.
 XX KW retinopathy of prematurity; neonatal; somatostatin; Woc-4D; octreotide;
 XX KW lanreotide; vapreotide; Woc-2A; Woc-2B; Woc-3A; Woc-4; Woc-4D;
 XX KW Woc-5; Woc-8; octreotide acetate; cyclic.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 1. 4
 XX FT /note= "D form residues"
 XX FT Disulfide-bond 5..10
 XX FT /note= Forms a cyclic region of the peptide
 XX FT Misc-difference 7
 XX FT /note= "D form residue"
 XX FT Modified-site 11
 XX FT /note= "C-terminal amide"
 XX US2003207811-A1.
 XX 06-NOV-2003.
 XX 03-MAY-2002; 2002US-00138554.
 XX 03-MAY-2002; 2002US-00138554.

XX PA (SCHR/) SCHRIER B K.
 XX PA (HIGG/) HIGGINS R D.
 XX PI Schrier BK, Higgins RD;
 XX DR WPI; 2004-069300/07.
 XX FT Treatment or prevention of retinopathy of prematurity in neonatal mammal,
 XX FT comprises administering somatostatin analog having composition that
 XX FT provides therapeutic benefit to mammal.
 XX PS Example; Page 5; 12pp; English.
 XX CC The invention relates to a method of treating retinopathy of prematurity
 XX CC in a neonatal mammal. The condition is treated or prevented by
 XX CC administering to the mammal a somatostatin analogue. Also described is a
 XX CC pharmaceutical composition Woc-4D and carrier for treating or preventing
 XX CC retinopathy of prematurity in neonatal mammal. The somatostatin analogue
 XX CC is octreotide, Woc4D, somatostatin analogue having serum half-life of
 XX CC octreotide, or somatostatin analogue having serum half-life more than that
 XX CC of octreotide, or somatostatin analogue having serum half-life of Woc-4D.
 XX CC It is selected from octreotide, lanreotide, vapreotide, Woc-2A, Woc-2B,
 XX CC Woc-3A, Woc-3B, Woc-4, Woc-4D, Woc-5, or Woc-8. The invention provides a
 XX CC therapeutic benefit without affecting growth of the neonates. The present
 XX CC sequence represents somatostatin analogue, Woc-4D.
 XX SQ Sequence 11 AA;
 Query Match 86.2%; Score 69; DB 8; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.086;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYCYCFWKTCCT 11
 |||||
 Db 1 YYCYCFWKTCCT 11
 |||||

RESULT 4
 ADM95422
 ID ADM95422 standard; peptide; 11 AA.
 XX AC ADM95422;
 XX DT 07-APR-2005 (first entry)
 XX DE Amino acid sequence of WOC4D.
 XX KW cytostatic; dispersed phase formulation; microspheres;
 XX KW sustained drug release; controlled drug release;
 XX KW testosterone dependent disorder; prostate disease; prostate cancer;
 XX KW octreotide drug; WOC4D.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 1
 XX FT /note= "D-form residue with H attached"
 XX FT Misc-difference 2
 XX FT /note= "D-form residue"
 XX FT Misc-difference 3
 XX FT /note= "D-form residue"
 XX FT Misc-difference 4
 XX FT /note= "D-form residue"
 XX FT Disulfide-bond 5..10
 XX FT Misc-difference 7
 XX FT /note= "D-form residue"
 XX FT Modified-site 11
 XX FT /note= "NH2 attached"
 XX WO2005007122-A2.
 XX 27-JAN-2005.

XX 19-JUL-2004; 2004WO-US023324.
 XX PF
 XX PI
 XX PR 18-JUL-2003; 2003US-0488573P.
 XX PA (OAKW-) OAKWOOD LAB LLC.
 XX PI Thanoo BC, Murtagh J, Johns G;
 XX PR WPI; 2005-122673/13.
 XX DR
 XX XX
 XX PF Dispersed phase formulation useful for providing sustained release of
 XX PT drug suppressing gonadotropin releasing hormone comprises nucleophilic
 XX PT substance catalyzing ester bond cleavage and causing molecular weight
 XX PT reduction of polymer.
 XX XX
 XX PS Example; Page 63; 114pp; English.
 XX XX
 XX CC The specification describes a dispersed phase formulation which comprises
 XX CC a biocompatible and biodegradable polymer, at least one nucleophilic
 XX CC substance capable of catalyzing ester bond cleavage and causing molecular
 XX CC weight reduction of the polymer, and acid additive in an amount such that
 XX CC the polymer is less susceptible to molecular reduction as compared to the
 XX CC formulation without the acid additive. The formulation of the invention
 XX CC is useful for preparing microspheres providing a sustained or controlled
 XX CC release of drug. This is useful for suppressing gonadotropin releasing
 XX CC hormone in the treatment of testosterone dependent disorder, benign
 XX CC prostate hypertrophy or prostate cancer. The present sequence represents
 XX CC WO4d (a somatostatin analog), a peptide which was contained in
 XX CC microspheres of the invention.
 XX SQ Sequence 11 AA;
 XX
 Query Match 86.2%; Score 69; DB 9; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.086;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YYCYCFWKTCCT 11
 DB 1 YYCYCFWKTCCT 11
 RESULT 5
 ADS74377
 ID ADS74377 standard; peptide; 11 AA.
 XX AC ADS74377;
 XX DT 16-DEC-2004 (first entry)
 XX DE Somatostatin analogue.
 XX KW Somatostatin analogue; cytostatic; gene therapy.
 XX OS Synthetic.
 XX OS Key Location/Qualifiers
 XX FH Misc-difference 1..4 /note= "D-form residues"
 XX FT Disulfide-bond 5..10
 XX FT Misc-difference 7 /note= "D-form residue"
 XX FT Modified-site 11 /note= "C-terminal amide or alcohol"
 XX FT
 XX PN WO2004081031-A2.
 XX PD 23-SEP-2004.
 XX PF 10-MAR-2004; 2004WO-US007143.
 XX PR 10-MAR-2003; 2003US-0452928P.
 XX XX

(BIOG-) BIOGEN IDEC INC.
 Bratislasky GR, Chinn P;
 WPI; 2004-668933/65.
 A composition comprising a somatostatin analog useful for thiol-specific
 drug attachment to somatostatin and other targeting peptides, or for
 diagnosing or treating somatostatin receptor-associated disorders, e.g.
 cancer.
 Claim 4; SEQ ID NO 5; 43pp; English.
 The present sequence is that of a synthetic somatostatin analogue. The
 peptide can be used as component B in a claimed composition comprising a
 somatostatin analogue of formula (A-B), where A is Cys, or a peptide
 chain comprising one or more Cys residues, which is suitable for binding
 to a drug or chelator via a thiol linkage, and B is a naturally occurring
 or synthetic somatostatin peptide, or its fragment, that binds to the
 somatostatin receptor (SSTR). The drug or chelator is bound to the Cys
 residue(s) of component A by a thiol linkage. The drug is a therapeutic
 drug such as a radioisotope, a cytotoxin, an immunostimulant, an
 antiangiogenic agent, a therapeutic gene, or a chemotherapeutic agent.
 The somatostatin analogue preferably binds to SSTR-positive cells,
 especially human cancer cells. A claimed method for detecting SSTR-
 positive cells comprises administering the somatostatin analogue in which
 a detectable label is bound to the Cys residue(s) of component A, and
 detecting the label. A claimed method for treating an SSTR-associated
 disorder comprises administering a somatostatin analogue in which a
 therapeutic agent is bound to the Cys residue(s) of component A. The SSTR
 -associated disorder is especially cancer. Thiol-mediated drug attachment
 can also be used with other targeting peptides.
 Sequence 11 AA;
 Query Match 78.1%; Score 62.5; DB 8; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.5;
 Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 2 YC-YCFWKTCCT 11
 DB 1 YCYCFWKTCCT 11
 RESULT 6
 ADS74378
 ID ADS74378 standard; peptide; 11 AA.
 XX AC ADS74378;
 XX DT 16-DEC-2004 (first entry)
 XX DE Somatostatin analogue.
 XX KW Somatostatin analogue; cytostatic; gene therapy.
 XX OS Synthetic.
 XX OS Key Location/Qualifiers
 XX FH Misc-difference 1..4 /note= "D-form residues"
 XX FT Disulfide-bond 5..10
 XX FT Misc-difference 7 /note= "D-form residue"
 XX FT Modified-site 11 /note= "C-terminal amide or alcohol"
 XX FT
 XX PN WO2004081031-A2.
 XX PD 23-SEP-2004.
 XX PF 10-MAR-2004; 2004WO-US007143.
 XX XX

PR 10-MAR-2003; 2003US-0452928P.
 XX (BIOG-) BIOGEN IDEC INC.
 FA
 XX Braslawsky GR, Chinn P;
 XX WPI; 2004-668933/65.
 DR
 XX A composition comprising a somatostatin analog useful for thiol-specific
 PT drug attachment to somatostatin and other targeting peptides, or for
 PT diagnosing or treating somatostatin receptor-associated disorders, e.g.
 PT cancer.
 XX
 XX Claim 4; SEQ ID NO 6; 43pp; English.
 PS
 XX The present sequence is that of a synthetic somatostatin analogue. The
 CC peptide can be used as component B in a claimed composition comprising a
 CC somatostatin analogue of formula (A-B), where A is Cys, or a peptide
 CC chain comprising one or more Cys residues, which is suitable for binding
 CC to a drug or chelator via a thiol linkage, and B is a naturally occurring
 CC or synthetic somatostatin peptide, or its fragment, that binds to the
 CC somatostatin receptor (SSTR). The drug or chelator is bound to the Cys
 CC residue(s) of component A by a thiol linkage. The drug is a therapeutic
 CC drug such as a radioisotope, a cytotoxin, an immunostimulant, an
 CC antiangiogenic agent, a therapeutic gene, or a chemotherapeutic agent.
 CC The somatostatin analogue preferably binds to SSTR-positive cells,
 CC especially human cancer cells. A claimed method for detecting SSTR-
 CC positive cells comprises administering the somatostatin analogue in which
 CC a detectable label is bound to the Cys residue(s) of component A, and
 CC detecting the label. A claimed method for treating an SSTR-associated
 CC disorder comprises administering a somatostatin analogue in which a
 CC therapeutic agent is bound to the Cys residue(s) of component A. The SSTR
 CC -associated disorder is especially cancer. Thiol-mediated drug attachment
 CC can also be used with other targeting peptides.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 77.5%; Score 62; DB 8; Length 11;
 Best Local Similarity 90.0%; Pred. NO. 0.58;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YCYCFWTKCT 11
 Db 2 YYCFWTKCT 11
 |:|||||
 |:|||||
 RESULT 7
 ADC68595
 ID ADC68595 standard; peptide; 13 AA.
 XX
 AC ADC68595;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Thiol-containing peptide linker #5.
 XX
 KW Protein conjugate; thiol-reactive diagnostic;
 KW thiol-reactive therapeutic agent; disulfide-containing targeting protein;
 KW thiol-containing peptide linker.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "D-form residue"
 FT Modified-site 5
 FT /note= "H2NCSNHCHC(O)-thiemicarbazonylglyoxy1"
 FT Misc-difference 6 /note= "D-form residue"
 FT /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 13
 FT /note= "ol (not defined)"
 FT

XX US2003092198-A1.
 XX 15-MAY-2003.
 XX 13-OCT-1999; 99US-00417109.
 XX 13-OCT-1999; 99US-00417109.
 XX (MCBR/) MCBRIDE W J.
 PA (GRIF/) GRIFFITHS G L.
 PA
 XX Mcbride WJ, Griffiths GL;
 PI
 XX WPI; 2003-874590/81.
 DR
 XX Production of diagnostic or therapeutic conjugate of protein containing
 PT disulfide bonds, by contacting protein, polypeptide or peptide with a
 PT thiol-reactive agent to form therapeutic conjugate without cleavage of
 PT disulfide bond.
 XX
 XX Example 10; Page 9; 11pp; English.
 PS
 XX The invention describes a method of producing a diagnostic or therapeutic
 CC conjugate of a protein, polypeptide or peptide containing one disulfide
 CC bond(s). The method involves contacting protein, polypeptide or peptide
 CC with a thiol-reactive diagnostic or therapeutic agent, either performed
 CC or generated in situ to form a stable diagnostic therapeutic conjugate of
 CC protein, polypeptide or peptide without substantial cleavage of disulfide
 CC bond(s). The polypeptides are useful for introducing thiol-containing
 CC linkers into disease targeting agents e.g. polypeptide and peptides. The
 CC method enables the formation of conjugates of disulfide-containing
 CC targeting proteins, polypeptides, peptides e.g. divalent antibody
 CC fragments and with thiol-containing ligands without cleaving the
 CC disulfide bonds of the targeting proteins. This is the amino acid
 CC sequence of a thiol-containing peptide linker that can be conjugated to a
 CC disulfide-containing protein.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 77.5%; Score 62; DB 7; Length 13;
 Best Local Similarity 88.9%; Pred. NO. 0.66;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CYCFWTKCT 11
 Db 5 CFCFWTKCT 13
 |:|||||
 |:|||||
 RESULT 8
 AAO26828
 ID AAO26828 standard; peptide; 8 AA.
 XX
 AC AAO26828;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Somatostatin agonist compound #11.
 XX
 KW Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipaeamic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4 /note= "Modified by N-Methyl. D-form residue"
 FT Modified-site 8 /note= "C-terminal amide"
 FT
 XX WO200281499-A2.
 PN

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XX PD 17-OCT-2002.
XX
XX PF 08-APR-2002; 2002WO-US010882.
XX
XX PR 09-APR-2001; 2001US-0282526P.
XX
XX PA (TULA ) TULANE EDUCATIONAL FUND.
XX
XX PI Coy DH, Rajeswaran WG;
XX
XX DR WPI; 2003-247842/24.
XX
XX PT Novel somatostatin agonist, useful for treating Cushing's syndrome,
XX hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
XX Zollinger-Ellison syndrome, characterized by alkylation of amide
XX nitrogen.
XX
XX PS Claim 19; Page 31; 43pp; English.
XX
XX CC The invention relates to novel somatostatin agonists, typically
XX characterised by alkylation of the amide nitrogen, or its
XX pharmaceutically acceptable salt. The novel somatostatin agonists are
XX useful for binding one or more of human somatostatin subtype receptors -
XX 1.-2.-3.-4 and -5, and for eliciting a somatostatin agonist effect, by
XX administering a somatostatin agonist or a pharmaceutically acceptable
XX salt of it to a recipient in need of it. The somatostatin agonists are
XX useful for treating a disease or condition in a human or other animal,
XX including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
XX Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
XX Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
XX immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
XX syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
XX cancer, peoriasis, hypotension, panic attacks, scleroderma, small bowel
XX obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
XX disease, polycystic ovary disease, upper gastrointestinal bleeding,
XX pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
XX cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
XX inhibiting the accelerated growth of a solid tumour and decreasing body
XX weight, treating insulin resistance, Syndrome X, prolonging the survival
XX of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
XX hyperprolactinaemia and prolactinomas. This sequence represents a peptide
XX of a somatostatin agonist compound of the invention
XX
XX SQ Sequence 8 AA;
XX
XX Query Match 71.2%; Score 57; DB 6; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 YCFWKTKCT 11
XX | | | | |
XX 1 YCFWKTKCT 8
XX
XX Db
XX
XX RESULT 9
XX AAO26832
XX ID AAO26832 standard; peptide; 8 AA.
XX
XX AC AAO26832;
XX
XX DT 27-AUG-2003 (first entry)
XX
XX DE Somatostatin agonist compound #15.
XX
XX KW Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
XX hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
XX antilipaeic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
XX hyperparathyroidism; cancer.
XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers

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FT Misc-difference 4 /note= "D-form residue"
FT Modified-site 8 /note= "Modified by N-Methyl. C-terminal amide"
FT
XX WO200281499-A2.
XX
XX PN 17-OCT-2002.
XX
XX PD
XX
XX PF 08-APR-2002; 2002WO-US010882.
XX
XX PR 09-APR-2001; 2001US-0282526P.
XX
XX PA (TULA ) TULANE EDUCATIONAL FUND.
XX
XX PI Coy DH, Rajeswaran WG;
XX
XX DR WPI; 2003-247842/24.
XX
XX PT Novel somatostatin agonist, useful for treating Cushing's syndrome,
XX hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
XX Zollinger-Ellison syndrome, characterized by alkylation of amide
XX nitrogen.
XX
XX PS Claim 23; Page 32; 43pp; English.
XX
XX CC The invention relates to novel somatostatin agonists, typically
XX characterised by alkylation of the amide nitrogen, or its
XX pharmaceutically acceptable salt. The novel somatostatin agonists are
XX useful for binding one or more of human somatostatin subtype receptors -
XX 1.-2.-3.-4 and -5, and for eliciting a somatostatin agonist effect, by
XX administering a somatostatin agonist or a pharmaceutically acceptable
XX salt of it to a recipient in need of it. The somatostatin agonists are
XX useful for treating a disease or condition in a human or other animal,
XX including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
XX Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
XX Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
XX immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
XX syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
XX cancer, peoriasis, hypotension, panic attacks, scleroderma, small bowel
XX obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
XX disease, polycystic ovary disease, upper gastrointestinal bleeding,
XX pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
XX cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
XX inhibiting the accelerated growth of a solid tumour and decreasing body
XX weight, treating insulin resistance, Syndrome X, prolonging the survival
XX of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
XX hyperprolactinaemia and prolactinomas. This sequence represents a peptide
XX of a somatostatin agonist compound of the invention
XX
XX SQ Sequence 8 AA;
XX
XX Query Match 71.2%; Score 57; DB 6; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 YCFWKTKCT 11
XX | | | | |
XX 1 YCFWKTKCT 8
XX
XX Db
XX
XX RESULT 10
XX AAO26830
XX ID AAO26830 standard; peptide; 8 AA.
XX
XX AC AAO26830;
XX
XX XX 27-AUG-2003 (first entry)
XX
XX DT 27-AUG-2003 (first entry)
XX
XX DE Somatostatin agonist compound #13.
XX
XX KW Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
XX hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;

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antilipaemic; somatostatin agonist; Cushing's syndrome; gonadotropinoma; hyperparathyroidism; cancer.

Unidentified.

Key Location/Qualifiers
 Misc-difference 4 /note= "D-form residue"
 Modified-site 6 /note= "Modified by N-Methyl"
 Modified-site 8 /note= "C-terminal amide"

WO200281499-A2.
 17-OCT-2002.
 08-APR-2002; 2002WO-US010882.
 09-APR-2001; 2001US-0282526P.
 (TULA) TULANE EDUCATIONAL FUND.
 Coy DH, Rajeswaran WG;
 WPI; 2003-247842/24.

Novel somatostatin agonist, useful for treating Cushing's syndrome, hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and Zollinger-Ellison syndrome, characterized by alkylation of amide nitrogen.

Claim 21; Page 32; 43pp; English.

The invention relates to novel somatostatin agonists, typically characterised by alkylation of the amide nitrogen, or its pharmaceutically acceptable salt. The novel somatostatin agonists are useful for binding one or more of human somatostatin subtype receptors - 1,2,3,4 and -5, and for eliciting a somatostatin agonist effect, by administering a somatostatin agonist or a pharmaceutically acceptable salt of it to a recipient in need of it. The somatostatin agonists are useful for treating a disease or condition in a human or other animal, including Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma, immunodeficiency syndrome (AIDS) and other conditions, irritable bowel syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid cancer, psoriasis, hypotension, panic attacks, scleroderma, small bowel obstruction, gastrosophageal reflux, duodenogastric reflux, Grave's disease, polycystic ovary disease, upper gastrointestinal bleeding, cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma, inhibiting the accelerated growth of a solid tumour and decreasing body weight, treating insulin resistance, Syndrome X, prolonging the survival of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia, hyperprolactinaemia and prolactinomas. This sequence represents a peptide of a somatostatin agonist compound of the invention

Sequence 8 AA;
 Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
 DB 1 YCFWKTCCT 8

RESULT 11
 AAO26825
 ID AAO26825 standard; peptide; 8 AA.
 XX

AAO26825;
 27-AUG-2003 (first entry)
 Somatostatin agonist compound #8.

Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic; hypertensive; dermatological; antithyroid; immunomodulator; vasotropic; antilipaemic; somatostatin agonist; Cushing's syndrome; gonadotropinoma; hyperparathyroidism; cancer.

Unidentified.

Key Location/Qualifiers
 Modified-site 1 /note= "Modified by N-Methyl"
 Misc-difference 4 /note= "D-form residue"
 Modified-site 8 /note= "C-terminal amide"

WO200281499-A2.
 17-OCT-2002.
 08-APR-2002; 2002WO-US010882.
 09-APR-2001; 2001US-0282526P.
 (TULA) TULANE EDUCATIONAL FUND.
 Coy DH, Rajeswaran WG;
 WPI; 2003-247842/24.

Novel somatostatin agonist, useful for treating Cushing's syndrome, hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and Zollinger-Ellison syndrome, characterized by alkylation of amide nitrogen.

Claim 16; Page 31; 43pp; English.

The invention relates to novel somatostatin agonists, typically characterised by alkylation of the amide nitrogen, or its pharmaceutically acceptable salt. The novel somatostatin agonists are useful for binding one or more of human somatostatin subtype receptors - 1,2,3,4 and -5, and for eliciting a somatostatin agonist effect, by administering a somatostatin agonist or a pharmaceutically acceptable salt of it to a recipient in need of it. The somatostatin agonists are useful for treating a disease or condition in a human or other animal, including Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma, immunodeficiency syndrome (AIDS) and other conditions, irritable bowel syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid cancer, psoriasis, hypotension, panic attacks, scleroderma, small bowel obstruction, gastrosophageal reflux, duodenogastric reflux, Grave's disease, polycystic ovary disease, upper gastrointestinal bleeding, cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma, inhibiting the accelerated growth of a solid tumour and decreasing body weight, treating insulin resistance, Syndrome X, prolonging the survival of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia, hyperprolactinaemia and prolactinomas. This sequence represents a peptide of a somatostatin agonist compound of the invention

Sequence 8 AA;
 Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11

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Db          1 YCFWKTC T 8
|||||
RESULT 12
AAO26827
ID AAO26827 standard; peptide; 8 AA.
XX
AC AAO26827;
XX
DT 27-AUG-2003 (first entry)
XX
DE Somatostatin agonist compound #10.
XX
KW Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
XX hyperemetic; dermatological; antithyroid; immunomodulator; vasotropic;
XX antilipaemic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
XX hyperparathyroidism; cancer.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 3 /note= "Modified by N-Methyl"
FT Misc-difference 4 /note= "D-form residue"
FT Modified-site 8 /note= "C-terminal amide"
FT
XX WO200281499-A2.
XX
XX 17-OCT-2002.
XX
XX 08-APR-2002; 2002WO-US010882.
XX
XX 09-APR-2001; 2001US-0282526P.
XX
XX (TULA ) TULANE EDUCATIONAL FUND.
XX
XX Coy DH, Rajeswaran WG;
XX WPI; 2003-247842/24.
XX
XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
XX hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
XX Zollinger-Ellison syndrome, characterized by alkylation of amide
XX nitrogen.
XX
XX Claim 18; Page 31; 43pp; English.
XX
XX The invention relates to novel somatostatin agonists, typically
XX characterised by alkylation of the amide nitrogen, or its
XX pharmaceutically acceptable salt. The novel somatostatin agonists are
XX useful for binding one or more of human somatostatin subtype receptors -
XX 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
XX administering a somatostatin agonist or a pharmaceutically acceptable
XX salt of it to a recipient in need of it. The somatostatin agonists are
XX useful for treating a disease or condition in a human or other animal,
XX including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
XX Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
XX Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
XX immunodeficiency syndrome (AIDS) and other conditions. Irritable bowel
XX syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
XX cancer, peptasia, hypotension, panic attacks, scleroderma, small bowel
XX obstruction, gastrosophageal reflux, duodenogastric reflux, Grave's
XX disease, polycystic ovary disease, upper gastrointestinal bleeding,
XX pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
XX cachexia, acromegaly, tetanosis, hepatoma, lung cancer, melanoma,
XX inhibiting the accelerated growth of a solid tumour and decreasing body
XX weight, treating insulin resistance, Syndrome X, prolonging the survival
XX of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
XX hyperprolactinaemia and prolactinomas. This sequence represents a peptide
XX of a somatostatin agonist compound of the invention

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XX SQ Sequence 8 AA;
Query Match 71.2%; Score 57; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 YCFWKTC T 11
Db 1 YCFWKTC T 8
RESULT 13
AAO26826
ID AAO26826 standard; peptide; 8 AA.
XX
AC AAO26826;
XX
DT 27-AUG-2003 (first entry)
XX
DE Somatostatin agonist compound #9.
XX
KW Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
XX hyperemetic; dermatological; antithyroid; immunomodulator; vasotropic;
XX antilipaemic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
XX hyperparathyroidism; cancer.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 2 /note= "Modified by N-Methyl"
FT Misc-difference 4 /note= "D-form residue"
FT Modified-site 8 /note= "C-terminal amide"
FT
XX WO200281499-A2.
XX
XX 17-OCT-2002.
XX
XX 08-APR-2002; 2002WO-US010882.
XX
XX 09-APR-2001; 2001US-0282526P.
XX
XX (TULA ) TULANE EDUCATIONAL FUND.
XX
XX Coy DH, Rajeswaran WG;
XX WPI; 2003-247842/24.
XX
XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
XX hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
XX Zollinger-Ellison syndrome, characterized by alkylation of amide
XX nitrogen.
XX
XX Claim 17; Page 31; 43pp; English.
XX
XX The invention relates to novel somatostatin agonists, typically
XX characterised by alkylation of the amide nitrogen, or its
XX pharmaceutically acceptable salt. The novel somatostatin agonists are
XX useful for binding one or more of human somatostatin subtype receptors -
XX 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
XX administering a somatostatin agonist or a pharmaceutically acceptable
XX salt of it to a recipient in need of it. The somatostatin agonists are
XX useful for treating a disease or condition in a human or other animal,
XX including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
XX Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
XX Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
XX immunodeficiency syndrome (AIDS) and other conditions. Irritable bowel
XX syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
XX cancer, peptasia, hypotension, panic attacks, scleroderma, small bowel
XX obstruction, gastrosophageal reflux, duodenogastric reflux, Grave's
XX disease, polycystic ovary disease, upper gastrointestinal bleeding,
XX pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
XX cachexia, acromegaly, tetanosis, hepatoma, lung cancer, melanoma,
XX inhibiting the accelerated growth of a solid tumour and decreasing body
XX weight, treating insulin resistance, Syndrome X, prolonging the survival
XX of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
XX hyperprolactinaemia and prolactinomas. This sequence represents a peptide
XX of a somatostatin agonist compound of the invention

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CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
 CC pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
 CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 CC inhibiting the accelerated growth of a solid tumour and decreasing body
 CC weight, treating insulin resistance, Syndrome X, prolonging the survival
 CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
 CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
 CC of a somatostatin agonist compound of the invention

XX Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCT 11
 |||||
 Db 1 YCFWKTCT 8

RESULT 14
 AAO26829
 ID AAO26829 standard; peptide; 8 AA.
 XX
 AC AAO26829;

DT 27-AUG-2003 (first entry)

DE Somatostatin agonist compound #12.

XX Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipaeamic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.

OS Unidentified.

FH Key Location/Qualifiers
 FT Misc-difference 4 /note= "D-form residue"
 FT Modified-site 5 /note= "Modified by N-Methyl"
 FT Modified-site 8 /note= "C-terminal amide"

XX WO200281499-A2.

XX 17-OCT-2002.

XX 08-APR-2002; 2002WO-US010882.

XX 09-APR-2001; 2001US-0282526P.

XX (TULA) TULANE EDUCATIONAL FUND.

XX Coy DH, Rajeswaran WG;

XX WPI; 2003-247842/24.

XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
 PT hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
 PT Zollinger-Ellison syndrome, characterized by alkylation of amide
 PT nitrogen.

XX Claim 20; Page 31; 43pp; English.

CC The invention relates to novel somatostatin agonists, typically
 CC characterised by alkylation of the amide nitrogen, or its
 CC pharmaceutically acceptable salt. The novel somatostatin agonists are
 CC useful for binding one or more of human somatostatin subtype receptors -
 CC 1,-2,-3,-4 and -5, and for eliciting a somatostatin agonist effect, by
 CC administering a somatostatin agonist or a pharmaceutically acceptable
 CC salt of it to a recipient in need of it. The somatostatin agonists are

CC useful for treating a disease or condition in a human or other animal,
 CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
 CC Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
 CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
 CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
 CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
 CC cancer, psoriasis, hypotension, panic attacks, scleroderma, small bowel
 CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
 CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
 CC pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
 CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 CC inhibiting the accelerated growth of a solid tumour and decreasing body
 CC weight, treating insulin resistance, Syndrome X, prolonging the survival
 CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
 CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
 CC of a somatostatin agonist compound of the invention

XX Sequence 8 AA;

Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCT 11
 |||||
 Db 1 YCFWKTCT 8

RESULT 15

AAO26831

ID AAO26831 standard; peptide; 8 AA.

XX AAO26831;

DT 27-AUG-2003 (first entry)

DE Somatostatin agonist compound #14.

XX Osteopathic; cytostatic; antidiarrhoeic; antiinflammatory; antipsoriatic;
 KW hypertensive; dermatological; antithyroid; immunomodulator; vasotropic;
 KW antilipaeamic; somatostatin agonist; Cushing's syndrome; gonadotropinoma;
 KW hyperparathyroidism; cancer.

OS Unidentified.

FH Key Location/Qualifiers
 FT Misc-difference 4 /note= "D-form residue"
 FT Modified-site 7 /note= "Modified by N-Methyl"
 FT Modified-site 8 /note= "C-terminal amide"

XX WO200281499-A2.

XX 17-OCT-2002.

XX 08-APR-2002; 2002WO-US010882.

XX 09-APR-2001; 2001US-0282526P.

XX (TULA) TULANE EDUCATIONAL FUND.

XX Coy DH, Rajeswaran WG;

XX WPI; 2003-247842/24.

XX Novel somatostatin agonist, useful for treating Cushing's syndrome,
 PT hyperparathyroidism, Paget's disease, hyperinsulinism, gastrinoma and
 PT Zollinger-Ellison syndrome, characterized by alkylation of amide
 PT nitrogen.

XX Claim 22; Page 32; 43pp; English.

XX The invention relates to novel somatostatin agonists, typically
 CC characterised by alkylation of the amide nitrogen, or its
 CC pharmaceutically acceptable salt. The novel somatostatin agonists are
 CC useful for binding one or more of human somatostatin subtype receptors -
 CC 1,2,3,4 and -5, and for eliciting a somatostatin agonist effect, by
 CC administering a somatostatin agonist or a pharmaceutically acceptable
 CC salt of it to a recipient in need of it. The somatostatin agonists are
 CC useful for treating a disease or condition in a human or other animal,
 CC including Cushing's syndrome, gonadotropinoma, hyperparathyroidism,
 CC Paget's disease, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma,
 CC Zollinger-Ellison syndrome, hypersecretory diarrhoea related to acquired
 CC immunodeficiency syndrome (AIDS) and other conditions, irritable bowel
 CC syndrome, pancreatitis, Crohn's disease, systemic sclerosis, thyroid
 CC cancer, prolasia, hypotension, panic attacks, scleroderma, small bowel
 CC obstruction, gastroesophageal reflux, duodenogastric reflux, Grave's
 CC disease, polycystic ovary disease, upper gastrointestinal bleeding,
 CC pancreatic pseudocysts, pancreatic ascites, leukaemia, meningioma, cancer
 CC cachexia, acromegaly, restenosis, hepatoma, lung cancer, melanoma,
 CC inhibiting the accelerated growth of a solid tumour and decreasing body
 CC weight, treating insulin resistance, Syndrome X, prolonging the survival
 CC of pancreatic cells, fibrosis, hyperlipidaemia, hyperamylinemia,
 CC hyperprolactinaemia and prolactinomas. This sequence represents a peptide
 CC of a somatostatin agonist compound of the invention
 XX
 SQ Sequence 8 AA;
 Query Match 71.2%; Score 57; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YCFWKTKCT 11
 DB 1 YCFWKTKCT 8
 RESULT 16
 ID AAW48642
 AC AAW48642 standard; peptide; 9 AA.
 XX
 DT 04-AUG-1998 (first entry)
 DE Somatostatin peptide analog WOC-2B.
 XX
 KW Somatostatin; acromegaly; radiolocalisation; blood-brain barrier; cancer;
 KW halogen.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "D-form residue"
 FT Disulfide-bond 3..8
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site 9 /note= "C-terminal amide"
 FT
 XX WO9639161-A1.
 XX
 PD 12-DEC-1996.
 XX
 XX 03-JUN-1996; 96WO-US008437.
 XX
 XX 05-JUN-1995; 95US-00462223.
 XX
 XX (TULA) TULANE EDUCATIONAL FUND.
 PA (OHIS) UNIV OHIO STATE RES FOUND.
 PA (LOU) UNIV LOUISIANA STATE MEDICAL CENT FOUND.
 PA (CHIL-) CHILDRENS HOSPITAL INC.

XX Coy DH, Woltering EA, Odorizio MS, Odorizio TM, Murphy WA;
 XX WPI; 1997-042842/04.
 XX
 XX Multi-tyrosinated somatostatin analogues - useful for diagnosis and
 PT treatment of diseases related to altered somatostatin receptor
 PT expression.
 XX
 XX Claim 7; Page 60; 63pp; English.
 XX
 XX The invention provides for conventional somatostatin analogues (AAW48638-
 CC W48640 and AAW48664) and multi-tyrosinated analogues (AAW48641-W48645)
 CC such as the present one. The multi-tyrosinated somatostatin analogues
 CC bind to somatostatin receptors with practically the same affinity as
 CC native somatostatin. The somatostatin analogues are claimed to be useful
 CC for treating disease associated with increased production of factors
 CC which can be regulated by somatostatin, e.g. acromegaly. Also when
 CC radioactively labelled, the analogues are claimed to be useful for
 CC diagnosing cancer in vitro or in situ where aberrant expression of
 CC somatostatin receptors is involved. When halogenated, these analogues are
 CC found to bind somatostatin receptors with such high affinity that binding
 CC is nearly irreversible under physiological conditions. Therefore, by
 CC using radioactive halogenated analogues, the invention claims for
 CC improved sensitivity of radiolocalisation of the receptors. Multi-
 CC tyrosinated analogues have increased half-lives in vivo relative to
 CC conventional somatostatin analogues, are resistant to enzymatic
 CC degradation and have increased blood-brain barrier penetration
 XX
 SQ Sequence 9 AA;
 Query Match 71.2%; Score 57; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YCFWKTKCT 11
 DB 2 YCFWKTKCT 9
 RESULT 17
 ABG71792
 ID ABG71792 standard; peptide; 9 AA.
 XX
 AC ABG71792;
 XX
 DT 22-JAN-2003 (first entry)
 XX
 DE Paclitaxel-glutary 1-octreotide.
 XX
 KW Somatostatin; anticancer; drug; analogue; cytotoxic; toxic; side effect;
 KW drug delivery; cellular membrane receptor; somatostatin receptor; SSTF;
 KW tumour; carcinoid; islet of the pancreas; paraganglioma; carcinoma;
 KW therapeutic; Paclitaxel; glutarate; octreotide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT /note= "OTHER = covalently linked to paclitaxel-
 FT glutarate"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site 9 /label= OTHER
 FT /note= "OTHER = triphenylmethyl (Thr-ol)"
 FT
 XX US2002094964-A1.
 XX
 PD 18-JUL-2002.

CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis.
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 71.2%; Score 57; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YCFWKTCCT 11
 | | | | |
 DB 3 YCFWKTCCT 10
 RESULT 19
 ADU05247
 ID ADU05247 standard; peptide; 10 AA.
 AC ADU05247;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 D2 Cyclic somatostatin-dopamine chimeric peptide analogue #37.
 XX
 KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cystostatic; osteopathic; antihypertensive; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antiulcer;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipemic; analgesic;
 KW antianginal; anorectic; immunomodulator; cardiant; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "An N-terminal dopamine derivative (Dop1 to Dop6
 FT inclusive) is attached to a Lys(dopamine derivative)
 FT modified residue, where this second dopamine derivative
 FT must match the type occurring at the N-terminus, e.g.
 FT Dop1-Lys (Dop1), Dop2-Lys (Dop2) etc."
 FT Misc-difference 2
 FT /note= "D-form residue"
 FT Misc-difference 3
 FT /note= "D-form residue"
 FT Disulfide-bond 4..9
 FT /note= This disulphide bond cyclises the peptide
 FT Misc-difference 6

FT Modified-site 10 /note= "D-form residue"
 FT /note= "C-terminal alcohol"
 XX
 PN W02004091490-A2.
 PD 28-OCT-2004.
 XX
 PP 08-APR-2004; 2004WO-US010891.
 PR 11-APR-2003; 2003US-0462374P.
 XX
 PA (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX
 PI Dong ZX, Dewitt Culler M, Shen Y;
 XX WPI; 2004-784484/77.
 DR
 XX New chimeric analog comprising at least one moiety which binds to one or
 more somatostatin and dopamine receptor(s) useful to treat e.g.
 PT neuroendocrine tumor, vascular diseases, connective tissue disease,
 PT immune disease and cachexia.
 XX
 PS Claim 12; Page 103; 138pp; English.
 XX
 CC This invention relates to novel somatostatin-dopamine chimeric analogues
 that comprise at least one moiety that binds to one or more somatostatin
 receptors and at least one moiety that binds to one or more dopamine
 receptors, or a salt derived thereof. Specifically, it refers to
 CC analogues that may be used in vitro or in vivo for research, diagnostic
 and therapeutic agents to enhance the activity of somatostatin and
 CC dopamine i.e. working as receptor agonists. The present invention
 CC describes analogues with specificity for different types of somatostatin
 receptor subtypes that are accordingly associated with the treatment of
 CC particular diseases or conditions. As such, these analogues may be used
 CC to treat neoplasia and acromegaly as well as various neuroendocrine
 CC tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
 CC scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
 CC tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
 CC hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
 CC disorder or an opioid overdose. Accordingly, they exhibit activities that
 CC include cytostatic, osteopathic, antihypertensive, vasotropic, antiangiogenic,
 CC ophthalmological, antidiabetic, dermatological, immunosuppressive,
 CC antiarthritic, antirheumatic, antiinflammatory, antiulcer,
 CC antidiarrhoeic, nephrotropic, hepatotropic, antilipemic, analgesic,
 CC antianginal, anorectic, immunomodulator, cardiant, tranquilizer and
 CC antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
 CC analogue of the invention.
 SQ Sequence 10 AA;
 Query Match 71.2%; Score 57; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YCFWKTCCT 11
 | | | | |
 DB 3 YCFWKTCCT 10
 RESULT 20
 AD114956
 ID AD114956 standard; peptide; 11 AA.
 XX
 AC AD114956;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Somatostatin-dopamine chimeric analogue-related peptide 66.
 XX
 KW somatostatin-dopamine chimeric analogue; cytostatic; antihypertensive;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;

tranquilliser; antilipaeamic; nephrotropic; antiulcer; antiarthritic;
 somatostatin receptor agonist; lung cancer; glioma; anorexia;
 hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 pancreatic pseudocyst; ascite; VIPoma; nesidoblastosis; hyperinsulinism;
 gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 irritable bowel syndrome; pancreatitis; small bowel obstruction;
 gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 gonadotropinoma; hyperparathyroidism; Graves disease;
 diabetic neuropathy; Paget's disease; polycystic ovary disease;
 prolactin secreting adenoma; acromegaly; meningioma; cancer cachexia;
 thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 orthostatic; hypotension; postprandial hypotension; panic attack;
 GH secreting adenoma; acromegaly; TSH secreting adenoma;
 hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 proliferative retinopathy; dawn phenomenon; nephropathy;
 gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 pancreaticocutaneous fistula; dumping syndrome;
 watery diarrhoea syndrome; pancreatitis;
 gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 allograft rejection; graft vessel bleeding; portal hypertension;
 gastrointestinal bleeding; obesity; opioid overdose.

Synthetic.
 Unidentified.

Key Location/Qualifiers
 Modified-site 1 /note= "Amino acid is Doc. Bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidomethylsulfonyl acetic acid"
 Misc-difference 3. 4 /note= "D-form residue"
 Modified-site 5 /note= "Residue forms a bond to residue 10 to form a cyclic peptide"
 Misc-difference 7 /note= "D-form residue"
 Modified-site 10 /note= "Residue forms a bond to residue 5 to form a cyclic peptide"
 Modified-site 11 /note= "C-terminal amide"

WO2002100888-A1.
 19-DEC-2002.
 07-JUN-2002; 2002WO-US017859.
 08-JUN-2001; 2001US-0297059P.
 (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 Culler MD, Dong ZX, Kim SH, Moreau J;
 WPI; 2003-239103/23.
 New somatostatin-dopamine chimeric analogs useful for the treatment of e.g. lung cancer.
 Claim 3; Page 144; 85pp; English.
 This invention relates to novel somatostatin-dopamine chimeric analogues or their salts. The invention may be useful for the development of compounds with a cytostatic, antichryoid, vasotropic, anti-inflammatory, antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic, antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeamic, nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or antiaddictive activity through action as a dopamine receptor agonist and somatostatin receptor agonist. The invention may be useful for the

treatment of lung cancer, glioma, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and internal pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis, hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, thyroid cancer, cancer cachexia, orthostatic, hypotension, postprandial hypotension, prolactin secreting adenoma, acromegaly, TSH secreting adenoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity, Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon, nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea syndrome, pancreatitis, gastrointestinal hormone secreting tumour, angiogenesis, arthritis, allograft rejection, graft vessel bleeding, portal hypertension, gastrointestinal bleeding, obesity and opioid overdose. The compounds simultaneously elicit dopamine receptor agonist and somatostatin receptor agonist effects in vivo with enhanced biological activity over the native somatostatin and dopamine analogues alone. The present sequence is that of a peptide which was used to produce the somatostatin-dopamine chimeric analogues of the invention.

Sequence 11 AA;
 Query Match 71.2%; Score 57; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
 |||||
 Db 4 YCFWKTKT 11

RESULT 21
 ADI14951
 ID ADI14951 standard; peptide; 11 AA.
 XX
 AC ADI14951;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Somatostatin-dopamine chimeric analogue-related peptide 61.
 XX
 KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipaeamic; nephrotropic; antiulcer; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidoblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;

gastrointestinal bleeding; obesity; opioid overdose.

Synthetic.
Unidentified.

Key Location/Qualifiers

Modified-site 1

/note= "Amino acid is Doc. Bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methylsulfanyl-acetic acid"

Misc-difference 3..4

/note= "D-form residue"

Modified-site 5

/note= "Residue forms a bond to residue 10 to form a cyclic peptide"

Misc-difference 7

/note= "D-form residue"

Modified-site 10

/note= "Residue forms a bond to residue 5 to form a cyclic peptide"

Modified-site 11

/note= "C-terminal amide"

WO2002100888-A1.

19-DEC-2002.

07-JUN-2002; 2002WO-US017859.

08-JUN-2001; 2001US-0297059P.

(SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.

Culler MD, Dong ZX, Kim SH, Moreau J;

WPI; 2003-239103/23.

New somatostatin-dopamine chimeric analogs useful for the treatment of e.g. lung cancer.

Claim 3; Page 144; 85pp; English.

This invention relates to novel somatostatin-dopamine chimeric analogues or their salts. The invention may be useful for the development of compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory, antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic, antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeic, nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or antiaddictive activity through action as a dopamine receptor agonist and somatostatin receptor agonist. The invention may be useful for the treatment of lung cancer, glioma, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and internal pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia, meningioma, cancer cachexia, orthostatic, hypotension, postprandial hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH secreting adenomas, prolactin secreting adenomas, insulinoma, glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity, Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon, nephropathy, gastric acid secretion, peptic ulcer, dawn phenomenon, fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea syndrome, pancreatitis, gastrointestinal hormone secreting tumour, angioneurosis, arthritis, allograft rejection, graft vessel bleeding, portal hypertension, gastrointestinal bleeding, obesity and opioid overdose. The compounds simultaneously elicit dopamine receptor agonist and somatostatin receptor agonist effects in vivo with enhanced biological activity over the native somatostatin and dopamine analogues

CC alone. The present sequence is that of a peptide which was used to produce the somatostatin-dopamine chimeric analogues of the invention.

XX
SQ Sequence 11 AA;

Query Match 71.2%; Score 57; DB 7; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11

Db 4 YCFWKTCCT 11

RESULT 22

AD114959

ID AD114959 standard; peptide; 11 AA.

XX

AC AD114959;

DT 22-APR-2004 (first entry)

DE Somatostatin-dopamine chimeric analogue-related peptide 69.

XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
KW tranquiliser; antilipaeic; nephrotropic; antiulcer; antiarthritic;
KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
KW pancreatic pseudocyst; ascites; VIPoma; nesidioblastosis; hyperinsulinism;
KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
KW gonadotropinoma; hyperparathyroidism; Graves disease;
KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
KW orthostatic; hypotension; postprandial hypotension; panic attack;
KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
KW proliferative retinopathy; dawn phenomenon; nephropathy;
KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
KW pancreaticocutaneous fistula; dumping syndrome;
KW watery diarrhoea syndrome; pancreatitis;
KW gastrointestinal hormone secreting tumour; angioneurosis; arthritis;
KW allograft rejection; graft vessel bleeding; portal hypertension;
KW gastrointestinal bleeding; obesity; opioid overdose.

Synthetic.

Unidentified.

Key Location/Qualifiers

Modified-site 1

/note= "4-(2-aminoethyl)-1-carboxymethyl-piperazine. Bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-ethylureidomethylsulfanyl acetic acid"

Misc-difference 3..4

/note= "D-form residue"

Modified-site 5

/note= "Residue forms a bond to residue 10 to form a cyclic peptide"

Misc-difference 7

/note= "D-form residue"

Modified-site 10

/note= "Residue forms a bond to residue 5 to form a cyclic peptide"

Modified-site 11

/note= "C-terminal amide"

XX	FN	WO2002100888-A1.	DE	XX	Somatostatin-dopamine chimeric analogue-related peptide 64.
XX	PD	19-DEC-2002.	XX	KW	somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
XX	XX		KW	KW	vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
XX	XX		KW	KW	anti-diabetic; osteopathic; antiparasitic; immunomodulator; hypertensive;
XX	PP	07-JUN-2002; 2002WO-US017859.	XX	KW	tranquilliser; antileptemic; nephrotropic; antitumor; antiarthritic;
XX	XX		KW	KW	hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
XX	XX		KW	KW	somatostatin receptor agonist; lung cancer; glioma; anorexia;
XX	XX	08-JUN-2001; 2001US-0297059P.	KW	KW	hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
XX	XX		KW	KW	acromegaly; restenosis; Crohn's disease; systemic sclerosis;
XX	XX	(SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.	KW	KW	pancreatic pseudocyst; ascite; VIPoma; nesidoblastosis; hyperinsulinism;
XX	XX		KW	KW	Gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
XX	PI	Culler MD, Dong ZX, Kim SH, Moreau J;	KW	KW	AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
XX	XX	WPI; 2003-239103/23.	KW	KW	Irritable bowel syndrome; pancreatitis; small bowel obstruction;
XX	DR	New somatostatin-dopamine chimeric analogs useful for the treatment of	KW	KW	gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
XX	PT	e.g. lung cancer.	KW	KW	gonadotropinoma; hyperparathyroidism; Graves disease;
XX	XX		KW	KW	diabetic neuropathy; Paget's disease; polycystic ovary disease;
XX	XX		KW	KW	orthostatic; hypotension; postprandial hypotension; panic attack;
XX	XX		KW	KW	GH secreting adenoma; acromegaly; TSH secreting adenoma;
XX	XX		KW	KW	prolactin secreting adenoma; insulin insensitivity; Syndrome X; angiopathy;
XX	XX		KW	KW	proliferative retinopathy; dawn phenomenon; nephropathy;
XX	CC	This invention relates to novel somatostatin-dopamine chimeric analogues	KW	KW	gastric acid secretion; peptic ulcer; enterocutaneous fistula;
XX	CC	or their salts. The invention may be useful for the development of	KW	KW	pancreaticocutaneous fistula; dumping syndrome;
XX	CC	compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,	KW	KW	watery diarrhoea syndrome; pancreatitis;
XX	CC	antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,	KW	KW	gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
XX	CC	antibacterial, immunomodulator, hypertensive, tranquiliser, antileptemic,	KW	KW	allograft rejection; graft vessel bleeding; portal hypertension;
XX	CC	nephrotropic, antitumor, antiarthritic, hypotensive, anorectic or	XX	XX	gastrointestinal bleeding; obesity; opioid overdose.
XX	CC	antiaddictive activity through action as a dopamine receptor agonist and	OS	OS	Synthetic.
XX	CC	somatostatin receptor agonist. The invention may be useful for the	OS	OS	Unidentified.
XX	CC	treatment of lung cancer, glioma, anorexia, hypothyroidism,	XX	XX	Key
XX	CC	hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,	XX	XX	Modified-site 1
XX	CC	restenosis, Crohn's disease, systemic sclerosis, external and internal	XX	XX	/note= "4-(2-aminoethyl)-1-carboxymethyl-piperazine.
XX	CC	pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,	XX	XX	Bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3
XX	CC	hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS	XX	XX	-fg]quinolin-9-yl-methylsulfanyl-acetic acid"
XX	CC	related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable	XX	XX	Misc-difference 3. .4
XX	CC	bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal	XX	XX	/note= "D-form residue"
XX	CC	reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,	XX	XX	Modified-site 5
XX	CC	hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's	XX	XX	/note= "Residue forms a bond to residue 10 to form a
XX	CC	disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,	XX	XX	cyclic peptide"
XX	CC	meningioma, cancer cachexia, orthostatic, hypotension, postprandial	XX	XX	/note= "D-form residue"
XX	CC	fistula, pancreaticocutaneous fistula, dumping syndrome, enterocutaneous	XX	XX	Modified-site 7
XX	CC	hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH	XX	XX	/note= "Residue forms a bond to residue 5 to form a
XX	CC	secreting adenomas, prolactin secreting adenomas, insulinoma,	XX	XX	cyclic peptide"
XX	CC	glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,	XX	XX	Modified-site 10
XX	CC	Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon,	XX	XX	/note= "Residue forms a bond to residue 5 to form a
XX	CC	nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous	XX	XX	cyclic peptide"
XX	CC	fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea	XX	XX	Modified-site 11
XX	CC	syndrome, pancreatitis, gastrointestinal hormone secreting tumour,	XX	XX	/note= "C-terminal amide"
XX	CC	angiogenesis, arthritis, allograft rejection, graft vessel bleeding,	XX	XX	WO2002100888-A1.
XX	CC	portal hypertension, gastrointestinal bleeding, obesity and opioid	XX	XX	19-DEC-2002.
XX	CC	overdose. The compounds simultaneously elicit dopamine receptor agonist	XX	XX	07-JUN-2002; 2002WO-US017859.
XX	CC	and somatostatin receptor agonist effects in vivo with enhanced	XX	XX	08-JUN-2001; 2001US-0297059P.
XX	CC	biological activity over the native somatostatin and dopamine analogues	XX	XX	(SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
XX	CC	alone. The present sequence is that of a peptide which was used to	XX	XX	Culler MD, Dong ZX, Kim SH, Moreau J;
XX	CC	produce the somatostatin-dopamine chimeric analogues of the invention.	XX	XX	WPI; 2003-239103/23.
XX	XX		XX	XX	New somatostatin-dopamine chimeric analogs useful for the treatment of
XX	XX		XX	XX	e.g. lung cancer.
XX	XX		XX	XX	Claim 3; Page 144; 85pp; English.
XX	XX		XX	XX	This invention relates to novel somatostatin-dopamine chimeric analogues
XX	XX		XX	XX	or their salts. The invention may be useful for the development of
XX	XX		XX	XX	compounds with a cytostatic, antithyroid, vasotropic, chimeric analogues
XX	XX		XX	XX	analogues of their salts. The invention may be useful for the development of
XX	XX		XX	XX	compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,

Query Match

Best Local Similarity 71.2%; Score 57; DB 7; Length 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11

Db 4 YCFWKTCCT 11

RESULT 23

ID ADI14954

AC ADI14954 standard; peptide; 11 AA.

XX ADI14954;

DT 22-APR-2004 (first entry)

XX

CC anti-diarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquilizer, antilipaeamic,
 CC nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or
 CC antiaddictive activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC xeroderma, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiotensin, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 XX Sequence 11 AA;

Query Match 71.2%; Score 57; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
 DB 4 YCFWKTCCT 11

RESULT 24
 ADU05246
 ID ADU05246 standard; peptide; 11 AA.

AC ADU05246;

XX 13-JAN-2005 (first entry)

XX Cyclic somatostatin-dopamine chimeric peptide analogue #36.

XX somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective tissue disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytototoxic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antiulcer;
 KW anti-diarrhoeic; nephrotropic; hepatotropic; antilipaeamic; analgesic;
 KW antianginal; anorectic; immunomodulator; cardiant; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX Synthetic.

OS Key Location/Qualifiers

PH Modified-site 1
 FT /note= "An N-terminal dopamine derivative (Dop1 to Dop6
 FT inclusive) is attached to a Lys(dopamine derivative)
 FT modified residue, where this second dopamine derivative
 FT must match the type occurring at the N-terminus, e.g.
 FT Dop1-Lys (Dop1), Dop2-Lys (Dop2) etc."

FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Disulfide-bond 5.10
 FT /note= This disulphide bond cyclises the peptide
 FT Misc-difference 7 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal alcohol"

XX WO2004091490-A2.

XX 28-OCT-2004.

XX 08-APR-2004; 2004WO-US010891.

XX 11-APR-2003; 2003US-0462374P.

XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.

XX Dong ZX, Dewitt Culler M, Shen Y;

XX WPI; 2004-784484/77.

XX New chimeric analog comprising at least one moiety which binds to one or
 more somatostatin and dopamine receptor(s) useful to treat e.g.
 FT neuroendocrine tumor, vascular diseases, connective tissue disease,
 FT immune disease and cachexia.

XX Claim 12; Page 103; 138pp; English.

XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC that comprise at least one moiety that binds to one or more somatostatin
 CC receptors and at least one moiety that binds to one or more dopamine
 CC receptors, or a salt derived thereof. Specifically, it refers to
 CC analogues that may be used in vitro or in vivo for research, diagnostic
 CC and therapeutic agents to enhance the activity of somatostatin and
 CC dopamine i.e. working as receptor agonists. The present invention
 CC describes analogues with specificity for different types of somatostatin
 CC receptor subtypes that are accordingly associated with the treatment of
 CC particular diseases or conditions. As such, these analogues may be used
 CC to treat neoplasia and acromegaly as well as various neuroendocrine
 CC tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
 CC scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
 CC tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
 CC hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
 CC disorder or an opioid overdose. Accordingly, they exhibit activities that
 CC include cytostatic, osteopathic, antithyroid, vasotropic, antiangiogenic,
 CC ophthalmological, antidiabetic, dermatological, immunosuppressive,
 CC antiarthritic, antirheumatic, antiinflammatory, antiulcer, analgesic,
 CC anti-diarrhoeic, nephrotropic, hepatotropic, antilipaeamic, analgesic,
 CC antianginal, anorectic, immunomodulator, cardiant, tranquilizer and
 CC antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
 CC analogue of the invention.

XX Sequence 11 AA;

Query Match 71.2%; Score 57; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
 DB 4 YCFWKTCCT 11

RESULT 25

AD114894

ID AD114894 standard; peptide; 12 AA.

XX AC AD114894;

XX

cyclic peptide"

XX

DT 22-APR-2004 (first entry)
 XX Somatostatin-dopamine chimeric analogue-related peptide 67.
 DE
 XX
 KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipaeamic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antidiabetic; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothalamic; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis; external and internal
 KW pancreatic pseudocysts and ascites; VIPoma; nesidioblastosis;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma; irritable
 KW bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 OS Synthetic.
 OS Unidentified.
 XX

Key Location/Qualifiers
 Modified-site 1
 /note="Amino acid is Doc. Bound to 1-(7-allyl-
 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-
 carbonyl)-3-ethylureidomethylsulfonyl acetic acid"
 Modified-site 2. .3
 /note="Amino acid is Doc"
 Misc-difference 5. .6
 /note="D-form residue"
 Modified-site 7
 /note="Residue forms a bond to residue 12 to form a
 cyclic peptide"
 Misc-difference 9
 /note="D-form residue"
 Modified-site 12
 /note="Residue forms a bond to residue 7 to form a
 cyclic peptide"
 Modified-site 13
 /note="C-terminal amide"
 WO2002100888-A1.
 19-DEC-2002.
 07-JUN-2002; 2002WO-US017859.
 08-JUN-2001; 2001US-0297059P.
 (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 Culler MD, Dong ZX, Kim SH, Moreau J;
 WPI; 2003-239103/23.
 New somatostatin-dopamine chimeric analogs useful for the treatment of
 e.g. lung cancer.
 Claim 3; Page 145; 85pp; English.

XX
 CC This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeamic,
 CC nephrotropic, antitumor, antiarthritic, hypotensive, anorectic or
 CC antidiabetic activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegaly, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 13 AA;
 Query Match 71.2%; Score 57; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YCFWKTCCT 11
 Db 6 YCFWKTCCT 13
 RESULT 27
 ADI14895
 ID ADI14895 standard; peptide; 13 AA.
 XX
 AC ADI14895;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE
 XX Somatostatin-dopamine chimeric analogue-related peptide 8.
 KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipaeamic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antidiabetic; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothalamic; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis; hyperinsulinism;
 KW pancreatic pseudocysts; ascites; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;

KW GH secreting adenoma; acromegally; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; Glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose; cyclic; circular.
 XX Synthetic.
 OS Unidentified.
 XX

Key Location/Qualifiers
 Modified-site 1
 FT /note= "Amino acid is Doc. Optionally bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methylsulfanyl-acetic acid. Optionally bound to 7-propyl-
 FT 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 FT methyl-carbamic acid. Optionally bound to carbonic acid
 FT mono-(7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fg]quinolin-9-yl-methyl) ester. Optionally bound to 4-(7-
 FT -propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fg]quinolin-9-yl-methyl) carbonyl) butyric acid.
 FT Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carboxylic acid.
 FT Optionally bound to 1-(7-allyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
 FT ethylureidomethylsulfonyl acetic acid. Optionally bound
 FT to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fg]quinolin-9-carbonyl)-3-ethylureidopropyl)carbamic
 FT acid. Optionally bound to carbonic acid mono-(3-(1-(7-
 FT allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin
 FT -9-carbonyl)-3-ethylureido)propyl)carbamic acid.
 FT Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
 FT ethylureidopropyl)-Gly-. Optionally bound to 4-(3-(1-(7-
 FT allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin
 FT -9-carbonyl)-3-ethylureido)propyl)carbonyl)butyric acid"
 FT 2. 3
 FT Modified-site /note= "Amino acid is Doc"
 FT 5. .6
 FT Misc-difference /note= "D-form residue"
 FT 7
 FT Modified-site /note= "Residue forms a bond to residue 12 to form a
 FT cyclic peptide"
 FT 9
 FT Misc-difference /note= "D-form residue"
 FT 12
 FT Modified-site /note= "Residue forms a bond to residue 7 to form a
 FT cyclic peptide"
 FT 13
 FT Modified-site /note= "C-terminal amide"
 FT
 XX WO2002100888-A1.
 XX
 XX 19-DEC-2002.
 XX
 XX 07-JUN-2002; 2002WO-US017859.
 XX
 XX 08-JUN-2001; 2001US-0237059P.
 XX
 XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 XX
 XX Culler MD, Dong ZX, Kim SH, Moreau J;
 XX WPI; 2003-239103/23.
 XX
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 XX e.g. lung cancer.
 XX
 XX Claim 3; Page 103; 85pp; English.

XX This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeic,
 CC nephrotropic, antitumor, antiarthritic, hypotensive, anorectic or
 CC antidiabetic activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC restenosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, mesodiblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 13 AA;
 Query Match 71.2%; Score 57; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YCFWKTKT 11
 DB 6 YCFWKTKT 13
 RESULT 28
 ADI14952
 ID ADI14952 standard; peptide; 14 AA.
 XX
 AC ADI14952;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Somatostatin-dopamine chimeric analogue-related peptide 62.
 XX
 KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 KW tranquiliser; antilipaeic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antidiabetic; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis;
 KW pancreatic pseudocyst; ascite; VIPoma; mesodiblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;

GH secreting adenoma; acromegally; TSH secreting adenoma;
 prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 hyperlipidaemia; insulin insensitivity; Syndrome X; angiopathy;
 proliferative retinopathy; dawn phenomenon; nephropathy;
 gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 pancreaticocutaneous fistula; dumping syndrome;
 watery diarrhoea syndrome; pancreatitis;
 gastrointestinal hormone secreting tumour; angio genesis; arthritis;
 allograft rejection; graft vessel bleeding; portal hypertension;
 gastrointestinal bleeding; obesity; opioid overdose.
 Synthetic.
 Unidentified.

Key Location/Qualifiers
 Modified-site 1
 /note= "Amino acid is Doc. Bound to 7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-methylsulfanyl-acetic acid"
 Modified-site 2..4
 /note= "Amino acid is Doc"
 Misc-difference 6..7
 /note= "D-form residue"
 Modified-site 8
 /note= "Residue forms a bond to residue 13 to form a cyclic peptide"
 Misc-difference 10
 /note= "D-form residue"
 Modified-site 13
 /note= "Residue forms a bond to residue 8 to form a cyclic peptide"
 Modified-site 14
 /note= "C-terminal amide"

WO2002100888-A1.
 19-DEC-2002.
 07-JUN-2002; 2002WO-US017859.
 08-JUN-2001; 2001US-0297059P.
 (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 Culler MD, Dong ZX, Kim SH, Moreau J;
 WPI; 2003-239103/23.
 New somatostatin-dopamine chimeric analogs useful for the treatment of e.g. lung cancer.
 Claim 3; Page 144; 85pp; English.

This invention relates to novel somatostatin-dopamine chimeric analogues or their salts. The invention may be useful for the development of compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory, antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic, antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeamic, nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or antiaddictive activity through action as a dopamine receptor agonist and somatostatin receptor agonist. The invention may be useful for the treatment of lung cancer, glioma, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and internal pancreatic pseudocysts and ascites, VIPoma, nesidioblastosis, hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma, hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia, meningioma, cancer cachexia, orthostatic, hypotension, postprandial hypotension, panic attacks, GH secreting adenomas, acromegally, TSH

CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angio genesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 14 AA;
 Query Match 71.2%; Score 57; DB 7; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YCFWKTCCT 11
 Db |||||
 7 YCFWKTCCT 14
 RESULT 29
 ABR42184
 ID ABR42184 standard; peptide; 15 AA.
 XX
 AC ABR42184;
 XX
 DT 28-JUL-2003 (first entry)
 XX
 DE Somatostatin analogue peptide JF-08-87A.
 XX
 KW Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 KW antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 Modified-site 1
 /note= "Optional methotrexate-acetyl moiety or 2-bromo-acetyl-D-tert-butyl or D-tert butyl modification, D-form residue"
 Misc-difference 2
 /note= "D-form residue, optional tert-butyl modification"
 Misc-difference 3
 /note= "D-form residue, optional tert-butyl modification"
 Misc-difference 4
 /note= "D-form residue, optional tert-butyl modification"
 Misc-difference 5
 /note= "D-form residue, optional tert-butyl modification"
 Modified-site 6
 /note= "Optional epsilon-tert-butyloxycarbonyl modification"
 Misc-difference 7
 /note= "D-form residue, optional tert-butyl modification"
 Modified-site 8
 /note= "Optional tert-butyl modification"
 Disulfide-bond 9..14
 /note= "Optional Cys circularization"
 Modified-site 9
 /note= "Optional S-trityl modification"
 Misc-difference 11
 /note= "D-form residue"
 Modified-site 12
 /note= "Optional epsilon-tert-butyloxycarbonyl modification"
 Modified-site 13
 /note= "Optional tert-butyl modification"
 Modified-site 14
 /note= "Optional epsilon-tert-butyloxycarbonyl"

FT Modified-site 15 modification"
 FT /note= "C-terminal amide, optional tert-butyl
 FT modification"
 XX
 XX W02003028527-A2.
 XX
 XX 10-APR-2003.
 XX
 XX 20-SEP-2002; 2002WO-US030143.
 XX
 XX 21-SEP-2001; 2001US-0323851P.
 XX
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX
 XX Coy DH, Fuselier JA, Murphy WA, Sun L;
 XX WPI; 2003-441067/41.
 XX
 XX Biologically active peptides such as somatostatin or bombesin conjugated
 XX to chemical compounds through linkers, useful for treating tumors of the
 XX lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 XX vessels.
 XX
 XX Disclosure; Page 16; 86pp; English.
 XX
 XX The present sequence is that of somatostatin analogue peptide JP-08-87A.
 XX It is an example of peptide agents of the invention that comprise a
 XX biologically active peptide, such as somatostatin or bombesin, conjugated
 XX to a chemical compound through a linker that maintains the peptide's
 XX biological activity. The peptide agents may also include a cytostatic or
 XX therapeutic agent, label or chelating group and a peptide that increases
 XX the hydrophilic biodistribution of the agent. They are useful for
 XX treating tumors of the lung, breast, brain, eye, prostate, or colon,
 XX tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
 XX angiogenic blood vessels (claimed). Other diseases that can also be
 XX treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
 XX arthritis, neoplastic cells or aberrantly proliferating cells, and
 XX acromegaly. Peptide JP-08-87A has the ability to inhibit growth hormone
 XX release from primary cultures of rat pituitary cells, having an IC50 of
 XX 0.16 nM (compared with 0.15 nM for somatostatin-14). Note: The present
 XX sequence is identified as SEQ ID 2 in the disclosure (page 16), but it is
 XX not the same as the sequence given as SEQ ID 2 in the sequence listing
 XX
 XX SQ Sequence 15 AA;
 XX
 XX Query Match 71.2%; Score 57; DB 6; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 2.9;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 4 YCFWKTCCT 11
 XX |||||
 XX Db 8 YCFWKTCCT 15
 XX
 XX RESULT 30
 XX AD114935
 XX ID AD114935 standard; peptide; 15 AA.
 XX
 XX AC AD114935;
 XX
 XX DT 22-APR-2004 (first entry)
 XX
 XX DE Somatostatin-dopamine chimeric analogue-related peptide 46.
 XX
 XX somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 XX vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 XX anti-diabetic; osteopathic; antibacterial; immunomodulator; hypertensive;
 XX tranquiliser; antilipemic; nephrotoxic; antitumor; antiarthritic;
 XX hypotensive; anorectic; antidiabetic; dopamine receptor agonist;
 XX somatostatin receptor agonist; lung cancer; glioma; anorexia;
 XX hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 XX acromegaly; restenosis; Crohn's disease; systemic sclerosis;

KW pancreatic pseudocyst; ascite; VIPoma; nesidoblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiogenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 OS Synthetic.
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 XX Modified-site 1
 XX /note= "D-form residue. Optionally bound to 7-propyl-
 XX 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 XX methylsulfonyl-acetic acid. Optionally bound to 7-propyl-
 XX 4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin-9-yl-
 XX methyl-carbamate acid. Optionally bound to carbonic acid
 XX mono-(7-propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 XX fg]quinolin-9-yl-methyl) ester. Optionally bound to 4-((7-
 XX propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 XX fg]quinolin-9-yl-methyl) carbonyl) butyric acid.
 XX Optionally bound to 7-propyl-4,6,6a,7,8,9,10,10a-
 XX octahydroindolo[4,3-fg]quinolin-9-carboxylic acid.
 XX Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-
 XX octahydroindolo[4,3-fg]quinolin-9-carbonyl)-3-
 XX ethylureidopropyl)-Gly-"
 XX Misc-difference 2. .5 /note= "D-form residue"
 XX Misc-difference 7. .8 /note= "D-form residue"
 XX Modified-site 9 /note= "Residue forms a bond to residue 14 to form a
 XX cyclic peptide"
 XX Misc-difference 11 /note= "D-form residue"
 XX Modified-site 14 /note= "Residue forms a bond to residue 9 to form a
 XX cyclic peptide"
 XX Modified-site 15 /note= "C-terminal OL"
 XX
 XX W02002100888-A1.
 XX
 XX 19-DEC-2002.
 XX
 XX 07-JUN-2002; 2002WO-US017859.
 XX
 XX 08-JUN-2001; 2001US-0297059P.
 XX
 XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 XX
 XX Culler WD, Dong ZX, Kim SH, Moreau J;
 XX WPI; 2003-239103/23.
 XX
 XX New somatostatin-dopamine chimeric analogs useful for the treatment of
 XX e.g. lung cancer.
 XX
 XX Claim 3; Page 133; 85pp; English.

CC This invention relates to novel somatostatin-dopamine chimeric analogues
 CC or their salts. The invention may be useful for the development of
 CC compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 CC antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 CC antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaeamic,
 CC nephrotropic, antiulcer, antiarthritic, hypotensive, anorectic or
 CC antiaddictive activity through action as a dopamine receptor agonist and
 CC somatostatin receptor agonist. The invention may be useful for the
 CC treatment of lung cancer, glioma, anorexia, hypothyroidism,
 CC hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 CC renalosis, Crohn's disease, systemic sclerosis, external and internal
 CC pancreatic pseudocysts and ascites, VIPoma, nesidoblastosis,
 CC hyperinsulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 CC related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 CC bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 CC reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 CC hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 CC meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 CC hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 CC secreting adenomas, prolactin secreting adenomas, insulinoma,
 CC glucagonoma, diabetes mellitus, hyperlipidaemia, insulin insensitivity,
 CC Syndrome X, angiodopathy, proliferative retinopathy, dawn phenomenon,
 CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreaticocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angioneuroma, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 CC
 SQ Sequence 15 AA;

Query Match 71.2%; Score 57; DB 7; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCT 11
 |||||
 Db 8 YCFWKTCT 15

RESULT 32
 ABR42192
 ID ABR42192 standard; peptide; 20 AA.

AC ABR42192;

DT 28-JUL-2003 (first entry)

XX Peptide analogue conjugate.

DE Somatostatin; peptide conjugate; cytostatic; antidiabetic; antihypertensive;
 XX antinflammatory; antiarthritic; antirheumatic; cyclic.

OS Synthetic.

XX Key Location/Qualifiers

FH Modified-site 1 /note= "DOTA moiety or optional DOTA-O-benzyl or O-benzyl
 FT modification, D-form residue"

FT Misc-difference 2 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"

FT Misc-difference 3 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"

FT Misc-difference 4 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"

FT Misc-difference 5 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 6 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 7 /note= "optionally modified D-with O-benzyl, D-form
 FT residue"
 FT Misc-difference 8 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 9 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Misc-difference 10 /note= "optionally modified with D-O-benzyl, D-form
 FT residue"
 FT Modified-site 11 /note= "optionally modified with N-epsilon- (2-
 FT chlorobenzoyloxycarbonyl)"
 FT Modified-site 12 /note= "optionally modified with O-2,6- dichlorobenzyl"
 FT Modified-site 13 /note= "optionally modified with O-2,6- dichlorobenzyl"
 FT Disulfide-bond 14.19
 FT Modified-site 14 /note= "Optional Cys circularization"
 FT Misc-difference 16 /note= "optionally modified with S-4-methylbenzyl"
 FT Modified-site 17 /note= "D-form residue"
 FT Modified-site 19 /note= "optionally modified with N-epsilon- (2-
 FT (chlorobenzoyloxycarbonyl)"
 FT Misc-difference 20 /note= "optionally modified with O-benzyl, C-terminal
 FT amide, Rink-amide resin or MBHA resin"
 XX WO2003028527-A2.
 XX 10-APR-2003.
 XX 20-SEP-2002; 2002WO-US030143.
 XX 21-SEP-2001; 2001US-0323851P.
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX Coy DH, Fusellier JA, Murphy WA, Sun L;
 XX WPI; 2003-441067/41.
 XX Biologically active peptides such as somatostatin or bombesin conjugated
 XX to chemical compounds through linkers, useful for treating tumors of the
 XX lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 XX vessels.
 XX Example 15; Page 45; 86pp; English.
 XX The present sequence is that of a peptide analogue conjugate that is an
 XX example of peptide agents of the invention that comprise a biologically
 XX active peptide, such as somatostatin or bombesin, conjugated to a
 XX chemical compound through a linker that maintains the peptide's
 XX biological activity. The peptide agents may also include a cytostatic or
 XX therapeutic agent, label or chelating group and a peptide that increases
 XX the hydrophilic biotransformation of the agent. They are useful for
 XX treating tumors of the lung, breast, brain, eye, prostate, or colon,
 XX tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
 XX angiogenic blood vessels (claimed). Other diseases that can also be
 XX treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
 XX arthritis, neoplastic cells or aberrantly proliferating cells, and

CC acromegaly
 XX Sequence 20 AA;
 SQ

Query Match 71.2%; Score 57; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
 Db 13 YCFWKTCCT 20

RESULT 33
 ABR42198
 ID ABR42198 standard; peptide; 20 AA.
 XX AC ABR42198;
 DT 28-JUL-2003 (first entry)
 DE Somatostatin analogue peptide.
 XX
 KW Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 KW antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX
 OS Synthetic.

FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Misc-difference 6 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 8 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 10 /note= "D-form residue"
 FT Misc-difference 12 /note= "D-form residue"
 FT Misc-difference 13 /note= "D-form residue"
 FT Disulfide-bond 14. .19
 FT Misc-difference 16 /note= "D-form residue"
 FT Modified-site 20 /note= "C-terminal amide"
 FT
 XX WO2003028527-A2.
 FN 10-APR-2003.
 XX
 PD 20-SEP-2002; 2002MO-US030143.
 PF
 XX 21-SEP-2001; 2001US-0323851P.
 PR (TULA) TULANE EDUCATIONAL FUND.
 PA
 XX Coy DH, Fuselier JA, Murphy WA, Sun L;
 FI WPI; 2003-441067/41.
 DR
 XX

PT Biologically active peptides such as somatostatin or bombesin conjugated
 PT to chemical compounds through linkers, useful for treating tumors of the
 PT lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 PT vessels.
 XX
 XX Example 26; Page 55; 86pp; English.
 XX
 CC The present sequence is that of a somatostatin analogue peptide. It is an
 CC example of peptide agents of the invention that comprise a biologically
 CC active peptide, such as somatostatin or bombesin, conjugated to a
 CC chemical compound through a linker that maintains the peptide's
 CC biological activity. The peptide agents may also include a cytostatic or
 CC therapeutic agent, label or chelating group and a peptide that increases
 CC the hydrophilic biotribution of the agent. They are useful for
 CC treating tumors of the lung, breast, brain, eye, prostate, or colon,
 CC tumours of neuroendocrine origin (for e.g. carcinoid syndrome), and
 CC angiogenic blood vessels (claimed). Other diseases that can also be
 CC treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
 CC arthritis, neoplastic cells or aberrantly proliferating cells, and
 CC acromegaly. The present peptide has the ability to inhibit growth hormone
 CC release from primary cultures of rat pituitary cells, having an IC50 of
 CC 0.24 nM (compared with 0.15 nM for somatostatin-14)
 XX
 SQ Sequence 20 AA;
 Query Match 71.2%; Score 57; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
 Db 13 YCFWKTCCT 20

RESULT 34
 ADI14936
 ID ADI14936 standard; peptide; 20 AA.
 XX AC ADI14936;
 XX
 DT 22-APR-2004 (first entry)
 DE Somatostatin-dopamine chimeric analogue-related peptide 47.
 XX
 KW somatostatin-dopamine chimeric analogue; cytostatic; antithyroid;
 KW vasotropic; anti-inflammatory; antidiarrhoeic; anti-HIV; dermatological;
 KW anti-diabetic; osteopathic; antibacterial; immunomodulator; hypercensive;
 KW tranquiliser; anitlipaemic; nephrotropic; antitumor; antiarthritic;
 KW hypotensive; anorectic; antiaddictive; dopamine receptor agonist;
 KW somatostatin receptor agonist; lung cancer; glioma; anorexia;
 KW hypothyroidism; hyperaldosteronism; Helicobacter pylori proliferation;
 KW acromegaly; restenosis; Crohn's disease; systemic sclerosis; hyperinsulinism;
 KW pancreatic pseudocyst; ascite; VIPoma; nesidioblastosis; hyperinsulinism;
 KW gastrinoma; Zollinger-Ellison Syndrome; diarrhoea;
 KW AIDS related diarrhoea; chemotherapy related diarrhoea; scleroderma;
 KW irritable bowel syndrome; pancreatitis; small bowel obstruction;
 KW gastroesophageal reflux; duodenogastric reflux; Cushing's syndrome;
 KW gonadotropinoma; hyperparathyroidism; Graves disease;
 KW diabetic neuropathy; Paget's disease; polycystic ovary disease;
 KW thyroid cancer; hepatoma; leukaemia; meningioma; cancer cachexia;
 KW orthostatic; hypotension; postprandial hypotension; panic attack;
 KW GH secreting adenoma; acromegaly; TSH secreting adenoma;
 KW prolactin secreting adenoma; insulinoma; glucagonoma; diabetes mellitus;
 KW hyperlipidaemia; insulin insensitivity; Syndrome X; angiodopathy;
 KW proliferative retinopathy; dawn phenomenon; nephropathy;
 KW gastric acid secretion; peptic ulcer; enterocutaneous fistula;
 KW pancreaticocutaneous fistula; dumping syndrome;
 KW watery diarrhoea syndrome; pancreatitis;
 KW gastrointestinal hormone secreting tumour; angiodenesis; arthritis;
 KW allograft rejection; graft vessel bleeding; portal hypertension;
 KW gastrointestinal bleeding; obesity; opioid overdose.
 XX
 OS Synthetic.

FT methyl) carbonyl) butyric acid. Optionally bound to 7-
 FT propyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fg]quinolin-9-carboxylic acid. Optionally bound to 1-(7-
 FT allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-fg]quinolin
 FT -9-carbonyl)-3-ethylureidomethylsulfonyl acetic acid.
 FT Optionally bound to 3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carbonyl))-3-
 FT ethylureidopropyl)carbanic acid. Optionally bound to
 FT carbonic acid mono-(3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carbonyl))-3-
 FT ethylureido)propyl)carbanic acid. Optionally bound to 3-
 FT (1-(7-allyl-4,6,6a,7,8,9,10,10a-octahydroindolo[4,3-
 FT fg]quinolin-9-carbonyl))-3-ethylureidopropyl)-Gly-
 FT Optionally bound to 4-(3-(1-(7-allyl-4,6,6a,7,8,9,10,10a-
 FT octahydroindolo[4,3-fg]quinolin-9-carbonyl))-3-
 FT ethylureido)propyl)carbamoyl)butyric acid"
 FT 2. .10
 FT /note= "D-form residue"
 FT Misc-difference 12. .13
 FT /note= "D-form residue"
 FT Modified-site 14
 FT /note= "Residue forms a bond to residue 19 to form a
 FT cyclic peptide"
 FT Misc-difference 16
 FT /note= "D-form residue"
 FT Modified-site 19
 FT /note= "Residue forms a bond to residue 14 to form a
 FT cyclic peptide"
 FT Modified-site 20
 FT /note= "C-terminal amide"
 FT
 FT WO2002100888-A1.
 FT
 FT 19-DEC-2002.
 FT
 FT 07-JUN-2002; 2002WO-US017859.
 FT
 FT 08-JUN-2001; 2001US-0297059P.
 FT
 FT (SCRC) SCRAS SOC CONSRILS RECH & APPL SCI.
 FT
 FT Culler MD, Dong ZX, Kim SH, Moreau J;
 FT
 FT WPI; 2003-239103/23.
 FT
 FT New somatostatin-dopamine chimeric analogs useful for the treatment of
 FT e.g. lung cancer.
 FT
 FT Claim 3; Page 103; 85pp; English.
 FT
 FT This invention relates to novel somatostatin-dopamine chimeric analogues
 FT or their salts. The invention may be useful for the development of
 FT compounds with a cytostatic, antithyroid, vasotropic, anti-inflammatory,
 FT antidiarrhoeic, anti-HIV, dermatological, anti-diabetic, osteopathic,
 FT antibacterial, immunomodulator, hypertensive, tranquiliser, antilipaemic,
 FT nephrotropic, antitumor, antiarthritic, hypotensive, anorectic or
 FT anti-addictive activity through action as a dopamine receptor agonist and
 FT somatostatin receptor agonist. The invention may be useful for the
 FT treatment of lung cancer, glioma, anorexia, hypothyroidism,
 FT hyperaldosteronism, Helicobacter pylori proliferation, acromegaly,
 FT restenosis, Crohn's disease, systemic sclerosis, external and internal
 FT pancreatic pseudocysts and ascites, VIPoma, nasidoblastosis,
 FT hyperneulinism, gastrinoma, Zollinger-Ellison Syndrome, diarrhoea, AIDS
 FT related diarrhoea, chemotherapy related diarrhoea, scleroderma, irritable
 FT bowel syndrome, pancreatitis, small bowel obstruction, gastroesophageal
 FT reflux, duodenogastric reflux, Cushing's syndrome, gonadotropinoma,
 FT hyperparathyroidism, Graves disease, diabetic neuropathy, Paget's
 FT disease, polycystic ovary disease, thyroid cancer, hepatoma, leukaemia,
 FT meningioma, cancer cachexia, orthostatic, hypotension, postprandial
 FT hypotension, panic attacks, GH secreting adenomas, acromegally, TSH
 FT secreting adenomas, prolactin secreting adenomas, insulin insensitivity,
 FT glucagonoma, diabetes mellitus, hyperlipidemia, insulin insensitivity,
 FT Syndrome X, angiopathy, proliferative retinopathy, dawn phenomenon,

CC nephropathy, gastric acid secretion, peptic ulcer, enterocutaneous
 CC fistula, pancreatocutaneous fistula, dumping syndrome, watery diarrhoea
 CC syndrome, pancreatitis, gastrointestinal hormone secreting tumour,
 CC angiogenesis, arthritis, allograft rejection, graft vessel bleeding,
 CC portal hypertension, gastrointestinal bleeding, obesity and opioid
 CC overdose. The compounds simultaneously elicit dopamine receptor agonist
 CC and somatostatin receptor agonist effects in vivo with enhanced
 CC biological activity over the native somatostatin and dopamine analogues
 CC alone. The present sequence is that of a peptide which was used to
 CC produce the somatostatin-dopamine chimeric analogues of the invention.
 XX
 SQ Sequence 20 AA;
 Query Match 71.2%; Score 57; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YCFWKTCT 11
 Db 13 YCFWKTCT 20
 |||||
 |||||
 RESULT 36
 ABR42181
 ID ABR42181 standard; peptide; 22 AA.
 XX AC ABR42181;
 XX 28-JUL-2003 (first entry)
 XX Somatostatin analogue peptide JF-08-73.
 DE
 XX Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 KW antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "125I-Succinoyl-Aspartic acid, D-form residue"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Misc-difference 6 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 8 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 10 /note= "D-form residue"
 FT Misc-difference 11 /note= "D-form residue"
 FT Misc-difference 12 /note= "D-form residue"
 FT Misc-difference 13 /note= "D-form residue"
 FT Misc-difference 14 /note= "D-form residue"
 FT Misc-difference 15 /note= "D-form residue"
 FT Disulfide-bond 16. .21
 FT Misc-difference 18 /note= "D-form residue"
 FT Modified-site 22 /note= "C-terminal amide"
 FT

XX WO2003028527-A2.
 XX
 XX 10-APR-2003.
 XX
 XX 20-SEP-2002; 2002WO-US030143.
 XX
 XX 21-SEP-2001; 2001US-0323851P.
 XX
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX
 XX Coy DH, Fuselier JA, Murphy WA, Sun L;
 XX WPI; 2003-441067/41.
 XX
 XX Biologically active peptides such as somatostatin or bombesin conjugated
 XX to chemical compounds through linkers, useful for treating tumors of the
 XX lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 XX vessels.
 XX
 XX Example 19; Page 47; 86pp; English.
 XX
 XX The present sequence is that of somatostatin analogue peptide JP-08-73.
 XX It is an example of peptide agents of the invention that comprise a
 XX biologically active peptide, such as somatostatin or bombesin, conjugated
 XX to a chemical compound through a linker that maintains the peptide's
 XX biological activity. The peptide agents may also include a cytostatic or
 XX therapeutic agent, label or chelating group and a peptide that increases
 XX the hydrophilic biodistribution of the agent. They are useful for
 XX treating tumors of the lung, breast, brain, eye, prostate, or colon,
 XX tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
 XX angiogenic blood vessels (claimed). Other diseases that can also be
 XX treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
 XX arthritis, neoplastic cells or aberrantly proliferating cells, and
 XX acromegaly. Peptide JP-08-73 was used in an examination of the
 XX biodistribution of hydrophilic peptide agents. A lack of accumulation of
 XX radioactivity was noted in normal tissue including liver, but rapid and
 XX high efficiency elimination of the peptide agent in urine and faeces.
 XX Note: The present sequence is identified as SEQ ID 11 in the disclosure
 XX (page 14), but it is not the same as the sequence given as SEQ ID 11 in
 XX the sequence listing
 XX
 XX Sequence 22 AA;
 XX
 XX Query Match 71.2%; Score 57; DB 6; Length 22;
 XX Best Local Similarity 100.0%; Pred. No. 3.9;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 4 YCFWKTCCT 11
 XX |||||
 XX Db 15 YCFWKTCCT 22
 XX
 XX RESULT 37
 XX ABR42199
 XX ID ABR42199 standard; peptide; 25 AA.
 XX AC ABR42199;
 XX
 XX 28-JUL-2003 (first entry)
 XX
 XX Somatostatin analogue peptide.
 XX
 XX Somatostatin; peptide conjugate; cytostatic; antiangiogenic;
 XX antiinflammatory; antiarthritic; antirheumatic; cyclic.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal 3-N,N-dimethylaminobenzoic acid
 XX moiety, D-form residue"
 XX
 XX Misc-difference 2

FT Misc-difference 3 /note= "D-form residue"
 FT FT Misc-difference 4 /note= "D-form residue"
 FT FT Misc-difference 5 /note= "D-form residue"
 FT FT Misc-difference 6 /note= "D-form residue"
 FT FT Misc-difference 7 /note= "D-form residue"
 FT FT Misc-difference 8 /note= "D-form residue"
 FT FT Misc-difference 9 /note= "D-form residue"
 FT FT Misc-difference 10 /note= "D-form residue"
 FT FT Misc-difference 11 /note= "D-form residue"
 FT FT Misc-difference 12 /note= "D-form residue"
 FT FT Misc-difference 13 /note= "D-form residue"
 FT FT Misc-difference 14 /note= "D-form residue"
 FT FT Misc-difference 15 /note= "D-form residue"
 FT FT Misc-difference 17 /note= "D-form residue"
 FT FT Misc-difference 18 /note= "D-form residue"
 FT Disulfide-bond 19.24
 FT Misc-difference 21 /note= "D-form residue"
 FT Modified-site 25 /note= "C-terminal amide"
 FT
 XX WO2003028527-A2.
 XX
 XX 10-APR-2003.
 XX
 XX 20-SEP-2002; 2002WO-US030143.
 XX
 XX 21-SEP-2001; 2001US-0323851P.
 XX
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX
 XX Coy DH, Fuselier JA, Murphy WA, Sun L;
 XX WPI; 2003-441067/41.
 XX
 XX Biologically active peptides such as somatostatin or bombesin conjugated
 XX to chemical compounds through linkers, useful for treating tumors of the
 XX lung and breast, carcinoid syndrome, and tumors of angiogenic blood
 XX vessels.
 XX
 XX Example 26; Page 55; 86pp; English.
 XX
 XX The present sequence is that of a somatostatin analogue peptide. It is an
 XX example of peptide agents of the invention that comprise a biologically
 XX active peptide, such as somatostatin or bombesin, conjugated to a
 XX chemical compound through a linker that maintains the peptide's
 XX biological activity. The peptide agents may also include a cytostatic or
 XX therapeutic agent, label or chelating group and a peptide that increases
 XX the hydrophilic biodistribution of the agent. They are useful for
 XX treating tumors of the lung, breast, brain, eye, prostate, or colon,
 XX tumors of neuroendocrine origin (for e.g. carcinoid syndrome), and
 XX angiogenic blood vessels (claimed). Other diseases that can also be
 XX treated are inflammatory bowel disease, autoimmune disorders, rheumatoid
 XX arthritis, neoplastic cells or aberrantly proliferating cells, and
 XX acromegaly. The present peptide has the ability to inhibit growth hormone
 XX release from primary cultures of rat pituitary cells, having an IC50 of
 XX 0.27 nM (compared with 0.15 nM for somatostatin-14)

XX	SQ	Sequence 25 AA;
XX	FT	Misc-difference 26 /note= "D-form residue"
XX	FT	Modified-site 30
XX	FT	/note= "C-terminal amide"
XX	PV	WO2003028527-A2.
XX	PD	10-APR-2003..
XX	PP	20-SEP-2002; 2002WO-US030143.
XX	PR	21-SEP-2001; 2001US-0323851P.
XX	PA	(TULA) TULANE EDUCATIONAL FUND.
XX	PI	Coy DH, Fuselier JA, Murphy WA, Sun L;
XX	DR	WPI; 2003-441067/41.
XX	PT	Biologically active peptides such as somatostatin or bombesin conjugated to chemical compounds through linkers, useful for treating tumors of the lung and breast, carcinoid syndrome, and tumors of angiogenic blood vessels.
XX	PS	Example 26; Page 55; 86pp; English.
XX	CC	The present sequence is that of a somatostatin analogue peptide. It is an example of peptide agents of the invention that comprise a biologically active peptide, such as somatostatin or bombesin, conjugated to a chemical compound through a linker that maintains the peptide's biological activity. The peptide agents may also include a cytostatic or therapeutic agent, label or chelating group and a peptide that increases the hydrophilic biodistribution of the agent. They are useful for treating tumors of the lung, breast, brain, eye, prostate, or colon, tumours of neuroendocrine origin (for e.g. carcinoid syndrome), and angiogenic blood vessels (claimed). Other diseases that can also be treated are inflammatory bowel disease, autoimmune disorders, rheumatoid arthritis, neoplastic cells or aberrantly proliferating cells, and acromegaly
XX	SQ	Sequence 30 AA;
XX	Query Match	71.2%; Score 57; DB 6; Length 30;
XX	Best Local Similarity	100.0%; Pred.No. 5;
XX	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	Qy	4 YCFWKTCCT 11
XX	Dz	23 YCFWKTCCT 30
XX	RESULT 39	
XX	AAW48643	ID AAW48643 standard; peptide; 10 AA.
XX	AC	AAW48643;
XX	DT	04-AUG-1998 (first entry)
XX	DE	Somatostatin peptide analog WOC-3A.
XX	KW	Somatostatin; acromegaly; radiolocalisation; blood-brain barrier; cancer; halogen.
XX	OS	Synthetic.
XX	OS	Homo sapiens.
XX	FH	Key Location/Qualifiers
XX	FT	Misc-difference 3 /note= "D-form residue"
XX	FT	Disulfide-bond 4..9
XX	FT	Misc-difference 6 /note= "D-form residue"
XX	FT	Disulfide-bond 24..29
XX	SQ	Sequence 25 AA;
XX	Query Match	71.2%; Score 57; DB 6; Length 25;
XX	Best Local Similarity	100.0%; Pred.No. 4.3;
XX	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	Qy	4 YCFWKTCCT 11
XX	Dz	18 YCFWKTCCT 25
XX	RESULT 38	
XX	ABR42197	ID ABR42197 standard; peptide; 30 AA.
XX	AC	ABR42197;
XX	DT	28-JUL-2003 (first entry)
XX	DB	Somatostatin analogue peptide.
XX	KW	Somatostatin; peptide conjugate; cytostatic; antiangiogenic; antinflammatory; antiarthritic; antirheumatic; cyclic.
XX	OS	Synthetic.
XX	FH	Key Location/Qualifiers
XX	FT	Misc-difference 1 /note= "D-form residue"
XX	FT	Misc-difference 2 /note= "D-form residue"
XX	FT	Misc-difference 3 /note= "D-form residue"
XX	FT	Misc-difference 4 /note= "D-form residue"
XX	FT	Misc-difference 5 /note= "D-form residue"
XX	FT	Misc-difference 6 /note= "D-form residue"
XX	FT	Misc-difference 7 /note= "D-form residue"
XX	FT	Misc-difference 8 /note= "D-form residue"
XX	FT	Misc-difference 9 /note= "D-form residue"
XX	FT	Misc-difference 10 /note= "D-form residue"
XX	FT	Misc-difference 11 /note= "D-form residue"
XX	FT	Misc-difference 12 /note= "D-form residue"
XX	FT	Misc-difference 13 /note= "D-form residue"
XX	FT	Misc-difference 14 /note= "D-form residue"
XX	FT	Misc-difference 15 /note= "D-form residue"
XX	FT	Misc-difference 16 /note= "D-form residue"
XX	FT	Misc-difference 17 /note= "D-form residue"
XX	FT	Misc-difference 18 /note= "D-form residue"
XX	FT	Misc-difference 19 /note= "D-form residue"
XX	FT	Misc-difference 20 /note= "D-form residue"
XX	FT	Misc-difference 22 /note= "D-form residue"
XX	FT	Misc-difference 23 /note= "D-form residue"
XX	FT	Disulfide-bond 24..29

FT Modified-site 10
 FT /note= "C-terminal amide"
 FN WO9639161-A1.
 XX 12-DEC-1996.
 XX
 XX 03-JUN-1996; 96WO-US008437.
 XX
 XX 05-JUN-1995; 95US-00462223.
 XX
 XX (TULA) TULANE EDUCATIONAL FUND.
 PA (OHIS) UNIV OHIO STATE RES FOUND.
 PA (LOU) UNIV LOUISIANA STATE MEDICAL CENT FOUND.
 PA (CHIL-) CHILDRENS HOSPITAL INC.
 XX
 PI Coy DH, Woltering EA, Odorizio MS, Odorizio TM, Murphy WA;
 XX WPI; 1997-042842/04.
 DR
 XX Multi-tyrosinated somatostatin analogues - useful for diagnosis and
 XX treatment of diseases related to altered somatostatin receptor
 FT expression.
 FT
 XX Claim 7; Page 60; 63pp; English.
 FS
 XX The invention provides for conventional somatostatin analogues (AAW48638-
 CC W48640 and AAW48664) and multi-tyrosinated analogues (AAW48641-W48645)
 CC such as the present one. The multi-tyrosinated somatostatin analogues
 CC bind to somatostatin receptors with practically the same affinity as
 CC native somatostatin. The somatostatin analogues are claimed to be useful
 CC for treating disease associated with increased production of factors
 CC which can be regulated by somatostatin, e.g. acromegaly. Also when
 CC radioactively labelled, the analogues are claimed to be useful for
 CC diagnosing cancer in vitro or in situ where aberrant expression of
 CC somatostatin receptors is involved. When halogenated, these analogues are
 CC found to bind somatostatin receptors with such high affinity that binding
 CC is nearly irreversible under physiological conditions. Therefore, by
 CC using radioactive halogenated analogues, the invention claims for
 CC improved sensitivity of radiolocalisation of the receptors. Multi-
 CC tyrosinated analogues have increased half-lives in vivo relative to
 CC conventional somatostatin analogues, are resistant to enzymatic
 CC degradation and have increased blood-brain barrier penetration
 XX
 SQ Sequence 10 AA;

Query Match 70.0%; Score 56; DB 2; Length 10;
 Best Local Similarity 70.0%; Pred. No. 2.8;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YCYCFWKTCT 11
 | | | | | | | | | |
 Db 1 YAYCYWKTCT 10

RESULT 40
 ID ADU05266 standard; peptide; 10 AA.
 XX
 AC ADU05266;
 XX
 XX 13-JAN-2005 (first entry)
 XX
 XX Cyclic somatostatin-dopamine chimeric peptide analogue #56.
 XX somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective tissue disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytosstatic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antiulcer;

KW antiarrhythmic; nephrotropic; hepatotropic; antilipemic; analgesic;
 KW antiangiinal; anorectic; immunomodulator; cardiant; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "An N-terminal dopamine derivative (Dop1, Dop2 or
 FT Dop5) is attached to a Lys (dopamine derivative) modified
 FT residue, where this second dopamine derivative must match
 FT the type occurring at the N-terminus, e.g. Dop1-
 FT Lys (Dop1), Dop2-Lys (Dop2) etc. Optionally Lys can be a D-
 FT form residue."
 FT Misc-difference 2
 FT /note= "D-form residue"
 FT Misc-difference 3
 FT /note= "D-form residue"
 FT Disulfide-bond 4.9
 FT /note= This disulphide bond cyclises the peptide
 FT Modified-site 5
 FT /label= 3-iodo tyrosine
 FT Misc-difference 6
 FT /note= "D-form residue"
 FT Modified-site 10
 FT /note= "C-terminal amide"
 FT
 XX WO2004091490-A2.
 XX
 XX 28-OCT-2004.
 XX
 XX 08-APR-2004; 2004WO-US010891.
 XX
 XX 11-APR-2003; 2003US-0462374P.
 XX
 XX (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX
 XX Dong ZX, Dewitt Culler M, Shen Y;
 XX WPI; 2004-784484/77.
 XX
 XX New chimeric analog comprising at least one moiety which binds to one or
 XX more somatostatin and dopamine receptor(s) useful to treat e.g.
 XX neuroendocrine tumor, vascular diseases, connective tissue disease,
 XX immune disease and cachexia.
 XX
 PS Claim 12; Page 115; 138pp; English.
 XX
 CC This invention relates to novel somatostatin-dopamine chimeric analogues
 CC that comprise at least one moiety that binds to one or more somatostatin
 CC receptors and at least one moiety that binds to one or more dopamine
 CC receptors, or a salt derived thereof. Specifically, it refers to
 CC analogues that may be used in vitro or in vivo for research, diagnostic
 CC and therapeutic agents to enhance the activity of somatostatin and
 CC dopamine i.e. working as receptor agonists. The present invention
 CC describes analogues with specificity for different types of somatostatin
 CC receptor subtypes that are accordingly associated with the treatment of
 CC particular diseases or conditions. As such, these analogues may be used
 CC to treat neoplasia and acromegaly as well as various neuroendocrine
 CC tumours, vascular diseases e.g. angiogenesis, connective diseases e.g.
 CC scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal
 CC tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g.
 CC hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic
 CC disorder or an opioid overdose. Accordingly, they exhibit activities that
 CC include cytostatic, osteopathic, antithyroid, vasotropic, antiangiogenic,
 CC ophthalmological, antidiabetic, dermatological, immunosuppressive,
 CC antiarthritic, antirheumatic, antiinflammatory, antiulcer,
 CC antiarrhythmic, nephrotropic, hepatotropic, antilipemic, analgesic,
 CC antiangiinal, anorectic, immunomodulator, cardiant, tranquilizer and
 CC antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric
 XX analogue of the invention.
 XX Sequence 10 AA;

Query Match 67.5%; Score 54; DB 8; Length 10;
 Best Local Similarity 87.5%; Pred. No. 4.8;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YCFWKTCCT 11
 Db 3 YCYWKTCCT 10

RESULT 41
 ID ADU05270 standard; peptide; 11 AA.
 XX AC ADU05270;
 XX DT 13-JAN-2005 (first entry)
 XX DB Cyclic somatostatin-dopamine chimeric peptide analogue #60.
 XX KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytotatic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antitumor;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipemic; analgesic;
 KW antiangular; anorectic; immunomodulator; cardiant; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX OS Synthetic.

Key 1 Location/Qualifiers
 Modified-site 1 /note= "An N-terminal dopamine derivative (Dop1, Dop2 or Dop5) is attached to a Lys(dopamine derivative) modified residue, where this second dopamine derivative must match the type occurring at the N-terminus, e.g. Dop1-Lys(Dop1), Dop2-Lys(Dop2) etc. Optionally Lys can be a D-form residue."
 Misc-difference 3 /note= "D-form residue"
 Misc-difference 4 /note= "D-form residue"
 Disulfide-bond 5..10 /note= "This disulphide bond cyclises the peptide"
 Modified-site 6 /label= 3-iodo tyrosine
 Misc-difference 7 /note= "D-form residue"
 Modified-site 11 /note= "C-terminal amide"
 XX WO2004091490-A2.
 XX PD 28-OCT-2004.
 XX PF 08-APR-2004; 2004WO-US010891.
 XX PR 11-APR-2003; 2003US-0462374P.
 XX PA (SCRC) SAS SOC CONSEILS RECH & APPL SCI.
 XX PI Dong ZX, Dewitt Culler M, Shen Y;
 XX DR WPI, 2004-784484/77.
 XX New chimeric analog comprising at least one moiety which binds to one or more somatostatin and dopamine receptor(s) useful to treat e.g. neuroendocrine tumor, vascular diseases, connective tissue disease, immune disease and cachexia.

XX PS Claim 12; Page 115; 138pp; English.
 XX CC This invention relates to novel somatostatin-dopamine chimeric analogues that comprise at least one moiety that binds to one or more somatostatin receptors and at least one moiety that binds to one or more dopamine receptors, or a salt derived thereof. Specifically, it refers to analogues that may be used in vitro or in vivo for research, diagnostic and therapeutic agents to enhance the activity of somatostatin and dopamine i.e. working as receptor agonists. The present invention describes analogues with specificity for different types of somatostatin receptor subtypes that are accordingly associated with the treatment of particular diseases or conditions. As such, these analogues may be used to treat neoplasia and acromegaly as well as various neuroendocrine tumours, vascular diseases e.g. angiogenesis, connective diseases e.g. scleroderma, immune diseases e.g. rheumatoid arthritis, gastrointestinal tract disorders e.g. irritable bowel syndrome, metabolic diseases e.g. hyperlipidaemia, cachexia, cancer, a musculoskeletal disorder, panic disorder or an opioid overdose. Accordingly, they exhibit activities that include cytostatic, osteopathic, antithyroid, vasotropic, antiangiogenic, ophthalmological, antidiabetic, dermatological, immunosuppressive, antiarthritic, antirheumatic, antiinflammatory, antitumor, antidiarrhoeic, nephrotropic, hepatotropic, antilipemic, analgesic, antiangular, anorectic, immunomodulator, cardiant, tranquilizer and antiaddictive. This peptide sequence is a somatostatin-dopamine chimeric analogue of the invention.

XX SQ Sequence 11 AA;
 Query Match 67.5%; Score 54; DB 8; Length 11;
 Best Local Similarity 87.5%; Pred. No. 5.1;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YCFWKTCCT 11
 Db 4 YCYWKTCCT 11

RESULT 42
 ID ADU05281 standard; peptide; 11 AA.
 XX AC ADU05281;
 XX DT 13-JAN-2005 (first entry)
 XX DB Cyclic somatostatin-dopamine chimeric peptide analogue #71.
 XX KW somatostatin-dopamine chimeric analogue; agonist; cyclic;
 KW vascular disease; angiogenesis; connective disease; scleroderma;
 KW immune disease; rheumatoid arthritis; gastrointestinal tract disorder;
 KW irritable bowel syndrome; metabolic disease; hyperlipidaemia; cachexia;
 KW cancer; musculoskeletal disorder; panic disorder; opioid overdose;
 KW cytotatic; osteopathic; antithyroid; vasotropic; antiangiogenic;
 KW ophthalmological; antidiabetic; dermatological; immunosuppressive;
 KW antiarthritic; antirheumatic; antiinflammatory; antitumor;
 KW antidiarrhoeic; nephrotropic; hepatotropic; antilipemic; analgesic;
 KW antiangular; anorectic; immunomodulator; cardiant; tranquilizer;
 KW antiaddictive; acromegaly; neoplasia; neuroendocrine tumour.
 XX OS Synthetic.

Key 1 Location/Qualifiers
 Modified-site 1 /note= "An N-terminal dopamine derivative (Dop2) is attached to a Lys(dopamine derivative) modified residue, where this second dopamine derivative must match the type occurring at the N-terminus, i.e. Dop2-Lys(Dop2). Optionally Lys can be a D-form residue."
 Modified-site 2 /label= OTHER
 /note= "OTHER= Aepa, 4-(2-aminoethyl)-1-carboxy methyl-piperazine"


```
FT Disulfide-bond 2. .7
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 8 /label= THR, OTHER
FT /note= "THR-ol"
XX
XX EP29579-A.
XX
XX 03-JUN-1981.
XX
XX 27-NOV-1979; 79CH-00010524.
XX
XX 27-NOV-1979; 79CH-00010524.
XX
XX 13-JUN-1980; 80CH-00004574.
XX
XX (SANO ) SANDOZ AG.
XX
XX Bauer W, Pless J;
XX
XX WPI; 1981-42362D/24.
XX
XX Polypeptide(s) contg. cysteine-terminal hexa:peptide fragment - useful as
XX growth-hormone, gastric and pancreatic secretion inhibitors.
XX
XX Example 12; Page 24; 35pp; English.
XX
XX The peptide inhibits growth hormone secretion and can be used to treat
XX diabetes, angiodopathy and acromegaly. It also inhibits gastric and
XX pancreatic secretion and can be used to treat gastrointestinal disorders
XX
XX Sequence 8 AA;
XX
XX Query Match 66.2%; Score 53; DB 1; Length 8;
XX Best Local Similarity 87.5%; Pred. No. 2e+06;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 YCFWKTCT 11
XX :|||||
XX 1 FCFWKTCT 8
XX
XX RESULT 45
XX AAP20161
XX ID AAP20161 standard; peptide; 8 AA.
XX
XX AC AAP20161;
XX
XX DT 02-DEC-1992 (first entry)
XX
XX DE Peptide for inhibiting somatotropin secretion, and gastric and pancreatic
XX secretions.
XX
XX Somatotropin; gastric; pancreatic; hormone; protein secretion;
XX disulfide bond; diabetes mellitus; angiodopathy; acromegalia; ulcer;
XX acute pancreatis.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 1 /label= CH3(CH2)8-CO-D-Phe
XX Disulfide-bond 2. .7
XX Misc-difference 4 /label= D-Trp
XX Misc-difference 8 /label= Thr-ol
XX
XX BE892315-A.
XX
XX 01-SEP-1982.
XX
XX 06-MAR-1981; 81CH-00001531.
XX
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XX 06-MAR-1981; 81CH-00001531.
XX 04-SEP-1981; 81CH-00005723.
XX
XX (SANO ) SANDOZ AG.
XX
XX WPI; 1982-76690E/37.
XX
XX Polypeptide derivs. contg. two cysteine residues - inhibiting secretion
XX of growth hormone and gastric and pancreatic secretions.
XX
XX Claim 6; Page 23; 27pp; French.
XX
XX The peptide inhibits the secretion of somatotropin and so can be used to
XX treat diabetes mellitus, angiodopathy and acromegalia. It also inhibits
XX gastric and pancreatic secretions so is useful in the treatment of
XX gastric ulcers, gastro-intestinal bleeding and acute pancreatitis
XX
XX Sequence 8 AA;
XX
XX Query Match 66.2%; Score 53; DB 1; Length 8;
XX Best Local Similarity 87.5%; Pred. No. 2e+06;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 YCFWKTCT 11
XX :|||||
XX 1 FCFWKTCT 8
XX
XX RESULT 46
XX AAP40368
XX ID AAP40368 standard; peptide; 8 AA.
XX
XX AC AAP40368;
XX
XX DT 10-MAR-2003 (revised)
XX 11-FEB-1992 (first entry)
XX
XX DE Sequence of growth hormone secretion inhibitor.
XX
XX Diabetes therapy; angiodopathy; acromegalia; gastric ulcer; pancreatitis.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /label= benzyl-D-Phe
XX Disulfide-bond 2. .7
XX Modified-site 4 /label= D-Trp
XX Modified-site 8 /label= Thr-ol
XX
XX BE897546-A.
XX
XX 17-FEB-1984.
XX
XX 17-AUG-1983; 83BE-00897546.
XX
XX 24-AUG-1982; 82CH-00005031.
XX
XX (SANO ) SANDOZ SA.
XX
XX WPI; 1984-049502/09.
XX
XX Polypeptide(s) contg. a hepta:peptide defined fragment - are growth
XX hormone secretion inhibitors, used to treat ulcers, diabetes, angiodopathy,
XX acromegalia etc.
XX
XX Claim 4; Page 23; 28pp; French.
XX
XX The peptides of the invention are used in the treatment of diabetes,
XX angiodopathy, acromegalia and gastro-intestinal disorders, such as gastric
XX
```

CC ulcers, gastro-intestinal haemorrhage and acute pancreatitis. They are
 CC administered in daily doses of 2.0 mcg-10 mg as 2-4 unit doses of 0.5 mcg
 CC -5 mg. (Updated on 10-MAR-2003 to add missing OS field.)
 XX
 SQ Sequence 8 AA;

Query Match 66.2%; Score 53; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. NO. 2e+06;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
 :|||||
 Db 1 FCFWKTCCT 8

RESULT 47
 AAP50504
 ID AAP50504 standard; peptide; 8 AA.

XX AAP50504;

AC 08-DEC-1991 (first entry)

DT Mini-somatostatin derived from natural tetradecapeptide somatostatin.

DE Mini-somatostatin; somatostatin; hormone; Alzheimer disease;
 XX senile dementia; ss.

KW Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /label= D-Phe

FT Disulfide-bond 2..7

FT Modified-site 4

FT /label= D-Trp

XX BE900089-A.

XX 07-JAN-1985.

XX 05-JUL-1984; 84BE-00900089.

XX 08-JUL-1983; 83GB-00018552.

XX (SANO) SANDOZ SA.

XX Reubi JC, Palacios J;

XX WPI; 1985-018747/04.

XX Use of mini:somatostatin(s) - to treat evolutive senile dementia.

XX Claim 2; Page 13; 16pp; French.

XX The mini-somatostatin is derived from the natural tetradecapeptide
 CC somatostatin and contain 1 or more of the peptide sequences of this
 CC material either intact or as derivatives. It may be used to treat e.g.
 CC Alzheimer's disease. It may be given parenterally at a unit dose of
 CC 0.0005-1 mg in combination with glucose. See also AAP50505-07

XX Sequence 8 AA;

Query Match 66.2%; Score 53; DB 1; Length 8;

Best Local Similarity 87.5%; Pred. NO. 2e+06;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11

:|||||

Db 1 FCFWKTCCT 8

RESULT 48

AAP82525
 ID AAP82525 standard; peptide; 8 AA.

XX AAP82525;

XX 12-DEC-1990 (first entry)

DT Bridged somatostatin analog.

DE bridged somatostatin analog; peripherally mediated pain treatment;

XX analgesic agents.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 2..7

FT /note= "intramolecular."

XX EP255224-A.

XX 03-FEB-1988.

XX 23-JUN-1987; 87EP-00305551.

XX 30-JUN-1986; 86US-00880536.

XX (MERI) MERCK & CO INC.

XX Dallob AL, Moore VL, Goldenberg MM;

XX WPI; 1988-030436/05.

XX Use of cyclic and bridged cyclic somatostatin analog use - for prepn. of
 CC medicament for treating peripherally mediated pain.

XX Claim 1; Page 9; 11pp; English.

XX Phe(1) is in the D-form and Trp(4) is in the D-form. Analog is useful as
 CC analgesic. See also AAP82526-P82540

XX Sequence 8 AA;

Query Match 66.2%; Score 53; DB 1; Length 8;

Best Local Similarity 87.5%; Pred. NO. 2e+06;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11

:|||||

Db 1 FCFWKTCCT 8

RESULT 49

AAR05177

ID AAR05177 standard; peptide; 8 AA.

XX AAR05177;

XX 04-NOV-2004 (revised)

XX 25-MAR-2003 (revised)

XX 10-MAR-2003 (revised)

XX 11-OCT-1990 (first entry)

XX Somatostatin analogue or deriv. used as lung damage protectant.

XX Somatostatin; lung damage protection; respiratory distress syndrome;
 CC oxygen therapy.

XX Homo sapiens.

XX Unidentified.

XX Key Location/Qualifiers

FT Disulfide-bond 2..7

PN DE3937539-A.
 XX 31-MAY-1990.
 XX 10-NOV-1989; 89DE-03937539.
 XX 11-NOV-1988; 88DE-03838380.
 XX (SANO) SANDOZ AG.
 XX Chrubasik J, Chrubasik S;
 XX WPI; 1990-172518/23.
 XX Somatostatin and its analogues or derivs. - used for protection against
 PT lung damage, esp. respiratory distress syndrome or damage caused by
 PT oxygen therapy.
 XX Claim 5; Page 17; 18pp; German.
 CC Residues Phe and Trp at positions 1 and 4 are D-Phe and D-Trp. An H is
 CC attached to D-Phe and OH to Thr. Derivs of this sequence substd. on the N
 CC -terminal amino gp. by N alpha-(alpha-glucosyl(1-4)deoxyfructosyl) or N
 CC alpha-(beta-deoxyfructosyl) are pref. for oral administration. The cpds.
 CC are esp. used to prevent, inhibit or treat respiratory distress syndrome
 CC in children and adults, and to inhibit or treat lung damage caused by
 CC oxygen therapy. Opt. they are formulated with a glucocorticoid steroid.
 CC The y are also known to inhibit release of growth hormone, insulin, and
 CC glucagon, and to reduce gastric secretions. See also AAR05177-80,
 CC AAR05182-88, AAR05191-95, AAR06530 and AAR05197. (Updated on 10-MAR-2003
 CC to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)
 CC Revised record issued on 04-NOV-2004 : Correction to Feature table key
 XX Sequence 8 AA;
 SQ Query Match 66.2%; Score 53; DB 2; Length 8;
 Best Local Similarity 87.5%; Pred. No. 2e+06;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YCFWKTCCT 11
 Db :|||||
 1 FCFWKTCCT 8
 RESULT 50
 AAR05188
 ID AAR05188 standard; protein; 8 AA.
 XX AAR05188;
 XX 04-NOV-2004 (revised)
 DT 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 11-OCT-1990 (first entry)
 XX Somatostatin analogue or deriv. used as lung damage protectant.
 DE Somatostatin; lung damage protection; respiratory distress syndrome;
 XX oxygen therapy.
 KW Homo sapiens.
 OS Unidentified.
 XX Key Location/Qualifiers
 FH Disulfide-bond 2..7
 FT
 XX DE3937539-A.
 PN 31-MAY-1990.
 XX 10-NOV-1989; 89DE-03937539.
 XX

PR 11-NOV-1988; 88DE-03838380.
 XX (SANO) SANDOZ AG.
 PA Chrubasik J, Chrubasik S;
 XX WPI; 1990-172518/23.
 XX Somatostatin and its analogues or derivs. - used for protection against
 PT lung damage, esp. respiratory distress syndrome or damage caused by
 PT oxygen therapy.
 XX Disclosure; Page; 18pp; German.
 CC Residues Phe and Trp at positions 1 and 4 are D-Phe and D-Trp. An H is
 CC attached to D-Phe and OH to Thr. Derivs of this sequence substd. on the N
 CC -terminal amino gp. by N alpha-(alpha-glucosyl(1-4)deoxyfructosyl) or N
 CC alpha-(beta-deoxyfructosyl) are pref. for oral administration. The cpds.
 CC are esp. used to prevent, inhibit or treat respiratory distress syndrome
 CC in children and adults, and to inhibit or treat lung damage caused by
 CC oxygen therapy. Opt. they are formulated with a glucocorticoid steroid.
 CC The y are also known to inhibit release of growth hormone, insulin, and
 CC glucagon, and to reduce gastric secretions. See also AAR05177-80,
 CC AAR05182-88, AAR05191-95, AAR06530 and AAR05197. (Updated on 10-MAR-2003
 CC to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)
 CC Revised record issued on 04-NOV-2004 : Correction to Feature table key
 XX Sequence 8 AA;
 SQ Query Match 66.2%; Score 53; DB 2; Length 8;
 Best Local Similarity 87.5%; Pred. No. 2e+06;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YCFWKTCCT 11
 Db :|||||
 1 FCFWKTCCT 8
 Search completed: May 9, 2006, 12:08:19
 Job time : 59.6667 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:05:35 ; Search time 19.3333 Seconds
(without alignments)
54.744 Million cell updates/sec

Title: US-10-796-158-7

Perfect score: 80

Sequence: 1 YYCYCFWKTCT 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	58.8	1910	2 H88124	protein T12C9.3 [i
2	46	57.5	501	2 S51160	nitrate reductase
3	46	57.5	617	2 S19254	nitrate reductase
4	46	57.5	881	2 S25445	nitrate reductase
5	46	57.5	886	2 A59223	nitrate reductase
6	46	57.5	889	2 T02240	nitrate reductase
7	46	57.5	890	2 T11805	nitrate reductase
8	46	57.5	891	1 RDBHNP	nitrate reductase
9	46	57.5	898	1 RDBJNH	nitrate reductase
10	46	57.5	900	2 S47029	nitrate reductase
11	46	57.5	904	1 RDNTNS	nitrate reductase
12	46	57.5	904	1 RDNTNT	nitrate reductase
13	46	57.5	909	2 JN0665	nitrate reductase
14	46	57.5	911	1 RDTONH	nitrate reductase
15	46	57.5	912	1 RDBHNS	nitrate reductase
16	46	57.5	915	1 RDBHNN	nitrate reductase
17	46	57.5	918	2 A41667	nitrate reductase
18	46	57.5	920	2 S52301	nitrate reductase
19	45	56.2	152	1 VGBEY9	early glycoprotein
20	44	55.0	332	2 A81667	conserved hypother
21	44	55.0	332	2 B71508	hypothetical prote
22	44	55.0	334	2 G86565	CT484 hypothetical
23	44	55.0	334	2 D72057	conserved hypother
24	43	53.8	285	2 AG1214	methylases homolog
25	43	53.8	710	2 T52573	cyclic nucleotide
26	42	52.5	859	1 S65938	nitrate reductase
27	42	52.5	911	2 T08105	nitrate reductase
28	42	52.5	911	2 T08108	nitrate reductase
29	42	52.5	917	1 RDMUNH	nitrate reductase

30	42	52.5	917	2 B96807	nitrate reductase
31	42	52.5	917	2 S35228	nitrate reductase
32	42	52.5	926	1 RDSPNH	nitrate reductase
33	42	52.5	1839	1 RRWPEM	genome polyprotein
34	41	51.2	108	2 S19112	Ig kappa chain V r
35	41	51.2	115	1 KVMSK2	Ig kappa chain pre
36	41	51.2	218	2 T03383	zinc-induced prote
37	41	51.2	552	2 T23755	hypothetical prote
38	41	51.2	716	2 JQ1366	polyprotein - hepa
39	41	51.2	894	2 S52857	nitrate reductase
40	41	51.2	1428	2 T39475	mucin 2, intestina
41	41	51.2	1513	2 A54895	hypothetical prote
42	40	50.0	76	2 T28486	C7L protein - vari
43	40	50.0	121	2 F72156	hypothetical prote
44	40	50.0	121	2 T43130	Ig kappa chain pre
45	40	50.0	234	2 S01320	hypothetical prote
46	40	50.0	247	2 T27205	rod shape-determ
47	40	50.0	304	2 C71637	hypothetical prote
48	40	50.0	512	2 T30924	nitrate reductase
49	40	50.0	859	2 S70584	nitrate reductase
50	40	50.0	867	1 JQ1525	nitrate reductase
51	40	50.0	868	1 JC4283	nitrate reductase
52	40	50.0	884	2 S66308	nitrate reductase
53	40	50.0	893	2 S46442	nitrate reductase
54	40	50.0	905	1 JN0803	nitrate reductase
55	40	50.0	982	1 S16292	nitrate reductase
56	40	50.0	1787	2 AC2009	serine/threonine k
57	40	50.0	1800	2 A11918	serine/threonine k
58	39.5	49.4	186	1 B48560	U155 protein - hum
59	39.5	49.4	186	1 WMBEXB	U155 protein - hum
60	39.5	49.4	186	1 WMBEXB	U155 protein - hum
61	39	48.8	115	2 T33473	hypothetical prote
62	39	48.8	120	2 B69971	conserved hypother
63	39	48.8	130	2 T22920	hypothetical prote
64	39	48.8	173	2 D58893	NADH2 dehydrogen
65	39	48.8	212	2 C87585	hypothetical prote
66	39	48.8	215	2 A49677	endoplasmic reticu
67	39	48.8	301	2 AB0164	FecCD transport fa
68	39	48.8	311	2 T27203	hypothetical prote
69	39	48.8	317	2 B86183	hypothetical prote
70	39	48.8	337	2 T20644	hypothetical prote
71	39	48.8	426	2 S28374	genome polyprotein
72	39	48.8	464	2 A81247	glutamyl-tRNA synt
73	39	48.8	464	2 F82019	glutamate-tRNA lig
74	39	48.8	490	2 C70146	glutamate-tRNA lig
75	39	48.8	532	2 T28784	hypothetical prote
76	39	48.8	654	2 AH2445	hypothetical prote
77	39	48.8	738	2 E86294	hypothetical prote
78	39	48.8	844	1 T05179	S-receptor kinase
79	39	48.8	1045	2 JC5795	CDEP protein - hum
80	39	48.8	1046	2 T26384	hypothetical prote
81	39	48.8	2021	2 AD2267	serine/threonine k
82	39	48.8	2057	2 F90109	splicing factor Pr
83	39	48.8	2214	2 T16305	hypothetical prote
84	38.5	48.1	52	2 S66609	neurotoxin AaH IT4
85	38.5	48.1	65	2 A38394	melanin inhibito
86	38	47.5	12	1 UOQ82	urotensin II - lon
87	38	47.5	12	2 JS0423	urotensin II-A pep
88	38	47.5	12	2 S42765	urotensin II - tel
89	38	47.5	12	2 JS0424	urotensin II-B pep
90	38	47.5	13	2 PQ0445	urotensin II - lau
91	38	47.5	83	2 S10706	urotensin II precu
92	38	47.5	83	2 T03673	pit1 protein (clon
93	38	47.5	125	2 T50499	urotensin II-gamma
94	38	47.5	125	2 T50498	cholecystokinin B
95	38	47.5	163	2 S48050	hypothetical prote
96	38	47.5	177	2 S74636	hypothetical prote
97	38	47.5	197	2 T38235	hypothetical prote
98	38	47.5	246	2 T28166	hypothetical prote
99	38	47.5	285	2 S76841	hypothetical prote
100	38	47.5	401	2 S37815	aureobasidin A res
101	38	47.5	493	2 JC5486	membrane glycoprot
102	38	47.5	574	2 B84958	arginine-tRNA liga

103 38 47.5 616 2 T29234 hypothetical prote
104 38 47.5 650 2 A34498 glycoprotein anti
105 38 47.5 870 2 G96790 hypothetical prote
106 38 47.5 840 2 T33217 hypothetical prote
107 38 47.5 1804 2 AF2250 serine/threonine k
108 38 47.5 2105 1 A44059 genome polypeptide
109 38 47.5 2229 2 T16199 hypothetical prote
110 38 47.5 2233 2 T28669 surface protein 51
111 37.5 46.9 54 2 D37847 hypothetical prote
112 37.5 46.9 140 2 T01027 hypothetical prote
113 37.5 46.9 682 1 JH0560 cyclic nucleotide-
114 37 46.2 50 2 B60512 phospholipase A2
115 37 46.2 50 2 D60512 phospholipase A2
116 37 46.2 51 2 A60512 phospholipase A2
117 37 46.2 52 2 C60512 phospholipase A2
118 37 46.2 52 2 C6279 phospholipase A2
119 37 46.2 60 1 H3NJ3E cytoxin 3 - cbr
120 37 46.2 106 2 A11428 thioredoxin homolo
121 37 46.2 106 2 A1802 thioredoxin homolo
122 37 46.2 117 2 A34860 phospholipase A2
123 37 46.2 117 2 A2416 phospholipase A2
124 37 46.2 118 1 P8BGA phospholipase A2
125 37 46.2 118 1 P8SNT phospholipase A2
126 37 46.2 118 2 B34860 phospholipase A2
127 37 46.2 118 2 B34860 phospholipase A2
128 37 46.2 118 2 C34860 phospholipase A2
129 37 46.2 118 2 E34860 phospholipase A2
130 37 46.2 118 2 G34860 phospholipase A2
131 37 46.2 118 2 H34860 phospholipase A2
132 37 46.2 119 1 P8B2H phospholipase A2
133 37 46.2 119 1 P8NOA5 phospholipase A2
134 37 46.2 120 2 S13019 phospholipase A2
135 37 46.2 121 1 P8B2C phospholipase A2
136 37 46.2 121 2 S17860 phospholipase A2
137 37 46.2 121 1 P8SAE phospholipase A2
138 37 46.2 122 1 P8SAE phospholipase A2
139 37 46.2 122 1 P8VII phospholipase A2
140 37 46.2 122 2 A53872 phospholipase A2
141 37 46.2 122 2 A3290 phospholipase A2
142 37 46.2 122 2 S46979 phospholipase A2
143 37 46.2 122 2 S33267 phospholipase A2
144 37 46.2 122 2 S62780 phospholipase A2
145 37 46.2 122 2 S62781 phospholipase A2
146 37 46.2 122 2 S09314 phospholipase A2
147 37 46.2 123 2 B53872 phospholipase A2
148 37 46.2 124 2 A59420 phospholipase A2
149 37 46.2 124 2 A59420 phospholipase A2
150 37 46.2 124 2 S1190 phospholipase A2
151 37 46.2 127 2 S22388 phospholipase A2
152 37 46.2 138 1 I51381 phospholipase A2
153 37 46.2 138 1 P8RSB2 phospholipase A2
154 37 46.2 138 1 P8RSBT phospholipase A2
155 37 46.2 138 1 P8TVIF phospholipase A2
156 37 46.2 138 2 A49959 phospholipase A2
157 37 46.2 138 2 A48188 phospholipase A2
158 37 46.2 138 2 A46169 phospholipase A2
159 37 46.2 138 2 S23299 phospholipase A2
160 37 46.2 138 2 S25298 phospholipase A2
161 37 46.2 138 2 S59522 phospholipase A2
162 37 46.2 138 2 I50098 phospholipase A2
163 37 46.2 192 2 T15484 hypothetical prote
164 37 46.2 208 2 T41710 hypothetical prote
165 37 46.2 231 2 AD0773 hypothetical prote
166 37 46.2 231 2 T16020 hypothetical prote
167 37 46.2 384 2 F64338 hypothetical prote
168 37 46.2 501 2 T23011 pre-mrna splicing
169 37 46.2 558 2 T40651 protein M0G5.5 li
170 37 46.2 559 2 F88392 hypothetical prote
171 37 46.2 559 2 T33425 hypothetical prote
172 37 46.2 617 2 T23082 hypothetical prote
173 37 46.2 723 2 H85092 hypothetical prote
174 37 46.2 736 2 S47645 TMDC I protein - c
175 37 46.2 957 2 T03829 transcription fact

176 37 46.2 978 2 T03763 hypothetical prote
177 37 46.2 998 2 T09492 glycoprotein anti
178 37 46.2 1016 1 JS0428 hypothetical prote
179 37 46.2 1360 2 T12064 hypothetical prote
180 37 46.2 1776 1 RRWPYM serine/threonine k
181 37 46.2 1946 2 AC2141 genome polypeptide
182 37 46.2 2155 2 T30197 hypothetical prote
183 37 46.2 2481 2 A43908 fibronectin - Afri
184 36.5 45.6 123 2 S70222 hypothetical prote
185 36.5 45.6 262 2 T01562 hypothetical prote
186 36.5 45.6 343 2 T29547 hypothetical prote
187 36.5 45.6 581 2 B90539 hypothetical prote
188 36.5 45.6 875 2 T33434 hypothetical prote
189 36.5 45.6 1487 2 T02850 hypothetical prote
190 36 45.0 37 2 B95134 cytoxin 1 - cbr
191 36 45.0 60 1 H3NJ1B cytoxin 1 - Moza
192 36 45.0 60 1 H3NJ1M cytoxin 1 - Cape
193 36 45.0 60 1 H3NJ2C cytoxin 2 - cbr
194 36 45.0 60 1 H3NJ2E cytoxin 2 - Moza
195 36 45.0 60 1 H3NJ2M cytoxin 2 - Cape
196 36 45.0 60 1 H3NJ3C cytoxin 3 - Moza
197 36 45.0 60 1 H3NJ3M cytoxin 3 - Cape
198 36 45.0 60 1 H3NJ4E cytoxin 4 - cbr
199 36 45.0 60 1 H3NJ5B cytoxin 5 - Egyp
200 36 45.0 60 1 H3NJ5Y cytoxin 5 - Egyp
201 36 45.0 60 1 H3NJ6E cytoxin 6 - cbr
202 36 45.0 60 1 H3NJ6M cytoxin 6 - minor
203 36 45.0 60 1 H3NJ7E cytoxin 7 - cbr
204 36 45.0 60 1 H3NJ7M cytoxin 7 - minor
205 36 45.0 60 1 H3NJ8E cytoxin 8 - cbr
206 36 45.0 60 1 H3NJ8E cytoxin 3, minor
207 36 45.0 66 2 A31188 neurotoxin 1 - sco
208 36 45.0 66 2 S23080 toxin 3 - scorpion
209 36 45.0 78 2 S23822 hypothetical prote
210 36 45.0 87 2 JN0672 neurotoxin 4 precu
211 36 45.0 90 2 S30430 Mat26AB protein -
212 36 45.0 104 2 S19430 2-ketovallate oxi
213 36 45.0 105 2 C75047 probable ferredoxi
214 36 45.0 105 2 H71113 2-oxoisovalerate-f
215 36 45.0 105 2 T45084 repetitive protein
216 36 45.0 118 1 RPXFIK ig kappa chain pre
217 36 45.0 130 2 S08079 hypothetical prote
218 36 45.0 138 2 T34049 E6 protein - human
219 36 45.0 155 1 W6ML43 dihydrofolate redu
220 36 45.0 157 2 T40985 hypothetical prote
221 36 45.0 234 2 AF0673 hypothetical prote
222 36 45.0 281 2 C82547 probable phosphata
223 36 45.0 290 2 D96974 NADH2 dehydrogenas
224 36 45.0 325 2 T14227 ROK family protein
225 36 45.0 326 2 B82343 transcription regu
226 36 45.0 335 2 A13453 probable RAV-like
227 36 45.0 337 2 B96543 probable pectinest
228 36 45.0 344 2 T00536 hypothetical prote
229 36 45.0 344 2 T28729 hypothetical prote
230 36 45.0 347 2 T23944 testican - human
231 36 45.0 439 2 S33293 sensor histidine k
232 36 45.0 443 2 F95243 histidine kinase
233 36 45.0 443 2 C98108 hypothetical prote
234 36 45.0 497 2 T27169 pancreatic zymogen
235 36 45.0 530 2 G02091 hypothetical prote
236 36 45.0 530 2 G64480 protein C09G12.6
237 36 45.0 606 2 H88649 hypothetical prote
238 36 45.0 641 2 T51385 NAD ADP-ribosyltra
239 36 45.0 1013 1 S04200 NAD ADP-ribosyltra
240 36 45.0 1014 1 A29725 protein unc-31 (im
241 36 45.0 1186 2 H88869 hypothetical prote
242 36 45.0 1251 2 B86194 hypothetical prote
243 36 45.0 1270 2 T28087 genome polypeptide
244 36 45.0 2048 1 ZLNZSE genome polypeptide
245 36 45.0 2228 1 ZLNZSV genome polypeptide
246 36 45.0 3165 2 S15010 hypothetical prote
247 36 45.0 4488 1 RRIHM2 genome polypeptide
248 35.5 44.4 104 2 C97803 hypothetical prote

249	35.5	44.4	448	2	T15188	hypothetical prote	322	35	43.8	998	2	A36368	transcription fact
250	35.5	44.4	529	2	J80200	M orphan UDP-glucuro	323	35	43.8	1013	2	T46422	hypothetical prote
251	35.5	44.4	1551	1	A43364	Orphan polyprotein prec	324	35	43.8	1097	2	S68685	adenylate cyclase
252	35	43.8	27	2	S64717	formin binding pro	325	35	43.8	1099	2	A55405	adenylate cyclase
253	35	43.8	66	2	A27406	toxin CsaII - Mexi	326	35	43.8	1119	2	A88481	protein C16A3.6 [i
254	35	43.8	79	2	S59090	hypothetical prote	327	35	43.8	1211	2	T24415	hypothetical prote
255	35	43.8	84	1	NFSR2N	Na+-channel-blocki	328	35	43.8	1244	2	T08212	RNA-directed RNA p
256	35	43.8	87	2	S34083	ig kappa chain v r	329	35	43.8	2291	2	S11238	polymerase - Berne
257	35	43.8	88	2	S21528	ig kappa chain v r	330	35	43.8	2957	2	T33152	hypothetical prote
258	35	43.8	94	2	S28802	hypothetical prote	331	35	43.8	3020	2	A43932	mucin 2 precursor,
259	35	43.8	99	2	B54339	Beejin protein - s	332	35	43.8	3712	2	S18253	laminin alpha-1 ch
260	35	43.8	103	2	B34862	probable adhesio	333	34.5	43.1	42	2	T07581	hypothetical prote
261	35	43.8	108	2	G92611	hypothetical prote	334	34.5	43.1	62	2	S62862	toxin III-8 - Tity
262	35	43.8	109	2	B86050	hypothetical prote	335	34.5	43.1	62	2	S62866	toxin III-8 - Tity
263	35	43.8	137	2	H71163	hypothetical prote	336	34.5	43.1	62	2	B39510	toxin III-8 - Braz
264	35	43.8	141	2	H91203	hypothetical prote	337	34.5	43.1	214	2	T30425	hypothetical prote
265	35	43.8	144	2	F81106	hypothetical prote	338	34.5	43.1	229	2	JC4269	apolipoprotein B m
266	35	43.8	144	2	F81908	probable membrane	339	34.5	43.1	229	2	I48249	apolipoprotein B m
267	35	43.8	157	2	S58014	probable olfactory	340	34.5	43.1	261	2	I78559	cyclic nucleotide-
268	35	43.8	183	2	B84728	probable alanine a	341	34.5	43.1	348	2	T28806	olfactory receptor
269	35	43.8	211	2	S50545	hypothetical prote	342	34.5	43.1	663	2	S11521	CAMP-gated channel
270	35	43.8	211	2	C81001	probable pyrazinam	343	34.5	43.1	664	2	S11517	cyclic nucleotide-
271	35	43.8	211	2	H82018	probable nicotinam	344	34.5	43.1	732	2	S35691	cyclic nucleotide-
272	35	43.8	216	2	B84450	hypothetical prote	345	34.5	43.1	918	2	JC4361	scavenger receptor
273	35	43.8	238	2	C83194	conserved hypothet	346	34.5	43.1	3341	1	A42996	genome polyprotein
274	35	43.8	245	2	I51323	proteolipid protei	347	34	42.5	27	1	T2A23	toxin III - snake-
275	35	43.8	260	1	A36299	transcription fact	348	34	42.5	83	2	H89471	protein B0294.2 [i
276	35	43.8	260	2	S70589	cytochrome-c oxida	349	34	42.5	116	2	D86510	hypothetical prote
277	35	43.8	278	2	T32391	high choriolytic h	350	34	42.5	116	2	B72111	hypothetical prote
278	35	43.8	279	2	C48826	hypothetical prote	351	34	42.5	124	2	B86771	hypothetical prote
279	35	43.8	322	2	T23900	hypothetical prote	352	34	42.5	128	2	T48813	hypothetical prote
280	35	43.8	335	2	H84449	hypothetical prote	353	34	42.5	129	2	S40347	ig kappa chain - h
281	35	43.8	341	2	F87699	glycosyl transfera	354	34	42.5	136	2	S04226	hemoglobin II - cl
282	35	43.8	342	2	T26677	hypothetical prote	355	34	42.5	144	2	S14156	hypothetical prote
283	35	43.8	346	2	T26097	hypothetical prote	356	34	42.5	144	2	B84450	hypothetical prote
284	35	43.8	353	2	JC4875	zinc-finger protei	357	34	42.5	154	2	S36555	B6 protein - human
285	35	43.8	360	2	S36750	cannabinoid recept	358	34	42.5	154	2	S36584	B6 protein - human
286	35	43.8	369	2	T24022	hypothetical prote	359	34	42.5	180	2	C81557	KDO-transferase 2
287	35	43.8	379	1	B28940	cytochrome d ubiq	360	34	42.5	202	2	S11434	protease - bovin
288	35	43.8	379	2	A99725	cytochrome d ubiq	361	34	42.5	217	2	B70324	hypothetical prote
289	35	43.8	379	2	B85576	cytochrome d ubiq	362	34	42.5	226	2	AB0018	conserved hypothet
290	35	43.8	397	2	G84461	hypothetical prote	363	34	42.5	229	2	AB1417	SIR2 family regula
291	35	43.8	406	2	T04613	hypothetical prote	364	34	42.5	229	2	AD1792	SIR2 family regula
292	35	43.8	426	2	B84689	probable RING zinc	365	34	42.5	230	2	B81397	probable 1-acylgly
293	35	43.8	428	2	T46046	hypothetical prote	366	34	42.5	234	2	T48454	hypothetical prote
294	35	43.8	430	2	T16715	hypothetical prote	367	34	42.5	237	2	JN0302	hypothetical 237 p
295	35	43.8	432	2	B82240	cyclopropane-fatty	368	34	42.5	284	2	G64753	yagM protein - Esc
296	35	43.8	447	2	I56511	Zic protein - mous	369	34	42.5	289	2	T05078	hypothetical prote
297	35	43.8	466	2	F95041	hypothetical prote	370	34	42.5	310	2	T41985	hypothetical prote
298	35	43.8	470	2	A65168	hypothetical 49.9	371	34	42.5	317	2	T27485	hypothetical prote
299	35	43.8	485	2	C97022	glutamyl-tRNA synt	372	34	42.5	322	2	AF1031	hypothetical prote
300	35	43.8	506	2	A40679	transcription enha	373	34	42.5	334	2	JC4681	bradykinin B1 rece
301	35	43.8	523	2	B40679	transcription enha	374	34	42.5	344	2	AG3020	ferrochelatase [im
302	35	43.8	537	2	D71296	glutamate-tRNA lig	375	34	42.5	368	2	B98264	ferrochelatase (M9
303	35	43.8	537	2	B33485	spore coat protein	376	34	42.5	379	2	AI0591	cytochrome d ubiq
304	35	43.8	549	2	T49298	hypothetical prote	377	34	42.5	379	2	T04645	hypothetical prote
305	35	43.8	566	2	A81682	conserved hypothet	378	34	42.5	386	2	A35693	NADH2 dehydrogenas
306	35	43.8	566	2	G71525	probable outer mem	379	34	42.5	395	2	T32309	hypothetical prote
307	35	43.8	577	2	T43207	nuclear fusion pro	380	34	42.5	396	2	T19294	hypothetical prote
308	35	43.8	588	2	H84902	hypothetical prote	381	34	42.5	398	2	T19293	hypothetical prote
309	35	43.8	590	1	QQU7C5	NADH2 dehydrogenas	382	34	42.5	399	2	T21586	hypothetical prote
310	35	43.8	636	2	A84903	hypothetical prote	383	34	42.5	407	2	A41106	GTP-binding protei
311	35	43.8	640	2	T19346	hypothetical prote	384	34	42.5	407	2	T39970	guanine nucleotide
312	35	43.8	661	2	T42754	hypothetical prote	385	34	42.5	417	2	T23013	hypothetical prote
313	35	43.8	670	2	H96707	probable receptor	386	34	42.5	450	2	T39088	probable vacuolar
314	35	43.8	680	2	PN0510	integrin beta-3 ch	387	34	42.5	458	2	A84306	hypothetical prote
315	35	43.8	753	2	B36268	platelet glycoprot	388	34	42.5	481	2	C95920	hypothetical membr
316	35	43.8	778	2	A60798	platelet glycoprot	389	34	42.5	502	1	I30010	NADH2 dehydrogenas
317	35	43.8	788	2	A26547	platelet glycoprot	390	34	42.5	521	2	A29249	RNA-directed RNA p
318	35	43.8	788	2	I77349	platelet glycoprot	391	34	42.5	528	2	JN0620	UDP-glucuronosyltr
319	35	43.8	804	2	A36494	protein F7F22.16 [392	34	42.5	529	2	A35366	glucuronosyltransf
320	35	43.8	817	2	S51445	probable membrane	393	34	42.5	613	2	S55615	thymidine kinase (
321	35	43.8	903	2	T20804	hypothetical prote	394	34	42.5	630	2	G87753	protein C43811.8 [

395 34 42.5 636 2 D84823
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 456 33 41.2 155 2 A93773
 457 33 41.2 177 2 S37650
 458 33 41.2 184 2 T30063
 459 33 41.2 195 2 J01850
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 473 33 41.2 262 2 A65220
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 475 33 41.2 276 2 T28746
 476 33 41.2 278 2 E71293
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 520 33 41.2 442 2 T20594
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 523 33 41.2 454 1 IQJUBA
 524 33 41.2 454 2 D84931
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 526 33 41.2 470 2 T07673
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 536 33 41.2 509 1 S58399
 537 33 41.2 511 2 T22707
 538 33 41.2 511 2 C83828
 539 33 41.2 574 2 C83828
 540 33 41.2 607 2 A44490

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541	33	41.2	625	2	T26047	hypothetical prote	614	32	40.0	106	2	JQ0234	hypothetical 12.5K
542	33	41.2	632	2	T24405	hypothetical prote	615	32	40.0	111	2	S38497	Ig lambda chain -
543	33	41.2	633	2	T52506	hypothetical prote	616	32	40.0	112	2	AB0663	probable multidrug
544	33	41.2	635	2	J55896	killer cell inhibi	617	32	40.0	121	2	PH1661	Ig heavy chain V r
545	33	41.2	646	2	T38212	hypothetical prote	618	32	40.0	128	2	S69856	hypothetical prote
546	33	41.2	664	2	AB1430	hypothetical prote	619	32	40.0	129	2	S44114	Ig heavy chain V r
547	33	41.2	664	2	AB1803	hypothetical prote	620	32	40.0	145	1	TNLJBT	trans-activating t
548	33	41.2	680	2	J55895	killer cell inhibi	621	32	40.0	152	2	T34649	hypothetical prote
549	33	41.2	689	2	T08918	hypothetical prote	622	32	40.0	157	1	S04810	hypothetical prote
550	33	41.2	690	2	G84638	hypothetical prote	623	32	40.0	157	2	D83748	dihydrofolate redu
551	33	41.2	703	2	T15503	hypothetical prote	624	32	40.0	159	1	S27195	transforming growt
552	33	41.2	706	2	T51432	cyclic nucleotide	625	32	40.0	159	1	WFR11	transforming growt
553	33	41.2	741	2	T46488	hypothetical prote	626	32	40.0	159	2	I57497	transforming growt
554	33	41.2	810	1	A33380	interleukin-4 rece	627	32	40.0	161	2	B84946	dihydrofolate redu
555	33	41.2	816	2	T19049	hypothetical prote	628	32	40.0	162	2	C33739	hypothetical 17.8K
556	33	41.2	841	2	J55894	killer cell inhibi	629	32	40.0	167	2	B24988	NADH2 dehydrogenas
557	33	41.2	860	2	B85074	hypothetical prote	630	32	40.0	186	2	S46450	hypothetical prote
558	33	41.2	891	2	J56519	DNA topoisomerase	631	32	40.0	186	2	G82439	MutT/nudix family
559	33	41.2	934	1	A34372	complement C6 prec	632	32	40.0	191	2	S43595	R07E5.7 protein (c
560	33	41.2	952	2	T03158	tegument protein 6	633	32	40.0	196	2	T44516	bplG protein homol
561	33	41.2	982	2	T15967	hypothetical prote	634	32	40.0	196	2	S47481	tex261 protein - m
562	33	41.2	988	2	T18986	hypothetical prote	635	32	40.0	203	2	B83606	hypothetical prote
563	33	41.2	989	2	A54505	serine-repeat anti	636	32	40.0	205	2	H90532	hypothetical prote
564	33	41.2	997	2	B16137	SERA antigen/papai	637	32	40.0	212	2	H84979	hypothetical prote
565	33	41.2	1022	2	T30543	major surface gly	638	32	40.0	230	1	TLBPK3	tail fiber protein
566	33	41.2	1040	2	A57638	receptor tyrosine	639	32	40.0	230	2	G65067	hypothetical prote
567	33	41.2	1043	2	T13733	FT2-F1 protein - f	640	32	40.0	230	2	B85937	hypothetical prote
568	33	41.2	1094	2	S46021	probable regulator	641	32	40.0	230	2	G91091	hypothetical prote
569	33	41.2	1103	2	T22889	hypothetical prote	642	32	40.0	242	2	T31174	hypothetical prote
570	33	41.2	1162	2	C81297	proline dehydrogen	643	32	40.0	243	1	D70456	guFA protein homol
571	33	41.2	1185	2	B71980	proline dehydrogen	644	32	40.0	254	2	T05811	conserved hypotet
572	33	41.2	1185	2	H64526	proline dehydrogen	645	32	40.0	254	2	S07752	hypothetical prote
573	33	41.2	1208	2	S69015	AXL1 protein - yea	646	32	40.0	261	2	D86149	TIN6.19 protein -
574	33	41.2	1227	2	B96673	hypothetical prote	647	32	40.0	261	2	S07752	NADH2 dehydrogenas
575	33	41.2	1231	2	T30841	serine-repeat anti	648	32	40.0	273	2	F69199	conserved hypotet
576	33	41.2	1241	2	H84486	probable helicase	649	32	40.0	274	2	B81119	probable glucosylt
577	33	41.2	1501	2	T29094	ribulose-bisphosph	650	32	40.0	275	2	T26361	hypothetical prote
578	33	41.2	1541	2	T02831	AAA protein I4171.	651	32	40.0	277	2	T04441	hypothetical prote
579	33	41.2	1773	2	T05128	hypothetical prote	652	32	40.0	281	2	B81894	hypothetical prote
580	33	41.2	1879	2	T19481	hypothetical prote	653	32	40.0	281	2	B81126	conserved hypotet
581	33	41.2	2139	2	A35672	crumbs protein - f	654	32	40.0	288	2	B43253	zinc finger protei
582	33	41.2	2704	2	S09118	G surface protein	655	32	40.0	292	2	T16085	hypothetical prote
583	33	41.2	2718	2	A33475	G surface protein	656	32	40.0	294	1	MUSM1	lysosome (BC 3.2.1
584	33	41.2	2823	2	F87908	protein T22A3.8 [i	657	32	40.0	299	2	AB1341	fructose-1,6-bipho
585	33	41.2	2823	2	T33064	hypothetical prote	658	32	40.0	299	2	AC1712	fructose-1,6-bipho
586	33	41.2	3102	2	T83291	laminin alpha chai	659	32	40.0	305	2	T39639	conserved protein-
587	32.5	40.6	52	1	XBP1	bromelain inhibito	660	32	40.0	310	2	A70449	hypothetical prote
588	32.5	40.6	91	2	A49754	hypothetical prote	661	32	40.0	313	2	T26308	hypothetical prote
589	32.5	40.6	100	1	TNLJSI	trans-activating t	662	32	40.0	320	2	T31948	hypothetical prote
590	32.5	40.6	114	2	PH1667	Ig heavy chain V r	663	32	40.0	322	2	T25648	hypothetical prote
591	32.5	40.6	154	2	T46006	hypothetical prote	664	32	40.0	325	2	JC2193	melanocortin recep
592	32.5	40.6	226	2	B99079	alkyl hydroperoxid	665	32	40.0	330	2	S58255	hypothetical prote
593	32.5	40.6	377	2	A49885	MHC class I histoc	666	32	40.0	336	2	T19498	hypothetical prote
594	32.5	40.6	379	2	A35878	class I major hist	667	32	40.0	338	2	T05036	xyloglucan endo-1,
595	32.5	40.6	379	2	B35878	class I major hist	668	32	40.0	340	2	S75099	xyloglucan endo-1,
596	32.5	40.6	406	2	B35878	class I major hist	669	32	40.0	341	2	S71223	xyloglucan endo-1,
597	32.5	40.6	717	2	H84057	pullulanase amyl	670	32	40.0	342	2	A45678	probable transmem
598	32.5	40.6	730	2	B83540	hemolytic phosphol	671	32	40.0	343	2	B86446	probable endoxylg
599	32.5	40.6	730	2	A6391	phospholipase C (B	672	32	40.0	344	2	T18019	probable site-spec
600	32.5	40.6	830	2	S25198	vacuolar membrane	673	32	40.0	345	2	T16074	hypothetical prote
601	32.5	40.6	835	2	JF0076	nel protein - chic	674	32	40.0	346	2	T28718	hypothetical prote
602	32	40.0	75	2	T21519	hypothetical prote	675	32	40.0	357	1	QQBEG4	HWLF3 protein - hu
603	32	40.0	77	2	S70443	Ig kappa chain V r	676	32	40.0	365	2	E97315	membrane protease
604	32	40.0	81	2	JC7602	vacuolar type prot	677	32	40.0	367	1	A46355	site-specific DNA-
605	32	40.0	88	2	H91290	hypothetical prote	678	32	40.0	367	2	T18185	probable site-spec
606	32	40.0	89	2	G97365	hypothetical prote	679	32	40.0	371	1	H22848	ubiquinol-cytochro
607	32	40.0	92	2	S37531	Ig kappa chain V r	680	32	40.0	371	2	T21707	hypothetical prote
608	32	40.0	92	2	E46522	T-cell receptor et	681	32	40.0	377	2	T47791	hypothetical prote
609	32	40.0	95	2	JC7601	vesicular membrane	682	32	40.0	381	2	F59101	hypothetical prote
610	32	40.0	100	2	A1201	GLI-related finger	683	32	40.0	385	2	A23388	conserved hypotet
611	32	40.0	100	2	A10092	probable membrane	684	32	40.0	392	2	T33444	hypothetical prote
612	32	40.0	101	2	PH0981	Ig heavy chain V r	685	32	40.0	392	2	T09654	polygalacturonase
613	32	40.0	104	2	PH0981	Ig heavy chain V r	686	32	40.0	397	2	JW0075	cysteine-dependent

687	32	40.0	399	2	T21015	hypothetical prote	760	32	40.0	726	2	A85355	hypothetical prote
688	32	40.0	404	2	B85466	hypothetical prote	761	32	40.0	743	2	S48917	probable regulator
689	32	40.0	404	2	A31460	xylose repressor h	762	32	40.0	751	2	T23880	hypothetical prote
690	32	40.0	404	2	AC1097	xylose repressor h	763	32	40.0	777	2	B99591	conserved hypotet
691	32	40.0	411	2	AB0013	probable exported	764	32	40.0	795	2	T34468	hypothetical prote
692	32	40.0	413	2	AC2360	hypothetical prote	765	32	40.0	803	2	B84859	probable RNA-bindi
693	32	40.0	413	2	T23098	hypothetical prote	766	32	40.0	816	2	C69493	hypothetical prote
694	32	40.0	417	2	T19230	hypothetical prote	767	32	40.0	852	1	GNLJGA	pol polyprotein -
695	32	40.0	422	1	BNHJUY	synaptotagmin I -	768	32	40.0	852	1	GNLJGB	pol polyprotein -
696	32	40.0	422	1	BNRT2Y	synaptotagmin II -	769	32	40.0	852	1	S29358	pol protein - bovi
697	32	40.0	422	2	A55417	synaptotagmin II -	770	32	40.0	870	2	B71698	hypothetical prote
698	32	40.0	422	2	A45486	synaptotagmin I -	771	32	40.0	874	2	T29548	hypothetical prote
699	32	40.0	424	2	I51210	synaptotagmin p65	772	32	40.0	896	2	C85438	hypothetical prote
700	32	40.0	427	2	JH0413	synaptotagmin o-p6	773	32	40.0	901	2	T03726	capsid polyprotein
701	32	40.0	428	2	T48008	hypothetical prote	774	32	40.0	908	1	JN0804	nitrate reductase
702	32	40.0	428	2	T48284	hypothetical prote	775	32	40.0	919	2	T16459	hypothetical prote
703	32	40.0	430	2	T28338	ORF MSV157 hypothe	776	32	40.0	921	2	H84921	hypothetical prote
704	32	40.0	431	1	BVBYPD	probable protein p	777	32	40.0	947	2	G86420	probable receptor-
705	32	40.0	432	2	T16141	hypothetical prote	778	32	40.0	958	2	C86308	P20D23.9 protein -
706	32	40.0	442	2	T18917	hypothetical prote	779	32	40.0	972	2	T39876	hypothetical prote
707	32	40.0	446	2	T31539	hypothetical prote	780	32	40.0	990	2	H88733	hypothetical prote
708	32	40.0	451	2	F83793	DNA-damage-inducib	781	32	40.0	1003	2	T16740	hypothetical prote
709	32	40.0	465	2	T27415	hypothetical prote	782	32	40.0	1027	2	A56533	chromatin remodel
710	32	40.0	466	2	S45419	hypothetical prote	783	32	40.0	1029	2	T41386	RanBP7/importin-be
711	32	40.0	467	2	T18744	hypothetical prote	784	32	40.0	1064	2	T01960	hypothetical prote
712	32	40.0	472	1	A54870	cell adhesion rece	785	32	40.0	1073	1	OYHUHX	heat-stable entero
713	32	40.0	473	2	T17260	hypothetical prote	786	32	40.0	1107	2	T15884	hypothetical prote
714	32	40.0	475	2	T33943	hypothetical prote	787	32	40.0	1110	2	A43253	Large tra-1 protei
715	32	40.0	485	1	VHVUHU	nucleoprotein - Ha	788	32	40.0	1227	2	AG2504	hypothetical prote
716	32	40.0	493	2	S72196	X-Pro dipeptidase	789	32	40.0	1273	2	T42405	sax-3 protein - Ca
717	32	40.0	498	2	PC6300	synaptotagmin X -	790	32	40.0	1291	1	S05465	retrovirus-related
718	32	40.0	499	2	T32337	hypothetical prote	791	32	40.0	1294	2	T19982	hypothetical prote
719	32	40.0	504	2	T27914	hypothetical prote	792	32	40.0	1331	2	T29249	hypothetical prote
720	32	40.0	507	2	C71412	probable hydroxypr	793	32	40.0	1339	2	JC5508	DNA-directed DNA p
721	32	40.0	508	2	AH2688	Na+/H+ antiporter	794	32	40.0	1345	2	T00964	hypothetical prote
722	32	40.0	521	2	T38466	probable NRAMP-fam	795	32	40.0	1484	2	T29275	hypothetical prote
723	32	40.0	524	2	S07168	probable maturase,	796	32	40.0	1499	2	AC2555	hypothetical prote
724	32	40.0	525	2	S41763	histidine-tRNA lig	797	32	40.0	1516	2	B71619	RAD2 endonuclease
725	32	40.0	525	2	C27470	probable NADH dehy	798	32	40.0	1571	2	T13711	polyprotein - frui
726	32	40.0	530	2	T23255	hypothetical prote	799	32	40.0	1621	2	S62356	TRP-185 protein -
727	32	40.0	543	2	S65462	glucose transport	800	32	40.0	1786	1	MMMSB1	laminin beta-1 cha
728	32	40.0	550	2	A57519	parathyroid hormon	801	32	40.0	2352	2	T32021	Notch homolog prot
729	32	40.0	554	2	S43897	methyl coenzyme M	802	32	40.0	2505	1	XYRTFA	enoyl-1-acyl-carrie
730	32	40.0	555	2	H96720	probable peptide t	803	32	40.0	2769	1	UIBO	throglobulin prec
731	32	40.0	560	2	A82437	NADH dehydrogenase	804	32	40.0	3106	1	S53868	laminin alpha-2 ch
732	32	40.0	560	2	S23313	hypothetical prote	805	31.5	39.4	38	2	JN0613	defensin 4K - scor
733	32	40.0	566	1	HMVISA	hemagglutinin prec	806	31.5	39.4	83	2	T48068	hypothetical prote
734	32	40.0	582	2	F84807	hypothetical prote	807	31.5	39.4	87	2	JN0670	Na+-channel-blocki
735	32	40.0	597	2	S65673	GABA transport pro	808	31.5	39.4	106	2	T49958	GASA4 - Arabidopsi
736	32	40.0	597	2	A30814	development-specif	809	31.5	39.4	106	2	S60232	gibberellin-regula
737	32	40.0	607	2	H88065	protein T16A1.1 li	810	31.5	39.4	116	2	T38410	RP3 candidate gene
738	32	40.0	609	2	A49839	odd-paired - fruit	811	31.5	39.4	118	2	A24754	Ig heavy chain V r
739	32	40.0	617	2	F84681	hypothetical prote	812	31.5	39.4	118	2	D84918	hypothetical prote
740	32	40.0	617	2	T00601	hypothetical prote	813	31.5	39.4	188	2	F95944	hypothetical prote
741	32	40.0	625	2	S48941	regulatory protein	814	31.5	39.4	194	2	T41796	AcMNPV orf52 - Bom
742	32	40.0	626	1	RGBY23	cell division cont	815	31.5	39.4	316	2	T27194	hypothetical prote
743	32	40.0	627	2	B84482	probable gag-prote	816	31.5	39.4	344	2	T27410	hypothetical prote
744	32	40.0	639	2	C95342	nitrous-oxide redu	817	31.5	39.4	354	2	B88650	protein C09G12.4 (
745	32	40.0	640	2	T29784	hypothetical prote	818	31.5	39.4	370	2	JC7998	platelet-derived g
746	32	40.0	642	2	S36511	E1 protein - human	819	31.5	39.4	370	2	JC7592	spinal cord-derive
747	32	40.0	643	1	W1WL42	E1 protein - human	820	31.5	39.4	379	2	T20394	hypothetical prote
748	32	40.0	650	2	T44660	nitrous-oxide redu	821	31.5	39.4	444	2	F71916	probable lipopolys
749	32	40.0	650	2	T00617	endostyle-specific	822	31.5	39.4	536	2	A71491	probable integral
750	32	40.0	652	2	T39409	hypothetical prote	823	31.5	39.4	546	2	G71348	probable apolipop
751	32	40.0	663	1	A54075	arachidonate 12-li	824	31.5	39.4	634	2	H64508	hypothetical prote
752	32	40.0	663	1	A38283	arachidonate 12-li	825	31.5	39.4	678	2	S48412	probable membrane
753	32	40.0	669	2	S65551	factor H - bovine	826	31.5	39.4	681	2	T23455	hypothetical prote
754	32	40.0	669	2	B70186	translation elonga	827	31.5	39.4	698	2	T13657	NADH2 dehydrogenas
755	32	40.0	672	2	E72391	beta-D-galactosida	828	31.5	39.4	843	1	JDVLJ2	DNA-directed DNA p
756	32	40.0	672	2	G84112	beta-galactosidase	829	31.5	39.4	1053	2	S34172	sucrose-phosphate
757	32	40.0	678	2	G84682	hypothetical prote	830	31.5	39.4	1145	1	GNLJEV	HIV-1 retropepsin
758	32	40.0	696	2	T01951	hypothetical prote	831	31.5	39.4	1146	1	GNLJ22	HIV-1 retropepsin
759	32	40.0	705	2	T06682	hypothetical prote	832	31.5	39.4	1146	1	GNLJEW	HIV-1 retropepsin

833	31.5	39.4	1327	2	T09402	immunoglobulin-lik	906	31	38.8	159	2	E82592	hypothetical prote
834	31.5	39.4	1501	2	S50992	SNQ2 protein - yea	907	31	38.8	161	2	E88541	protein ZK637.14 [
835	31.5	39.4	2895	2	T08437	hyperplastic discs	908	31	38.8	164	2	T44054	glycoprotein gp82/
836	31.5	39.4	2907	2	A54728	fibrillin-2 precu	909	31	38.8	165	2	T29176	hypothetical prote
837	31.5	39.4	2918	2	A54105	fibrillin-2 precu	910	31	38.8	168	2	S16294	T-cell receptor ga
838	31	38.8	18	2	C49254	TcR C gamma 1 chai	911	31	38.8	174	1	TVVPA4	small T antigen -
839	31	38.8	48	2	JN0355	neurotoxin 1 - sea	912	31	38.8	174	2	T10997	NADH2 dehydrogen
840	31	38.8	54	2	E64007	hypothetical prote	913	31	38.8	178	2	A81687	conserved hypothet
841	31	38.8	55	2	D64392	rubredoxin - Metha	914	31	38.8	181	2	B64223	signal peptidase I
842	31	38.8	56	1	WTFP	testis-specific pr	915	31	38.8	185	2	AB2241	hypothetical prote
843	31	38.8	60	2	S31723	metallothionein -	916	31	38.8	189	2	JK0235	core protein MGC-2
844	31	38.8	60	2	B27490	metallothionein B	917	31	38.8	193	2	E82171	DNA-3-methyladenin
845	31	38.8	60	2	JC2420	metallothionein -	918	31	38.8	194	2	AE1101	hypothetical prote
846	31	38.8	60	2	S30567	metallothionein A	919	31	38.8	195	2	S39967	hypothetical prote
847	31	38.8	61	2	JC1449	metallothionein -	920	31	38.8	196	2	T22609	hypothetical prote
848	31	38.8	61	2	T02733	hypothetical prote	921	31	38.8	198	2	JE0316	cytochrome c oxida
849	31	38.8	64	2	S28486	hypothetical prote	922	31	38.8	205	2	B97453	hypothetical cytos
850	31	38.8	70	1	XISRIA	insect toxin 1 - S	923	31	38.8	205	2	AH3407	hypothetical prote
851	31	38.8	71	2	A06683	hypothetical prote	924	31	38.8	207	2	H95002	hypothetical prote
852	31	38.8	78	2	C90872	hypothetical prote	925	31	38.8	210	2	T16744	hypothetical prote
853	31	38.8	80	2	H96775	GAST1-like protein	926	31	38.8	214	2	T20683	hypothetical prote
854	31	38.8	84	2	G95202	conserved hypothet	927	31	38.8	217	2	A88115	protein F53C3.5 [i
855	31	38.8	84	2	G98069	conserved hypothet	928	31	38.8	219	2	T25904	hypothetical prote
856	31	38.8	87	2	JN0669	Na+-channel-blocki	929	31	38.8	220	2	S52005	nodulin-30 (NpV30)
857	31	38.8	87	2	T33285	hypothetical prote	930	31	38.8	221	2	T29509	hypothetical prote
858	31	38.8	88	2	G34444	insect toxin 2 pre	931	31	38.8	221	2	H82999	probable hydrolase
859	31	38.8	89	2	F69268	hypothetical prote	932	31	38.8	225	2	C82893	hypothetical prote
860	31	38.8	92	2	S37509	Ig kappa chain V r	933	31	38.8	227	2	T28351	ORF MSV190 probabl
861	31	38.8	92	2	D37057	epithelial cell gl	934	31	38.8	229	2	A69762	hypothetical prote
862	31	38.8	96	2	S43910	gibberellin-regula	935	31	38.8	232	2	A60095	larval glue protei
863	31	38.8	97	2	S1272	hypothetical prote	936	31	38.8	236	1	XMBS7A	transcription acti
864	31	38.8	97	2	S71371	gibberellin-regula	937	31	38.8	243	2	T46221	PRE-mRNA SPLICING
865	31	38.8	100	2	G90427	hypothetical prote	938	31	38.8	244	2	AD2671	cytochrome C oxida
866	31	38.8	101	2	S26337	Ig light chain V r	939	31	38.8	244	2	A39365	cyanamide hydrat
867	31	38.8	101	2	C48219	S-100 calcium-bind	940	31	38.8	249	2	D71942	hypothetical prote
868	31	38.8	106	2	A48868	carbon-monoxide de	941	31	38.8	251	2	S01047	hemolymph 30K prot
869	31	38.8	107	2	S36275	Ig lambda chain V	942	31	38.8	253	2	T47303	hypothetical prote
870	31	38.8	107	2	A49442	Ig heavy chain V r	943	31	38.8	256	2	D83336	probable thiol-dis
871	31	38.8	107	2	G82461	hypothetical prote	944	31	38.8	257	2	S55612	hypothetical prote
872	31	38.8	108	2	F82598	hypothetical prote	945	31	38.8	258	2	B69297	CODH nickel-insert
873	31	38.8	110	2	S69897	Ig heavy chain V r	946	31	38.8	261	2	G72867	hypothetical prote
874	31	38.8	110	2	C24775	T-cell receptor ga	947	31	38.8	263	2	S17661	hemolymph 30K prot
875	31	38.8	110	2	T51963	GAS5-like protein	948	31	38.8	263	2	T06655	hypothetical prote
876	31	38.8	110	2	F90830	integral membrane	949	31	38.8	263	2	T32081	hypothetical prote
877	31	38.8	110	2	C85688	hypothetical prote	950	31	38.8	264	2	S01046	hemolymph 30K prot
878	31	38.8	110	2	S03329	ethidium efflux pr	951	31	38.8	264	2	S01048	hemolymph 30K prot
879	31	38.8	112	2	S40284	protein-tyrosine-p	952	31	38.8	266	2	I49363	natural killer cel
880	31	38.8	112	2	S22151	gibberellin-regula	953	31	38.8	266	2	I49363	Ly49H - mouse
881	31	38.8	112	2	S54832	gipi protein - gar	954	31	38.8	266	2	I49059	zinc finger protei
882	31	38.8	112	2	C81123	hypothetical prote	955	31	38.8	268	2	T39595	transcription regu
883	31	38.8	112	2	T29620	hypothetical prote	956	31	38.8	268	2	AG1408	high chorionlytic h
884	31	38.8	120	2	B24775	T-cell receptor ga	957	31	38.8	270	2	B48826	dimethyladenosine
885	31	38.8	120	2	S43030	hypothetical prote	958	31	38.8	277	2	H86822	transcription regu
886	31	38.8	121	2	A49590	Ig heavy chain V r	959	31	38.8	277	2	H72001	hypothetical prote
887	31	38.8	123	2	S30530	Ig heavy chain V r	960	31	38.8	285	2	E86833	hypothetical prote
888	31	38.8	123	2	S00531	insulin-like prote	961	31	38.8	285	2	A40657	probable 3-oxoacyl
889	31	38.8	124	1	MLHUS1	Ig heavy chain V-I	962	31	38.8	287	1	A45168	oxygen-independent
890	31	38.8	125	2	C83138	hypothetical prote	963	31	38.8	287	2	F69413	hypothetical prote
891	31	38.8	125	2	T34449	hypothetical prote	964	31	38.8	288	2	T32212	probable bifunctio
892	31	38.8	128	2	S26786	Ig heavy chain V r	965	31	38.8	289	1	S25286	probable dehydroge
893	31	38.8	129	1	F7HUB	folitropin beta c	966	31	38.8	290	2	E96706	probable bifunctio
894	31	38.8	131	2	AH2304	hypothetical prote	967	31	38.8	291	2	G71300	probable protein-m
895	31	38.8	132	2	PH1427	Ig heavy chain V r	968	31	38.8	293	2	AE1517	conserved hypothet
896	31	38.8	132	2	A10244	probable rhodanese	969	31	38.8	293	2	T47708	hypothetical prote
897	31	38.8	135	2	PC4252	hypothetical 135 p	970	31	38.8	295	2	AE0993	glycerol-3-phospha
898	31	38.8	140	2	T33284	hypothetical prote	971	31	38.8	296	1	S37312	transcription acti
899	31	38.8	141	2	JC7786	lectin CBL-I, N-ac	972	31	38.8	298	2	AD3336	sulfate transport
900	31	38.8	141	2	S15788	intermediate early	973	31	38.8	299	2	AG1033	hypothetical prote
901	31	38.8	143	2	T40635	clathrin coat asse	974	31	38.8	303	2	T20624	hypothetical prote
902	31	38.8	146	2	C91158	hypothetical prote	975	31	38.8	304	2	AB0390	conserved hypothet
903	31	38.8	146	2	AB6004	hypothetical prote	976	31	38.8	304	2	D82304	glutamyl-tRNA synt
904	31	38.8	151	2	T08002	glycine-rich prote	977	31	38.8	310	2	T32006	hypothetical prote
905	31	38.8	158	1	TVVPM4	small T antigen -	978	31	38.8	311	1	QQBEC1	HKLF1 protein - hu

A:Reference number: S25445
A:Accession: S25445
A:Molecule type: DNA
A:Residues: 1-881 <HOF>
A:Cross-references: UNIPROT:P39865; UNIPARC:UPI0000130051; EMBL:X53603; NID:g21018; PIDN
A:Experimental source: cv. Saxonia
C:Genetics:
A:Introns: 322/1; 369/1; 446/3
C:Complex: homodimer
C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C:Keywords: electron transfer; PAD; flavoprotein; heme; homodimer; iron; metalloprotein;
F:63-455/Domain: molybdopterin-binding domain homology <PCO>
F:515-589/Domain: cytochrome b5 core homology <CB5>
F:632-881/Domain: cytochrome-b5 reductase homology <CBR>
F:167/Binding site: molybdopterin (Cys) (covalent) #status predicted
F:550,573/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 57.5%; Score 46; DB 2; Length 881;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
|:|:|
Db 404 YWCWCFW 410

RESULT 5
A59223
nitrate reductase (NADH) (EC 1.7.1.1) 1, substrate-inducible [similarity] - soybean
C:Species: Glycine max (soybean)
C:Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: A59223; S72503; S66307
R:Wu, S.; Lu, Q.; Križ, A.L.; Harper, J.E.
submitted to the EMBL Data Library, April 1996
A:Reference number: A59223
A:Accession: A59223
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-886 <WU51>
A:Cross-references: UNIPROT:P54233; UNIPARC:UPI0000130052; GB:L23854; NID:g1262165; PIDN
A:Experimental source: cultivar Williams 82; dev stage seedling; tissue type leaf
R:Wu, S.; Lu, Q.; Križ, A.L.; Harper, J.E.
submitted to the EMBL Data Library, November 1993
A:Reference number: S72503
A:Accession: S72503
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 7-886 <WU5>
A:Cross-references: UNIPARC:UPI000017510B; EMBL:L23854; NID:g1262165
R:Wu, S.; Lu, Q.; Križ, A.L.; Harper, J.E.
Plant Mol. Biol. 29, 491-506, 1995
A:Title: Identification of cDNA clones corresponding to two inducible nitrate reductase
A:Reference number: S66307; MUID:96123229; PMID:8534848
A:Accession: S66307
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 7-95, 'A', '97', 'A', '99-188', 'A', '190-886' <WU2>
A:Cross-references: UNIPARC:UPI000017510C; EMBL:L23854; NID:g1262165
C:Genetics:
A:Gene: INRI1
C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C:Keywords: electron transfer; PAD; flavoprotein; heme; homodimer; iron; metalloprotein;
F:61-453/Domain: molybdopterin-binding domain homology <PCO>
F:513-587/Domain: cytochrome b5 core homology <CB5>
F:637-886/Domain: cytochrome-b5 reductase homology <CBR>
F:165/Binding site: molybdopterin (Cys) (covalent) #status predicted
F:548,571/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 57.5%; Score 46; DB 2; Length 886;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7

Db 402 YWCWCFW 408
|:|:|

RESULT 6
T02240

nitrate reductase [NAD(P)H] (EC 1.7.1.2) - maize
C:Species: Zea mays (maize)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02240
R:Campbell, W.H.; Redinbaugh, M.G.; Ingemarsson, B.; Dougherty, E.S.; Campbell, E.R.
submitted to the EMBL Data Library, January 1995
A:Description: A third nitrate reductase gene is expressed in corn tissues and suspension
A:Reference number: Z14635
A:Accession: T02240
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-889 <CAM>
A:Cross-references: UNIPROT:P49102; UNIPARC:UPI000013005A; EMBL:U20450; NID:g676849; PID
A:Experimental source: strain B73; seedling
C:Genetics:
A:Introns: 336/1; 383/1; 460/3
C:Function:
A:Description: catalyzes the reduction of nitrate to nitrite using NAD(P)H as the electron
A:Pathway: nitrate assimilation
C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; molybdenum; molybdopterin;
F:82-469/Domain: molybdopterin-binding domain homology <PCO>
F:520-594/Domain: cytochrome b5 core homology <CB5>
F:637-889/Domain: cytochrome-b5 reductase homology <CBR>
F:181/Binding site: molybdopterin (Cys) (covalent) #status predicted
F:420/Disulfide bonds: interchain #status predicted
F:555,578/Binding site: heme iron (His) (axial ligands) #status predicted
F:701,861/Binding site: NAD(P) (Lys, Cys) #status predicted
F:741/Binding site: PAD (Tyr) #status predicted

Query Match 57.5%; Score 46; DB 2; Length 889;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
|:|:|
Db 418 YWCWCFW 424

RESULT 7
T11805

nitrate reductase (NADH) (EC 1.7.1.1) 2 [similarity] - kidney bean
C:Species: Phaseolus vulgaris (kidney bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11805
R:Jensen, P.E.; Hoff, T.; Stummann, B.M.; Henningsen, K.W.
submitted to the EMBL Data Library, August 1993
A:Description: Structure and expression of a nitrate reductase gene from bean containing
A:Reference number: Z17348
A:Accession: T11805
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-890 <JEN>
A:Cross-references: UNIPROT:P39866; UNIPARC:UPI0000130057; EMBL:U01029; NID:g392991; PID
A:Experimental source: strain saxonia
C:Genetics:
A:Gene: NR2
A:Introns: 320/1; 367/1; 444/3; 591/1
C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C:Keywords: heme; iron; metalloprotein; molybdenum; molybdopterin; oxidoreductase; phospho
F:61-453/Domain: molybdopterin-binding domain homology <PCO>
F:513-587/Domain: cytochrome b5 core homology <CB5>
F:641-890/Domain: cytochrome-b5 reductase homology <CBR>
F:165/Binding site: molybdopterin (Cys) (covalent) #status predicted
F:548,571/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 57.5%; Score 46; DB 2; Length 890;

Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
|:|:|
Db 402 YMCWCFW 408

RESULT 8
RDBNHP
nitrate reductase [NAD(P)H] (EC 1.7.1.2) - barley
C/Species: Hordeum vulgare (barley)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: S16895
R;Miyaizaki, J.; Juricek, M.; Angelis, K.; Schnorr, K.M.; Kleinhofs, A.; Warner, R.L.
Mol. Gen. Genet. 228, 329-334, 1991
A/Title: Characterization and sequence of a novel nitrate reductase from barley.
A/Reference number: S16895; MUID:91375416; PMID:1896007
A/Accession: S16895
A/Molecule type: DNA
A/Residues: 1-891 <MIY>
A/Cross-references: UNIPROT:P27968; UNIPARC:UPI000013005B; EMBL:X60173; NID:gl9064; PIDN
C/Genetics:
A/Gene: Nar-7
A/Introns: 321/3; 368/3
C/Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
P/64-455/Domain: molybdopter-in-binding domain homology <PCO>
P/515-589/Domain: cytochrome b5 core homology <CB5>
P/637-891/Domain: cytochrome-b5 reductase homology <CBR>
F/168/Binding site: molybdopterin (Cys) (covalent) #status predicted
F/406/Disulfide bonds: interchain #status predicted
F/550,573/Binding site: heme iron (His) (axial ligands) #status predicted
F/701,863/Binding site: NAD(P) (Lys, Cys) #status predicted
F/741/Binding site: FAD (Tyr) #status predicted

Query Match 57.5%; Score 46; DB 1; Length 891;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
|:|:|
Db 404 YMCWCFW 410

RESULT 9
RDBUNH
nitrate reductase [NAD(P)H] (EC 1.7.1.2) - European white birch
C/Species: Betula pendula (European white birch)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: S15959
R;Friedmann, A.; Brinkmann, K.; Hachtel, W.
Mol. Gen. Genet. 227, 97-105, 1991
A/Title: Sequence of a cDNA encoding the bi-specific NAD(P)H-nitrate reductase from the
A/Reference number: S15959; MUID:91260687; PMID:1675424
A/Accession: S15959
A/Molecule type: mRNA
A/Residues: 1-898 <FRI>
A/Cross-references: UNIPROT:P27783; UNIPARC:UPI0000130060; EMBL:X54097; NID:gl7924; PIDN
A/Note: the authors translated the codon CAC for residue 31 as Arg and CGG for residue 3
C/Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
P/76-468/Domain: molybdopter-in-binding domain homology <PCO>
F/528-602/Domain: cytochrome b5 core homology <CB5>
F/648-898/Domain: cytochrome-b5 reductase homology <CBR>
F/180/Binding site: molybdopterin (Cys) (covalent) #status predicted
F/419/Disulfide bonds: interchain #status predicted
F/563,586/Binding site: heme iron (His) (axial ligands) #status predicted
F/713,870/Binding site: NAD(P) (Lys, Cys) #status predicted
F/753/Binding site: FAD (Tyr) #status predicted

Query Match 57.5%; Score 46; DB 1; Length 898;
Best Local Similarity 71.4%; Pred. No. 37;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
|:|:|
Db 417 YMCWCFW 423

RESULT 10
S47029
nitrate reductase (NADH) (EC 1.7.1.1) nia - Lotus japonicus
C/Species: Lotus japonicus
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S47029
R;Waterhouse, R.N.; Smyth, A.J.; Prosser, I.M.; Forde, B.G.; Clarkson, D.T.
submitted to the EMBL Data Library, July 1994
A/Description: Cloning and characterization of the nitrate reductase gene in Lotus japon.
A/Reference number: S47029
A/Accession: S47029
A/Molecule type: DNA
A/Residues: 1-900 <WAT>
A/Cross-references: UNIPROT:P39869; UNIPARC:UPI0000130067; EMBL:X80670; NID:gs17355; PIDI
A/Experimental source: strain B-129; cultivar GIFU
C/Genetics:
A/Gene: nia
A/Introns: 327/1; 374/1; 451/3
C/Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; iron; metalloprote
P/68-460/Domain: molybdopter-in-binding domain homology <PCO>
P/521-595/Domain: cytochrome b5 core homology <CB5>
F/651-900/Domain: cytochrome-b5 reductase homology <CBR>
F/172/Binding site: molybdopterin (Cys) (covalent) #status predicted
F/411/Disulfide bonds: interchain #status predicted
F/556,579/Binding site: heme iron (His) (axial ligands) #status predicted
F/715,872/Binding site: NAD(P) (Lys, Cys) #status predicted
F/755/Binding site: FAD (Tyr) #status predicted

Query Match 57.5%; Score 46; DB 2; Length 900;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
|:|:|
Db 409 YMCWCFW 415

RESULT 11
RDNVNS
nitrate reductase (NADH) (EC 1.7.1.1) nia-2 - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: S04839; S25375; S22779
R;Vaucheret, H.; Kronenberger, J.; Rouze, P.; Caboche, M.
Plant Mol. Biol. 12, 597-600, 1989
A/Title: Complete nucleotide sequence of the two homeologous tobacco nitrate reductase g
A/Reference number: S04839
A/Accession: S04839
A/Molecule type: DNA
A/Residues: 1-904 <VAU>
A/Cross-references: UNIPROT:P08509; UNIPARC:UPI0000130059; EMBL:X14059; NID:gl9890; PIDN
R;Galangau, F.; Cherel, I.; Deng, M.; Meyer, C.; Moureaux, T.; Rouze, P.; Vaucheret, H.;
Curr. Top. Plant Biochem. Physiol. 7, 26-34, 1988
A/Title: Nitrate reductase expression in tobacco and tomato.
A/Reference number: S25375
A/Accession: S25375
A/Molecule type: DNA
A/Residues: 1-904 <GAL>
A/Cross-references: UNIPARC:UPI0000130059
R;Calza, R.; Huttner, E.; Vincentz, M.; Rouze, P.; Galangau, F.; Vaucheret, H.; Cherel,
Mol. Gen. Genet. 209, 552-562, 1987
A/Title: Cloning of DNA fragments complementary to tobacco nitrate reductase mRNA and en
A/Reference number: S22779
A/Accession: S22779
A/Molecule type: mRNA

nitrates reductase (NADH) (EC 1.7.1.1) - petunia
N;Alternate names: nitrate reductase apoenzyme
C;Species: Petunia sp. (petunia)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 03-Jun-2002
C;Accession: JN0665
R;Salanoubat, M.; Ha, D.B.D.
Gene 128, 147-154, 1993
A;Title: Analysis of the petunia nitrate reductase apoenzyme-encoding gene: A first step
A;Reference number: JN0665; PMID:93292981; PMID:8514183
A;Accession: JN0665
A:Molecule type: DNA
A;Residues: 1-909 <SAL>
A;Cross-references: UNIPARC:UPI000013006B; GB:L13691; NID:g294113; PIDN:AAA33713.1; PID:
C;Comment: This enzyme catalyzes the rate-limiting and regulated step in the process of .
C;Comment: This enzyme catalyzes the reduction of nitrate to nitrite using NAD(P)H as th
C;Genetics:
A:Gene: nia
A;Introns: 342/1; 389/1; 466/3
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red
C;Keywords: chromoprotein; dimer; electron transfer; FAD; flavoprotein; heme; iron; meta
F;83-475/Domain: molybdopterin-binding domain homology <PCO>
F;535-609/Domain: cytochrome b5 core homology <CB5>
F;659-909/Domain: cytochrome-b5 reductase homology <CBR>
F;187/Binding site: molybdopterin (Cys) (covalent) #status predicted
F;142/disulfide bonds: interchain #status predicted
F;570,593/Binding site: heme iron (His) (axial ligands) #status predicted
F;723,881/Binding site: NAD (Lys, Cys) #status predicted
F;763/Binding site: PAD (Tyr) #status predicted

Query Match 57.5%; Score 46; DB 2; Length 909;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 424 YWCWCFW 430

RESULT 14
RDTONH
nitrates reductase (NADH) (EC 1.7.1.1) - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JQ0373
R;Daniel-Vedele, F.; Dorbe, M.F.; Caboche, M.; Rouze, P.
Gene 85, 371-380, 1989
A;Title: Cloning and analysis of the tomato nitrate reductase-encoding gene: protein dom
A;Reference number: JQ0373; PMID:90185211; PMID:2628174
A;Accession: JQ0373
A:Molecule type: DNA
A;Residues: 1-911 <DAN>
A;Cross-references: UNIPROT:P17570; UNIPARC:UPI0000130069; GB:X14060; NID:g19282; PIDN:C
C;Comment: This enzyme catalyzes the reduction of nitrate to nitrite in cytoplasm; each
me involved in the first step of nitrate assimilation in plants, fungi, and bacteria.
C;Genetics:
A:Gene: nia
A;Introns: 343/1; 390/1; 467/3
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red
C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
F;84-476/Domain: molybdopterin-binding domain homology <PCO>
F;536-610/Domain: cytochrome b5 core homology <CB5>
F;661-911/Domain: cytochrome-b5 reductase homology <CBR>
F;188/Binding site: molybdopterin (Cys) (covalent) #status predicted
F;142/disulfide bonds: interchain #status predicted
F;571,594/Binding site: heme iron (His) (axial ligands) #status predicted
F;725,883/Binding site: NAD (Lys, Cys) #status predicted
F;765/Binding site: PAD (Tyr) #status predicted

Query Match 57.5%; Score 46; DB 1; Length 911;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Ov 1 YYCYCFW 7

F:734,892/Binding site: NAD (lys, cys) #status predicted
F:774/Binding site: FAD (fyr) #status predicted

Query Match 57.5%; Score 46; DB 2; Length 920;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
: : : : :
: : : : :
DB 422 YMCWCFW 428

RESULT 19

VB9EY9
early glycoprotein gp48 precursor - human cytomegalovirus (strain AD169)
N:Alternate names: early glycoprotein UL4
C:Species: human cytomegalovirus, human herpesvirus 5
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S09767
R:Chen, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;
M.; Barrell, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A:Reference number: S09749; MUID:90269039; PMID:2161319

A:Accession: S09767
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-152 <CH>

A:Cross-references: UNIPROT:P17146; UNIPARC:UPI0000137B31; EMBL:X17403; NID:G59591; PIDN

A:Note: possible protein-coding frames are given
A:Note: the DNA sequence was submitted to the EMBL Data Library, December 1989, in compu

C:Superfamily: cytomegalovirus early glycoprotein gp48

C:Keywords: early protein; glycoprotein

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-152/Product: early glycoprotein gp48 #status predicted <MAT>

F:48,53,61,69,108,112,122,139,148/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 56.2%; Score 45; DB 1; Length 152;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YCYCFWKTCT 11
: : : : :
: : : : :
DB 19 YCYCFVGTCS 28

RESULT 20

AB1667
conserved hypothetical protein TC0771 [imported] - Chlamydia muridarum (strain Nigg)

C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: AB1667

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.P.; White, O.; Hickey,

, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: AB1500; MUID:20150255; PMID:10684935

A:Accession: AB1667

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-332 <TEP>

A:Cross-references: UNIPROT:Q9PJQ7; UNIPARC:UPI0000057A5A; GB:AE002345; GB:AE002160; NID

A:Experimental source: strain Nigg (MoPn)

C:Genetics:

A:Gene: TC0771

Query Match 55.0%; Score 44; DB 2; Length 332;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYCYCFWK 8
: : : : :
: : : : :
DB 151 FSCFCFWK 158

DB 150 FSCFCFWK 157

RESULT 21

B71508

hypothetical protein CT484 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C:Accession: B71508

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach

A:Reference number: A71570; MUID:99000809; PMID:9784136

A:Accession: B71508

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-332 <ARN>

A:Cross-references: UNIPROT:O84491; UNIPARC:UPI00000C0B5B; GB:AE001322; GB:AE001273; NID

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT484

Query Match 55.0%; Score 44; DB 2; Length 332;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYCYCFWK 8
: : : : :
: : : : :
DB 150 FSCFCFWK 157

RESULT 22

G86565

CT484 hypothetical protein [imported] - Chlamydia pneumoniae (strain J138)

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: G86565

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: G86565

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-334 <STO>

A:Cross-references: UNIPROT:Q9Z7V2; UNIPARC:UPI00000D41BD; GB:BA000008; NID:G8978974; PI

A:Experimental source: strain J138

C:Genetics:

A:Gene: CPJ0602

Query Match 55.0%; Score 44; DB 2; Length 334;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYCYCFWK 8
: : : : :
: : : : :
DB 151 FSCFCFWK 158

RESULT 23

D72057

conserved hypothetical protein CP0145 [imported] - Chlamydia pneumoniae (strains CWL

N:Alternate names: ct484 hypothetical protein

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: D72057; D81607

R:Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: D72057

A:Status: preliminary

A:Molecule type: DNA

A/Residues: 1-334 <ARN>
A/Cross-references: UNIPROT:Q9ZVU2; UNIPARC:UPI00000D41BD; GB:AE001645; GB:AE001363; NID
A/Experimental source: strain CWL029
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.
A/Reference number: A61500; MUID:20150255; PMID:10684935
A/Accession: D81607
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-334 <REA>
A/Cross-references: UNIPARC:UPI00000D41BD; GB:AE002176; GB:AE002161; NID:g7189080; PIDN:
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Gene: CPn0602; CP0145

Query Match 55.0%; Score 44; DB 2; Length 334;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVCYCFWK 8
: |||||
Db 151 FSCFCFWK 158

RESULT 24
AG1214
methyldases homolog lmo119 [imported] - *Listeria monocytogenes* (strain EGD-e)
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C/Accession: AG1214
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A/Title: Comparative Genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AG1214
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-285 <GLA>
A/Cross-references: UNIPROT:Q8Y800; UNIPARC:UPI0000055118; GB:NC_003210; PIDN:CAC99197.1
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: lmo119
C/Superfamily: modification methylase (adenine-specific), M.EcoRV type

Query Match 53.8%; Score 43; DB 2; Length 285;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YVCYCFWK 9
: |||||
Db 61 YSVCYCFWKS 69

RESULT 25
TS2573
cyclic nucleotide and calmodulin-regulated ion channel [imported] - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C/Accession: TS2573
R/Kohler, C.; Merkle, T.; Neuhaus, G.
Plant J. 18, 97-104, 1999
A/Title: Characterisation of a novel gene family of putative cyclic nucleotide- and cal
A/Reference number: Z6120
A/Accession: TS2573
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: mRNA
A/Residues: 1-710 <KOH>

A/Cross-references: UNIPROT:Q8RWS9; UNIPARC:UPI0000048C95; EMBL:Y17913; PIDN:CAB40130.1
A/Experimental source: cultivar Columbia
C/Genetics:
A/Gene: cngc5

Query Match 53.8%; Score 43; DB 2; Length 710;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YCYCFW 7
: |||||
Db 360 YCYCLW 365

RESULT 26
S65938
nitrate reductase [NAD(P)H] (EC 1.7.1.2) - yeast (*Pichia angusta*)
N/Alternate names: assimilatory nitrate reductase
C/Species: *Pichia angusta*
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S65938; T43157
R/Avila, J.; Perez, M.D.; Brito, N.; Gonzalez, C.; Siverio, J.M.
FEBS Lett. 366, 137-142, 1995
A/Title: Cloning and disruption of the YNR1 gene encoding the nitrate reductase apoenzym
A/Reference number: S65938; MUID:95309418; PMID:7789531
A/Accession: S65938
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-859 <AVI>
A/Cross-references: UNIPROT:P49050; UNIPARC:UPI000000094B; EMBL:Z49110; NID:g902625; PID
R/Siverio, J.M.
submitted to the EMBL Data Library, January 1998
A/Reference number: Z22318
A/Accession: T43157
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-859 <STV>
A/Cross-references: UNIPARC:UPI000000094B; EMBL:AJ223294; PIDN:CAAL1232.1
C/Genetics:
A/Gene: YNR1
C/Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu
C/Keywords: heme; iron; metalloprotein; molybdenum; molybdopterin; NADP; oxidoreductase;
P:30-432/Domain: molybdopterin-binding domain homology <PCO>
P:504-577/Domain: cytochrome b5 core homology <CB5>
P:609-859/Domain: cytochrome-b5 reductase homology <CBR>
P:137/Binding site: molybdopterin (Cys) (covalent) #status predicted
P:538,561/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 52.5%; Score 42; DB 1; Length 859;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CYCFWK 8
: |||||
Db 383 CWCFWK 388

RESULT 27
T08105
nitrate reductase (EC 1.7.1.-) 1 - rape
C/Species: *Brassica napus* (rape)
C/Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C/Accession: T08105
R/Fukuoka, H.; Ogawa, T.; Minami, H.; Yano, H.; Ohkawa, Y.
Plant Physiol. 111, 39-47, 1996
A/Title: Developmental stage-specific and nitrate-independent regulation of nitrate redu
A/Reference number: Z16358; MUID:96222419; PMID:8695274
A/Accession: T08105
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: mRNA
A/Residues: 1-911 <FUK>
A/Cross-references: UNIPROT:P39867; UNIPARC:UPI000013004D; EMBL:D38219; NID:g540484; PID
A/Experimental source: cv. Lisandra; developmental stage: 14dap; microspore-derived embr

C;Comment: This enzyme catalyzes the reduction of nitrate to nitrite in cytoplasm; each me involved in the first step of nitrate assimilation in plants, fungi, and bacteria.
C;Genetics:
A:Gene: NTA2
A:Map position: 1
C;Complex: homodimer
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase; chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
F:87-482/Domain: molybdopterin-binding domain homology <PCO>
F:542-616/Domain: cytochrome b5 core homology <CB5>
F:667-917/Domain: cytochrome-b5 reductase homology <CBR>
F:191/Binding site: molybdopterin (Cys) (covalent) #status predicted
F:433/disulfide bonds: interchain #status predicted
F:731,600/Binding site: heme iron (His) (axial ligands) #status predicted
F:731,889/Binding site: NAD (Lys, Cys) #status predicted
F:771/Binding site: FAD (Tyr) #status predicted

Query Match 52.5%; Score 42; DB 1; Length 917;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
:::|::|
DB 431 FWCWCFW 437

RESULT 30
E96807
Nitrate reductase 1 (NR1), 46724-43362 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E96807
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
C;Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ket, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96807
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-917 <STO>
A;Cross-references: UNIPROT:P11832; UNIPARC:UPI0000001AFA; GB:AE005173; NID:G6437524; P11832
C;Genetics:
A:Gene: T32E8.9
A:Map position: 1
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase; chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
F:580,603/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 52.5%; Score 42; DB 2; Length 917;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
:::|::|
DB 434 FWCWCFW 440

RESULT 31
S35228
Nitrate reductase (NADH) (EC 1.7.1.1) 1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S35228; S01640; S16495; S32018
R;Wilkinson, J.Q.; Crawford, N.M.
Mol. Gen. Genet. 239, 289-297, 1993
A;Title: Identification and characterization of a chlorate-resistant mutant of Arabidopsis

A;Reference number: 835228; MUID:93287999; PMID:8510658
 A;Accession: 835228
 A;Molecule type: DNA
 A;Residues: 1-917 <WIL>
 A;Cross-references: UNIPROT:P11832; UNIPARC:UPI000016DB93; EMBL:Z19050; NID:G22756; PIDN:R1Cheng, C.; Dewdney, J.; Nam, H.; den Boer, B.G.W.; Goodman, H.M. EMBO J. 7, 3309-3314, 1988
 A;Title: A new locus (NIA1) in Arabidopsis thaliana encoding nitrate reductase.
 A;Reference number: S01640; MUID:89091069; PMID:2905260
 A;Accession: S01640
 A;Molecule type: mRNA
 A;Residues: 525-917 <CHE1>
 A;Cross-references: UNIPARC:UPI000016DB95; EMBL:X13434; NID:G16402; PIDN:CAA31786.1; PID: A;Note: translation of nucleotide sequence not complete
 A;Accession: S16495
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 342-360 <CHE2>
 A;Cross-references: UNIPARC:UPI000016DB94; EMBL:X13436; NID:G16401; PIDN:CAA31788.1; PID: C;Genetics:
 A;Gene: NIA1
 A;Map position: 1
 A;Intons: 352/1; 399/1; 476/3
 A;Complex: homodimer
 C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
 C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron; P;93-485/Domain: molybdopterin-binding domain homology <PCO>
 P;545-619/Domain: cytochrome b5 core homology <CB5>
 P;667-917/Domain: cytochrome-b5 reductase homology <CBR>
 P;197/Binding site: molybdopterin (Cys) (covalent) #status predicted
 P;436/Disulfide bonds: interchain #status predicted
 P;580, 603/Binding site: heme iron (His) (axial ligands) #status predicted
 P;731, 889/Binding site: NAD (Lys, Cys) #status predicted
 P;771/Binding site: FAD (Tyr) #status predicted

Query Match 52.5%; Score 42; DB 2; Length 917;
 Best Local Similarity 57.1%; Pred. No. 1.4e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
 ::|||
 Db 434 FWCWCFW 440

RESULT 32
 RSPNH
 nitrate reductase (NADH) (EC 1.7.1.1) - spinach
 C;Species: Spinacia oleracea (spinach)
 C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
 C;Accession: S11868; PQ0694; PQ0695; S62777; A45589; B45589; S68383
 R;Prosser, I.M.; Lazarus, C.M. 1990
 Plant Mol. Biol. 15, 187-190, 1990
 A;Title: Nucleotide sequence of a spinach nitrate reductase cDNA.
 A;Reference number: S11868; MUID:91355858; PMID:2103436
 A;Accession: S11868
 A;Molecule type: mRNA
 A;Residues: 1-326 <PRO>
 A;Cross-references: UNIPROT:P23312; UNIPARC:UPI000013006D; GB:M32600; NID:G170118; PIDN: R;Shiraiishi, N.; Kubo, Y.; Takeba, G.; Kiyota, S.; Sakano, K.; Nakagawa, H. Plant Cell Physiol. 32, 1031-1038, 1991
 A;Title: Sequence analysis of cloned cDNA and proteolytic fragments for nitrate reductase
 A;Reference number: PQ0694
 A;Accession: PQ0694
 A;Molecule type: mRNA
 A;Residues: 287-926 <SH1>
 A;Cross-references: UNIPARC:UPI000016DB7F
 A;Experimental source: cv. Hoyo
 A;Accession: PQ0695
 A;Molecule type: protein
 A;Residues: 541-550; 659-667 <SH2>
 A;Cross-references: UNIPARC:UPI0000172110; UNIPARC:UPI0000172111
 R;Quinn, G.B.; Trimboli, A.J.; Prosser, I.M.; Barber, M.J. Arch. Biochem. Biophys. 327, 151-160, 1996

A;Title: Spectroscopic and kinetic properties of a recombinant form of the flavin domain
 A;Reference number: S62777; MUID:96201358; PMID:8615685
 A;Accession: S62777
 A;Molecule type: protein
 A;Residues: 639-673; 722-731; 758-766; 789-798; 802-814; 829-833; 846-852; 853-858; 859-864; 874-119; UNIPARC:UPI0000172112; UNIPARC:UPI0000172113; UNIPARC:UPI0000172114; UNIPARC:UPI0000172115; UNIPARC:UPI0000172116; UNIPARC:UPI0000172117; UNIPARC:UPI0000172118; UNIPARC:UPI0000172119; UNIPARC:UPI0000172120; UNIPARC:UPI0000172121; UNIPARC:UPI0000172122; UNIPARC:UPI0000172123; UNIPARC:UPI0000172124; UNIPARC:UPI0000172125; UNIPARC:UPI0000172126; UNIPARC:UPI0000172127; UNIPARC:UPI0000172128; UNIPARC:UPI0000172129; UNIPARC:UPI0000172130; UNIPARC:UPI0000172131; UNIPARC:UPI0000172132; UNIPARC:UPI0000172133; UNIPARC:UPI0000172134; UNIPARC:UPI0000172135; UNIPARC:UPI0000172136; UNIPARC:UPI0000172137; UNIPARC:UPI0000172138; UNIPARC:UPI0000172139; UNIPARC:UPI0000172140; UNIPARC:UPI0000172141; UNIPARC:UPI0000172142; UNIPARC:UPI0000172143; UNIPARC:UPI0000172144; UNIPARC:UPI0000172145; UNIPARC:UPI0000172146; UNIPARC:UPI0000172147; UNIPARC:UPI0000172148; UNIPARC:UPI0000172149; UNIPARC:UPI0000172150; 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UNIPARC:UPI0000172459; UNIPARC:UPI0000172460; UNIPARC:UPI0000172461; UNIPARC:UPI0000172462; UNIPARC:UPI0000172463; UNIPARC:UPI0000172464; UNIPARC:UPI0000172465; UNIPARC:UPI0000172466; UNIPARC:UPI0000172467; UNIPARC:UPI0000172468; UNIPARC:UPI0000172469; UNIPARC:UPI0000172470; UNIPARC:UPI0000172471; UNIPARC:UPI0000172472; UNIPARC:UPI0000172473; UNIPARC:UPI0000172474; UNIPARC:UPI0000172475; UNIPARC:UPI0000172476; UNIPARC:UPI0000172477; UNIPARC:UPI0000172478; UNIPARC:UPI0000172479; UNIPARC:UPI0000172480; UNIPARC:UPI0000172481; UNIPARC:UPI0000172482; UNIPARC:UPI0000172483; UNIPARC:UPI0000172484; UNIPARC:UPI0000172485; UNIPARC:UPI0000172486; UNIPARC:UPI0000172487; UNIPARC:UPI0000172488; UNIPARC:UPI0000172489; UNIPARC:UPI0000172490; UNIPARC:UPI0000172491; UNIPARC:UPI0000172492; UNIPARC:UPI0000172493; UNIPARC:UPI0000172494; UNIPARC:UPI0000172495; UNIPARC:UPI0000172496; UNIPARC:UPI0000172497; UNIPARC:UPI0000172498; UNIPARC:UPI0000172499; UNIPARC:UPI0000172500; UNIPARC:UPI0000172501; UNIPARC:UPI0000172502; UNIPARC:UPI0000172503; UNIPARC:UPI0000172504; UNIPARC:UPI0000172505; UNIPARC:UPI0000172506; UNIPARC:UPI0000172507; UNIPARC:UPI0000172508; UNIPARC:UPI0000172509; UNIPARC:UPI0000172510; UNIPARC:UPI0000172511; UNIPARC:UPI0000172512; UNIPARC:UPI0000172513; UNIPARC:UPI0000172514; UNIPARC:UPI0000172515; UNIPARC:UPI0000172516; UNIPARC:UPI0000172517; UNIPARC:UPI0000172518; UNIPARC:UPI0000172519; UNIPARC:UPI0000172520; UNIPARC:UPI0000172521; UNIPARC:UPI0000172522; UNIPARC:UPI0000172523; UNIPARC:UPI0000172524; UNIPARC:UPI0000172525; UNIPARC:UPI0000172526; UNIPARC:UPI0000172527; UNIPARC:UPI0000172528; UNIPARC:UPI0000172529; UNIPARC:UPI0000172530; UNIPARC:UPI0000172531; UNIPARC:UPI0000172532; UNIPARC:UPI0000172533; UNIPARC:UPI0000172534; UNIPARC:UPI0000172535; UNIPARC:UPI0000172536; UNIPARC:UPI0000172537; UNIPARC:UPI0000172538; UNIPARC:UPI0000172539; UNIPARC:UPI0000172540; UNIPARC:UPI0000172541; UNIPARC:UPI0000172542; UNIPARC:UPI0000172543; UNIPARC:UPI0000172544; UNIPARC:UPI0000172545; UNIPARC:UPI0000172546; UNIPARC:UPI0000172547; UNIPARC:UPI0000172548; UNIPARC:UPI0000172549; UNIPARC:UPI0000172550; UNIPARC:UPI0000172551; UNIPARC:UPI0000172552; UNIPARC:UPI0000172553; UNIPARC:UPI0000172554; UNIPARC:UPI0000172555; UNIPARC:UPI0000172556; UNIPARC:UPI0000172557; UNIPARC:UPI0000172558; UNIPARC:UPI0000172559; UNIPARC:UPI0000172560; UNIPARC:UPI0000172561; UNIPARC:UPI0000172562; UNIPARC:UPI0000172563; UNIPARC:UPI0000172564; UNIPARC:UPI0000172565; UNIPARC:UPI0000172566; UNIPARC:UPI0000172567; UNIPARC:UPI0000172568; UNIPARC:UPI0000172569; UNIPARC:UPI0000172570; UNIPARC:UPI0000172571; UNIPARC:UPI0000172572; UNIPARC:UPI0000172573; UNIPARC:UPI0000172574; UNIPARC:UPI0000172575; UNIPARC:UPI0000172576; UNIPARC:UPI0000172577; UNIPARC:UPI0000172578; UNIPARC:UPI0000172579; UNIPARC:UPI0000172580; UNIPARC:UPI0000172581; UNIPARC:UPI0000172582; UNIPARC:UPI0000172583; UNIPARC:UPI0000172584; UNIPARC:UPI0000172585; UNIPARC:UPI0000172586; UNIPARC:UPI0000172587; UNIPARC:UPI0000172588; UNIPARC:UPI0000172589; UNIPARC:UPI0000172590; UNIPARC:UPI0000172591; UNIPARC:UPI0000172592; UNIPARC:UPI0000172593; UNIPARC:UPI0000172594; UNIPARC:UPI0000172595; UNIPARC:UPI0000172596; UNIPARC:UPI0000172597; UNIPARC:UPI0000172598; UNIPARC:UPI0000172599; UNIPARC:UPI0000172600; UNIPARC:UPI0000172601; UNIPARC:UPI0000172602; UNIPARC:UPI0000172603; UNIPARC:UPI0000172604; UNIPARC:UPI0000172605; UNIPARC:UPI0000172606; UNIPARC:UPI0000172607; UNIPARC:UPI0000172608; UNIPARC:UPI0000172609; UNIPARC:UPI0000172610; UNIPARC:UPI0000172611; UNIPARC:UPI0000172612; UNIPARC:UPI0000172613; UNIPARC:UPI0000172614; UNIPARC:UPI0000172615; UNIPARC:UPI0000172616; UNIPARC:UPI0000172617; UNIPARC:UPI0000172618; UNIPARC:UPI0000172619; UNIPARC:UPI0000172620; UNIPARC:UPI0000172621; UNIPARC:UPI0000172622; UNIPARC:UPI0000172623; UNIPARC:UPI0000172624; UNIPARC:UPI0000172625; UNIPARC:UPI0000172626; UNIPARC:UPI0000172627; UNIPARC:UPI0000172628; UNIPARC:UPI0000172629; UNIPARC:UPI0000172630; UNIPARC:UPI0000172631; UNIPARC:UPI0000172632; UNIPARC:UPI0000172633; UNIPARC:UPI0000172634; UNIPARC:UPI0000172635; UNIPARC:UPI0000172636; UNIPARC:UPI0000172637; UNIPARC:UPI0000172638; UNIPARC:UPI0000172639; UNIPARC:UPI0000172640; UNIPARC:UPI0000172641; UNIPARC:UPI0000172642; UNIPARC:UPI0000172643; UNIPARC:UPI0000172644; UNIPARC:UPI0000172645; UNIPARC:UPI0000172646; UNIPARC:UPI0000172647; UNIPARC:UPI0000172648; UNIPARC:UPI0000172649; UNIPARC:UPI0000172650; UNIPARC:UPI0000172651; UNIPARC:UPI0000172652; UNIPARC:UPI0000172653; UNIPARC:UPI0000172654; UNIPARC:UPI0000172655; UNIPARC:UPI0000172656; UNIPARC:UPI0000172657; UNIPARC:UPI0000172658; UNIPARC:UPI0000172659; UNIPARC:UPI0000172660; UNIPARC:UPI0000172661; UNIPARC:UPI0000172662; UNIPARC:UPI0000172663; UNIPARC:UPI0000172664; UNIPARC:UPI0000172665; UNIPARC:UPI0000172666; UNIPARC:UPI0000172667; UNIPARC:UPI0000172668; UNIPARC:UPI0000172669; UNIPARC:UPI0000172670; UNIPARC:UPI0000172671; UNIPARC:UPI0000172672; UNIPARC:UPI0000172673; UNIPARC:UPI0000172674; UNIPARC:UPI0000172675; UNIPARC:UPI0000172676; UNIPARC:UPI0000172677; UNIPARC:UPI0000172678; 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UNIPARC:UPI0000172723; UNIPARC:UPI0000172724; UNIPARC:UPI0000172725; UNIPARC:UPI0000172726; UNIPARC:UPI0000172727; UNIPARC:UPI0000172728; UNIPARC:UPI0000172729; UNIPARC:UPI0000172730; UNIPARC:UPI0000172731; UNIPARC:UPI0000172732; UNIPARC:UPI0000172733; UNIPARC:UPI0000172734; UNIPARC:UPI0000172735; UNIPARC:UPI0000172736; UNIPARC:UPI0000172737; UNIPARC:UPI0000172738; UNIPARC:UPI0000172739; UNIPARC:UPI0000172740; UNIPARC:UPI0000172741; UNIPARC:UPI0000172742; UNIPARC:UPI0000172743; UNIPARC:UPI0000172744; UNIPARC:UPI0000172745; UNIPARC:UPI0000172746; UNIPARC:UPI0000172747; UNIPARC:UPI0000172748; UNIPARC:UPI0000172749; UNIPARC:UPI0000172750; UNIPARC:UPI0000172751; UNIPARC:UPI0000172752; UNIPARC:UPI0000172753; UNIPARC:UPI0000172754; UNIPARC:UPI00001727

Query Match 52.5%; Score 42; DB 1; Length 1839;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CYCFW 7
|||
DB 1090 CYCFW 1094

RESULT 34
S19112
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004
C:Accession: S19112
R:Myivaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A:Title: Biochemical implications from the variable gene sequences of an anti-cytochrome forms.
A:Reference number: S17586; MUID:92015240; PMID:1656053
A:Accession: S19112
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <MYL>
A:Cross-references: UNIPROT:Q9QVF0; UNIPROT:Q920B6; UNIPARC:UPI0000176CC7; EMBL:X60684
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:16-90/Domain: immunoglobulin homology <IMM>

Query Match 51.2%; Score 41; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YYCYCFWKT 9
|||
DB 86 YYCQHFNST 94

RESULT 35
KVMSK2
Ig kappa chain precursor V region (K2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Jul-1980 #sequence_revision 31-Jul-1980 #text_change 09-Jul-2004
C:Accession: A01918
R:Nishioaka, Y.; Leder, P.
J. Biol. Chem. 255, 3691-3694, 1980
A:Title: Organization and complete sequence of identical embryonic and plasmacytoma kappa
A:Reference number: A01918; MUID:80159999; PMID:6767723
A:Accession: A01918
A:Molecule type: DNA
A:Residues: 1-115 <NIS>
A:Cross-references: UNIPROT:P01635; UNIPARC:UPI00002A0AA; GB:V00778; GB:J00545; NID:G51
A:Note: the sequence was determined from the germline gene
A:Note: the gene was isolated and sequenced separately from two different sources, embryo
C:Genetics:
A:Introns: 17/1
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 14
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Product: Ig kappa chain V region (K2) #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>
F:43-108/Disulfide bonds: #status predicted

Query Match 51.2%; Score 41; DB 1; Length 115;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YYCYCFWKT 9
|||
DB 106 YYCQHFNST 114

Query Match 51.2%; Score 41; DB 2; Length 218;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCF 6
|||
DB 202 YYCF 207

RESULT 37
T23755
hypothetical protein M117.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23755
R:Kershaw, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19794
A:Accession: T23755
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-552 <WIL>
A:Cross-references: UNIPROT:Q21538; UNIPARC:UPI000016419F; EMBL:Z733910; PIDN:CAA98134.1;
A:Experimental source: clone M117
C:Genetics:
A:Gene: CESP:M117.1
A:Map position: 4
A:Introns: 44/3; 73/3; 94/2; 148/3; 268/3; 371/3; 463/2; 499/1

Query Match 51.2%; Score 41; DB 2; Length 552;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YYCYCFWKT 9
:|:|:|
DB 53 FYAYCLWDT 61

RESULT 38
JQ1366
Polyprotein - hepatitis C virus (French isolate) (fragments)
C:Species: hepatitis C virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C:Accession: JQ1366
R:Kremsdorf, D.; Porchon, C.; Kim, J.P.; Reyes, G.R.; Brechot, C.
J. Gen. Virol. 72, 2557-2561, 1991
A:Title: Partial nucleotide sequence analysis of a French hepatitis C virus: implication
A:Reference number: JQ1366; MUID:92013977; PMID:1655961
A:Accession: JQ1366
A:Molecule type: Genomic RNA
A:Residues: 1-716 <KRE>
A:Cross-references: UNIPROT:Q9PX22; UNIPARC:UPI0000178531
C:Keywords: glycoprotein; polyprotein
F:84,90,97,115,143,199,223,243,290,312/Binding site: carbohydrate (Asn) (covalent) #stat

Query Match 51.2%; Score 41; DB 2; Length 716;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 YCYCFWKT 10
 DB 399 CSQLMNTC 406
 |||||

RESULT 39
 S2857
 nitrate reductase (NADH) (EC 1.7.1.1) - Beauveria bassiana
 C:Species: Beauveria bassiana
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S52857
 R:Maurer, P.
 submitted to the EMBL Data Library, February 1995
 A:Reference number: S52857
 A:Accession: S52857
 A:Molecule type: DNA
 A:Residues: 1-894 <MAU>
 A:Cross-references: UNIPROT:P43100; UNIPARC:UPI000013005F; EMBL:X84950; NID:G693925; PID
 C:Genetics:
 A:Introns: 593/1
 C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu
 C:Keywords: heme; iron; metalloprotein; molybdenum; molybdopterin; oxidoreductase; phosph
 P:62-467/Domain: molybdopterin-binding domain homology <PCO>
 F:535-609/Domain: cytochrome b5 core homology <CB5>
 F:645-894/Domain: cytochrome-b5 reductase homology <CBR>
 F:169/Binding site: molybdopterin (Cys) (covalent) #status predicted
 F:570,593/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 51.2%; Score 41; DB 2; Length 894;
 Best Local Similarity 57.1%; Pred. No. 1.8e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YCYCFWK 8
 DB 417 FCWCFWE 423
 |||||

RESULT 40
 T39475
 probable ATP-dependent RNA helicase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T39475
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
 submitted to the EMBL Data Library, May 1998
 A:Reference number: Z21857
 A:Accession: T39475
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1428 <LYN>
 A:Cross-references: UNIPROT:O60114; UNIPARC:UPI000006C2ED; EMBL:AL023290; PIDN:CAA18896.
 A:Experimental source: strain 972h-; cosmid c15C4
 C:Genetics:
 A:Gene: SPDB:SPBC15C4.05
 A:Map position: 2

Query Match 51.2%; Score 41; DB 2; Length 1428;
 Best Local Similarity 62.5%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYCYCFWK 8
 DB 1178 YYAYCAWR 1185
 |||||

RESULT 41
 A34895
 mucin 2, intestinal/tracheal - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)

C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 31-Dec-2004
 C:Accession: A54895
 R:Omori, H.; Dohrman, A.F.; Gallup, M.; Tsuda, T.; Kai, H.; Gum Jr., J.R.; Kim, Y.S.; B
 J. Biol. Chem. 269, 17833-17840, 1994
 A:Title: Molecular cloning of the amino-terminal region of a rat MUC 2 mucin gene homolo
 A:Reference number: A54895; MUID:94299489; PMID:8027037
 A:Accession: A54895
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1513 <OHM>
 A:Cross-references: UNIPROT:Q62635; UNIPARC:UPI000012F8D0; GB:U07615
 C:Superfamily: von Willebrand factor type C repeat homology
 C:Keywords: intestine

Query Match 51.2%; Score 41; DB 2; Length 1513;
 Best Local Similarity 57.1%; Pred. No. 2.7e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKT 10
 DB 1234 FCYWETC 1240
 |||||

RESULT 42
 T28486
 hypothetical protein E7L - variola major virus
 C:Species: variola major virus
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T28486
 R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
 Nature 366, 748-751, 1993
 A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
 A:Reference number: Z20488; MUID:94088747; PMID:8264798
 A:Accession: T28486
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-76 <MAS>
 A:Cross-references: UNIPROT:Q85374; UNIPARC:UPI0000061D20; EMBL:L22579; NID:G623595; PID
 A:Experimental source: strain Bangladesh-1975

Query Match 50.0%; Score 40; DB 2; Length 76;
 Best Local Similarity 55.6%; Pred. No. 42;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYCYCFWKT 9
 DB 59 YHLLCFWRT 67
 |||||

RESULT 43
 F72156
 C7L protein - variola minor virus (strain Garcia-1966)
 C:Species: variola minor virus
 C>Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
 C:Accession: F72156
 R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Saifonov, P.F.; Massung, R.F.; Lopar
 submitted to GenBank, March 1998
 A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
 A:Reference number: A72150
 A:Accession: F72156
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-76 <SHC>
 A:Cross-references: UNIPROT:Q85374; UNIPARC:UPI0000061D20; GB:Y16780; NID:G5830555; PIDN
 A:Experimental source: strain Garcia-1966
 C:Genetics:
 A:Gene: C7L

Query Match 50.0%; Score 40; DB 2; Length 76;
 Best Local Similarity 55.6%; Pred. No. 42;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYCYCFWKT 9

Db 59 YHLLCFWRT 67

RESULT 44

hypothetical protein - Lactococcus lactis plasmid pMRC01
T43130
C:Species: Lactococcus lactis
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T43130
R:Dougherty, B.A.; Hill, C.; Weidman, J.F.; Richardson, D.R.; Venter, J.C.; Ross, R.P.
Mol. Microbiol. 29, 1029-1038, 1998
A:Title: Sequence and analysis of the 60 kb conjugative, bacteriocin-producing plasmid pMRC01
A:Reference number: Z22314
A:Accession: T43130
A>Status: preliminary; translated from GE/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-121 <DOU>
A:Cross-references: UNIPROT:O87259; UNIPARC:UPI00000BD2DD; EMBL:AE001272; PIDN:AAC56048.
A:Experimental source: strain DPC3147
C:Genetics:
A:Genome: plasmid pMRC01
A:Note: ORF00059
C:Superfamily: Lactococcus lactis hypothetical protein PL08712.5

Query Match 50.0%; Score 40; DB 2; Length 121;
Best Local Similarity 54.5%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

QY 1 YYC---YCFW 7
Db 103 YYCMLAPFCFW 113

RESULT 45

IG kappa chain precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C/Accession: S01320
R/de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A/Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A/Reference number: S01320; MUID:88329081; PMID:3138116
A/Accession: S01320
A/Molecule type: mRNA
A/Residues: 1-234 <DB1>
A/Cross-references: UNIPARC:UPT0000115DDA; EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID
A/Note: This sequence was determined from the differentiated gene
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-234/Product: Ig kappa chain #status predicted <MAT>
F/36-110/Domain: immunoglobulin homology <IMW>

Query Match	50.0%	Score 40;	DB 2;	Length 234;
Best Local Similarity	66.7%	Pred. No. 95;		
Matches	6;	Conservative	0;	Mismatches 3;
		Indels	0;	Gaps 0;

Qy 1 YCYCFWKT 9
pb 106 YCYCFWKT 106

RESULT 46

T27205
 hypothetical protein Y57A10C.9 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27205
 R:Smye, R.
 submitted to the EMBL Data Library, June 1998
 A:Reference number: Z20127

A,Accession: T27205
A,Status: preliminary;
A,Molecule type: DNA
A,Residues: 1-247 <WIL>
A,Cross-references: UNIPROT:O62493; UNIPARC:UPI00000
A,Experimental source: clone Y57A10C
A,Translated from: GB/EMBL/DBJ

C/Genetics:
A;Gene: CESP:Y57A10C.9
A;Map position: 2
A;Introns: 38/2; 110/3; 138/3; 200/1

Query Match 50.0%; Score 40; DB 2; Length 247;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YYCYCFWK 8
Db 31 YIIYCFWR 38

RESULT 47

C71637
rod shape-determining protein mreC (mreC) RP767 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: C71637
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: C71637
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-304 <AND>
A:Cross-references: UNIPROT:Q9ZCH5; UNIPARC:UPI000000D37EC; GB:AJ235269; NID
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: mreC; RP767

Query Match	50.0%	Score 40;	DB 2;	Length 304;
Best Local Similarity	53.3%	Pred. No. 1.2e+02;		
Matches	8:	Conservative	0:	Mismatches
			3:	Indels
			4:	Gaps

Qy 1 YYC---YCFWKTC 11
pb 274 YYCRSSNSCFKCT 28

RESULT 48

hypothetical protein D1007.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jan-2000
C:Accession: T30924
R:Davidson, S.; Kohlfing, T.
submitted to the EMBL Data Library, August 1999
A:Description: The sequence of *C. elegans* cosmid D1007.
A:Reference number: Z20934
A:Accession: T30924
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-512 <DAV>
A:Cross-references: UNIPARC:UPI0000179267; EMBL:AF003151; PIDN:AAB54224.1
A:Experimental source: strain Bristol N2; clone D1007
C:Genetics:

A; Map position: 1
A; Introns: 82/3; 110/3; 172/2; 207/2; 309/3; 430/3
A; Note: D1007.5
C; Superfamily: *Caenorhabditis elegans* hypothetical

Query Match 50.0%; Score 40; DB 2; Length 512;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YCYCFW 7
Db 398 FCWCFW 403

Search completed: May 9, 2006, 12:10:12
Job time : 42.3333 secs

```

Qy 5 CFWKTC 11
   |||||
Db 106 CFWKTI 112

RESULT 49
S70584
nitrate reductase (NADPH) (EC 1.7.1.3) - Aspergillus parasiticus
C/Species: Aspergillus parasiticus
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S70584
R/Chang, P.K.; Ehrlich, K.C.; Linz, J.E.; Bhatnagar, D.; Cleveland, T.E.; Bennett, J.W.
Curr. Genet. 30, 68-75, 1996
A/Title: Characterization of the Aspergillus parasiticus niad and niia gene cluster.
A/Reference number: S70584; MUID:96269932; PMID:8662212
A/Accession: S70584
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-859 <CHA>
A/Cross-references: UNIPROT:Q00284; UNIPARC:UPI000003CAAC; EMBL:U38948; NID:gl477473; PI
A/Experimental source: ATCC 56775
C/Genetics:
A/Gene: niad
A/Introns: 91/1; 124/2; 210/3; 289/2; 364/1; 572/1
C/Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu
C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; iron; metallopro
F/45-448/Domain: molybdopter-in-binding domain homology <PCO>
F/514-588/Domain: cytochrome b5 core homology <CB5>
F/622-859/Domain: cytochrome-b5 reductase homology <CBR>
F/152/Binding site: molybdopter-in (Cys) (covalent) #status predicted
F/549,572/Binding site: heme iron (His) (axial ligands) #status predicted
F/833/Binding site: NADP (Cys) #status predicted

Query Match 50.0%; Score 40; DB 2; Length 859;
Best Local Similarity 66.7%; Pred. NO. 2.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YCYCFW 7
   |||||
Db 398 FCWCFW 403

RESULT 50
JQ1525
nitrate reductase (NADPH) (EC 1.7.1.3) - Aspergillus niger
C/Species: Aspergillus niger
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: JQ1525
R/Unkles, S.E.; Campbell, E.I.; Punt, P.J.; Hawker, K.L.; Contreras, R.; Hawkins, A.R.;
Gene 111, 149-155, 1992
A/Title: The Aspergillus niger niad gene encoding nitrate reductase: upstream nucleotide
A/Reference number: JQ1525; MUID:92175518; PMID:1541396
A/Accession: JQ1525
A/Molecule type: DNA
A/Residues: 1-867 <UNK>
A/Cross-references: UNIPROT:P36858; UNIPARC:UPI000013005E; GB:M77022
C/Genetics:
A/Gene: niad
A/Introns: 91/1; 124/2; 210/3; 289/2; 364/1; 572/1
C/Complex: homodimer
C/Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu
C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
F/45-448/Domain: molybdopter-in-binding domain homology <PCO>
F/514-588/Domain: cytochrome b5 core homology <CB5>
F/622-867/Domain: cytochrome-b5 reductase homology <CBR>
F/152/Binding site: molybdopter-in (Cys) (covalent) #status predicted
F/399/Disulfide bonds: interchain #status predicted
F/549,572/Binding site: heme iron (His) (axial ligands) #status predicted
F/688,841/Binding site: NADP (Lys, Cys) #status predicted
F/725/Binding site: FAD (Tyr) #status predicted

Query Match 50.0%; Score 40; DB 1; Length 867;

```

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:05:00 ; Search time 67.3333 Seconds
(without alignments)
115.260 Million cell updates/sec

Title: US-10-796-158-7

Perfect score: 80

Sequence: 1 YYCYCPWKCT 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	62.5	405	2	Q8T609_BOMMO
2	48	60.0	507	2	Q7MNB7_VIBVY
3	48	60.0	1132	2	Q83861_NILPARVATA
4	47	58.8	891	2	Q4LEW9_PHYSCMITRE
5	47	58.8	892	2	Q4LEW8_PHYSCMITRE
6	47	58.8	1302	2	Q22426_CAENORHABDI
7	46	57.5	449	2	Q5Q1V6_9SOLA
8	46	57.5	487	2	Q92921_AGRGI
9	46	57.5	497	2	Q92922_AGRGI
10	46	57.5	501	2	Q43265_MAIZE
11	46	57.5	621	1	NIA1_MAIZE
12	46	57.5	629	2	P92920_AGRGI
13	46	57.5	750	2	Q8LT14_SOLITU
14	46	57.5	875	2	Q48930_SOYBN
15	46	57.5	881	1	NIA1_PHAVU
16	46	57.5	886	1	NIA1_SOYBN
17	46	57.5	889	1	NIA3_MAIZE
18	46	57.5	889	2	Q6ZHH7_ORYSA
19	46	57.5	890	1	NIA2_PHAVU
20	46	57.5	890	2	Q6SYRO_SOYBN
21	46	57.5	891	1	NIA7_HORVU
22	46	57.5	898	1	NIA1_BETVE
23	46	57.5	900	1	NIA1_LOTJA
24	46	57.5	904	1	NIA1_TOBAC
25	46	57.5	904	1	NIA2_TOBAC
26	46	57.5	906	2	Q93XS1_PRUPE
27	46	57.5	909	1	NIA1_PETHY
28	46	57.5	910	2	Q9XGW5_MAIZE
29	46	57.5	911	1	NIA1_LYCES
30	46	57.5	911	2	O04926_SOLITU
31	46	57.5	911	2	O24390_SOLITU

32	46	57.5	911	2	Q8LT13_SOLITU
33	46	57.5	912	1	NIA2_HORVU
34	46	57.5	914	2	Q9FUC2_RICCO
35	46	57.5	915	1	NIA1_HORVU
36	46	57.5	915	2	Q43042_PETHY
37	46	57.5	918	1	NIA_CUCWA
38	46	57.5	920	1	NIA_CICIN
39	45	56.2	152	1	UL01_HCNVA
40	45	56.2	261	2	Q4TAA1_TETNG
41	45	56.2	262	2	Q9FHA1_ARATH
42	45	56.2	334	2	Q96615_CAEBL
43	45	56.2	342	2	Q4N4M4_THEPA
44	45	56.2	843	2	Q8PI24_XANAC
45	45	56.2	2869	2	Q60PD2_CAEBR
46	44	55.0	227	2	Q8BKA5_MOUSE
47	44	55.0	315	2	Q706P3_PSEPU
48	44	55.0	332	2	O84491_CHLTR
49	44	55.0	332	2	Q9PJ07_CHLMU
50	44	55.0	334	2	Q9Z7V2_CHLPN
51	44	55.0	335	2	Q5L6X5_CHLAB
52	44	55.0	335	2	Q824K7_CHLCV
53	44	55.0	869	2	Q6MYK4_ASFPV
54	44	55.0	869	2	Q8TGB7_ASFPV
55	44	55.0	869	2	Q4WSG7_ASFPV
56	43.5	54.4	244	2	Q5HGA5_XANOR
57	43	53.8	148	2	Q911G9_HHV8
58	43	53.8	155	2	Q6ZU79_HUMAN
59	43	53.8	220	2	Q6VUT7_9BACT
60	43	53.8	220	2	Q6VV07_9BACT
61	43	53.8	246	2	Q8S8Q8_ARATH
62	43	53.8	285	2	Q8Y800_LISMO
63	43	53.8	323	2	Q4MV36_BACCE
64	43	53.8	529	2	Q4IN09_GIBZE
65	43	53.8	593	2	Q6TLC6_APIME
66	43	53.8	594	2	Q5JX99_HUMAN
67	43	53.8	630	2	Q7S3D2_NEUCR
68	43	53.8	646	2	Q6TLC7_APIME
69	43	53.8	714	2	Q6ZUT3_HUMAN
70	43	53.8	717	1	CNGC5_ARATH
71	43	53.8	773	2	Q7QRF9_GIALA
72	43	53.8	2267	2	Q4T578_TETNG
73	42	52.5	39	2	Q4XQ33_PLACH
74	42	52.5	108	2	Q5Z938_ORYSA
75	42	52.5	132	2	Q6Z212_ORYSA
76	42	52.5	144	2	Q6MEN5_BDEBA
77	42	52.5	171	2	Q4MLW6_BACCE
78	42	52.5	196	2	Q6HA18_BACHK
79	42	52.5	196	2	Q72WZ7_BACCI
80	42	52.5	196	2	Q81415_BACCR
81	42	52.5	196	2	Q81JK6_BACAN
82	42	52.5	196	2	Q630F5_BACCC
83	42	52.5	199	2	Q8EWV4_MYCPE
84	42	52.5	209	2	Q5DEV3_SCHJA
85	42	52.5	238	2	Q86FN7_CAEBL
86	42	52.5	266	2	Q9VI83_DROME
87	42	52.5	266	2	Q9SDR9_PRUDU
88	42	52.5	289	1	ATL5L1_ARATH
89	42	52.5	286	2	Q4JJ98_BRARC
90	42	52.5	296	2	Q4JJ99_BRARC
91	42	52.5	304	2	Q6P702_XENLA
92	42	52.5	321	2	Q6PAN0_MOUSE
93	42	52.5	328	2	Q6D9N0_ERWCT
94	42	52.5	380	2	Q8OU51_MOUSE
95	42	52.5	422	2	Q6GLM8_XENLA
96	42	52.5	423	1	TIC2_MOUSE
97	42	52.5	424	1	TIC2_HUMAN
98	42	52.5	543	2	Q8WTL1_CAEBL
99	42	52.5	562	2	Q61B18_CAEBR
100	42	52.5	563	2	Q95XX1_CAEBL
101	42	52.5	536	2	Q7PSK6_ANOGA
102	42	52.5	724	2	Q7X641_ORYSA
103	42	52.5	859	1	NIA_PICAN
104	42	52.5	859	2	Q7LLV6_PICAN

Q8LT13	solanum tub
P27969	hordeum vul
Q9FUC2	ricinus com
P27967	hordeum vul
Q43042	petunia hyb
P17569	cucurbita m
P43101	cichorium i
P17146	human cytom
Q4TAA1	tetradodon n
Q9FHA1	arabidopsis
Q96615	caenorhabdi
Q4N4M4	theileria p
Q8PI24	xanthomonas
Q60PD2	caenorhabdi
Q8BKA5	m mus muscu
O84491	chlamydia t
Q9PJ07	chlamydia m
Q9Z7V2	chlamydia p
Q5L6X5	chlamydophi
Q824K7	chlamydophi
Q6MYK4	aspergillus
Q8TGB7	aspergillus
Q4WSG7	aspergillus
Q5HGA5	xanthomonas
Q911G9	human herpe
Q6ZU79	homo sapien
Q6VUT7	uncultured
Q6VV07	uncultured
Q8S8Q8	arabidopsis
Q8Y800	listeria m
Q4MV36	bacillus ce
Q4IN09	gibberella
Q6TLC6	apis mellif
Q5JX99	homo sapien
Q7S3D2	neurospora
Q6TLC7	apis mellif
Q6ZUT3	homo sapien
Q8RW99	arabidopsis
Q7QRF9	giardia lam
Q4T578	tetradodon n
Q4XQ33	plasmodium
Q5Z938	oryza sativ
Q6Z212	oryza sativ
Q6MEN5	bdellovibri
Q4MLW6	bacillus ce
Q6HA18	bacillus th
Q72WZ7	bacillus ce
Q81415	bacillus ce
Q81JK6	bacillus an
Q630F5	bacillus ce
Q8EWV4	mycoplasma
Q5DEV3	schistosoma
Q86FN7	caenorhabdi
Q9VI83	drosophila
Q9SDR9	prunus dulc
Q9FIO0	arabidopsis
Q4JJ98	brassica ra
Q4JJ99	brassica ra
Q6P702	xenopus lae
Q6PAN0	mus musculu
Q6D9N0	erwinia car
Q8OU51	mus musculu
Q6GLM8	xenopus lae
Q9ER58	mus musculu
Q92563	homo sapien
Q8WTL1	caenorhabdi
Q61B18	caenorhabdi
Q95XX1	caenorhabdi
Q7PSK6	anopheles g
Q7X641	oryza sativ
P49050	pichia angu
Q7LLV6	pichia angu

105	42	52.5	894	2	Q8H1T7_TILPL	Q8H1T7_tilia platy	178	40	50.0	289	2	Q5LK68_BACHK	Q5LK68_bacillus th
106	42	52.5	911	1	N1A1_BRANA	P39867 brassica na	179	40	50.0	304	2	Q9ZCH5_RICPR	Q9ZCH5_rickettsia
107	42	52.5	911	1	N1A2_BRANA	P39868 brassica na	180	40	50.0	308	2	Q5N9N5_ORYSA	Q5N9N5_oryza sativ
108	42	52.5	917	1	N1A1_ARATH	P11832 arabidopsis	181	40	50.0	319	2	Q86M17_CAEL	Q86M17_caenorhabdi
109	42	52.5	917	1	N1A2_ARATH	P11035 arabidopsis	182	40	50.0	322	2	Q61UK4_CAEBR	Q61UK4_caenorhabdi
110	42	52.5	917	2	Q94C76_ARATH	Q94C76 arabidopsis	183	40	50.0	338	2	Q61UK6_DROME	Q61UK6_drosophila
111	42	52.5	926	1	N1A_SPTOL	P23112 spinacia ol	184	40	50.0	362	1	RF1_BUCBP	P59456 buchnera ap
112	42	52.5	1264	2	Q4N5D9_THEPA	Q4N5D9 theileria p	185	40	50.0	402	2	Q86GV0_CAEL	Q86GV0_caenorhabdi
113	42	52.5	1265	2	Q4UE53_THEAN	Q4UE53 theileria a	186	40	50.0	404	2	Q4RM39_TETNG	Q4RM39_tetradodon n
114	42	52.5	1839	1	P0LR_EPMV	P20126 eggplant mo	187	40	50.0	436	2	Q6CME3_KLULA	Q6CME3_kluyveromyc
115	42	52.5	2579	2	Q5XX25_CHAFE	Q5XX25 charybdis f	188	40	50.0	477	2	Q01870_CAEL	Q01870_caenorhabdi
116	42	52.5	2994	2	Q81I24_PLAF7	Q81I24 plasmodium	189	40	50.0	478	2	Q60PF1_CAEBR	Q60PF1_caenorhabdi
117	41.5	51.9	136	2	Q91IH2_HVH8	Q91IH2 human herpe	190	40	50.0	533	2	Q5BFG7_EMENI	Q5BFG7_aspergillus
118	41.5	51.9	237	2	Q7VFM5_HELHP	Q7VFM5 helicobacte	191	40	50.0	718	2	Q7R6F1_GIALA	Q7R6F1_giardia lam
119	41.5	51.9	284	2	Q91GW1_HVH8	Q91GW1 human herpe	192	40	50.0	787	2	Q891A4_CLOTE	Q891A4_clostridium
120	41	51.2	34	2	Q8PJK3_HUMAN	Q8PJK3 homo sapien	193	40	50.0	859	2	Q00284_ASPPA	Q00284_aspergillus
121	41	51.2	61	2	Q81Z26_BACAN	Q81Z26 bacillus an	194	40	50.0	867	1	N1A_ASPPG	P36858 aspergillus
122	41	51.2	97	2	Q82853_NRETR	Q82853 jembrana di	195	40	50.0	868	2	Q12561_ASPPR	P36858 aspergillus
123	41	51.2	105	2	Q5DT32_CARCH	Q5DT32 carcharodon	196	40	50.0	890	1	N1A2_SOYBN	P39870 glycine max
124	41	51.2	109	2	Q920B6_MOUSE	Q920B6 mus musculu	197	40	50.0	891	2	Q00101_PHANO	Q00101_phaeosphaer
125	41	51.2	110	2	Q5AHC7_CANAL	Q5AHC7 candida alb	198	40	50.0	893	1	N1A_LEPMC	P36842 leptosphaer
126	41	51.2	114	2	Q82854_NRETR	Q82854 jembrana di	199	40	50.0	905	1	N1A_FUSOX	P39853 fusarium ox
127	41	51.2	115	1	KV5C_MOUSE	P01635 mus musculu	200	40	50.0	907	2	Q92237_GIBFU	Q92237 gibberella
128	41	51.2	150	2	Q95WTO_TRYCR	Q95WTO trypanosoma	201	40	50.0	908	2	Q9UVH6_HEBCY	Q9UVH6_hebeloma cy
129	41	51.2	218	2	Q40647_ORYSA	Q40647 oryza sativ	202	40	50.0	982	1	N1A_NEUCR	P08619 neurospora
130	41	51.2	258	2	Q6C8A5_YARLI	Q6C8A5 yarrowia li	203	40	50.0	1275	2	Q5FGQ0_EHRRG	Q5FGQ0_ehrlichia r
131	41	51.2	277	2	Q4XU26_PLACH	Q4XU26 plasmodium	204	40	50.0	1787	2	Q8YV18_ANASP	Q8YV18_anabaena ap
132	41	51.2	289	2	Q5QYX8_ENTHI	Q5QYX8 entamoeba h	205	40	50.0	1800	2	Q8YF00_ANASP	Q8YF00_anabaena ap
133	41	51.2	299	2	Q6PPG7_9BACT	Q6PPG7 uncultured	206	40	50.0	3795	2	Q4Q754_LEIMA	Q4Q754_leishmania
134	41	51.2	329	2	Q6RUM6_9ROSI	Q6RUM6 cleome hass	207	40	50.0	4345	2	Q9VLA0_DROME	Q9VLA0_drosophila
135	41	51.2	338	2	Q5AYAT_EMENI	Q5AYAT aspergillus	208	40	50.0	4374	2	Q7KTG2_DROME	Q7KTG2_drosophila
136	41	51.2	356	1	PR44_LJCCU	Q52555 lucilia cup	209	39.5	49.4	186	1	UL55_HHV11	P10239 human herpe
137	41	51.2	423	2	Q5VH36_9ROSI	Q5VH36 podandrogy	210	39.5	49.4	186	1	UL55_HHV1E	P36236 human herpe
138	41	51.2	428	2	Q5VH36_9ROSI	Q5VH36 cleome pilo	211	39.5	49.4	186	1	UL55_HHV2H	P28251 human herpe
139	41	51.2	441	2	Q4Z4D2_PLABE	Q4Z4D2 plasmodium	212	39.5	49.4	253	2	Q4TB60_TETNG	Q4TB60_tetradodon n
140	41	51.2	468	2	Q816I9_HALARO	Q816I9 halocynthia	213	39.5	49.4	460	2	Q6F6A3_DAUCA	Q6F6A3_daucus caro
141	41	51.2	470	2	Q4Y4M5_PLACH	Q4Y4M5 plasmodium	214	39.5	49.4	461	2	Q84M29_HELAN	Q84M29_helianthus
142	41	51.2	480	2	Q7KSU2_PLAYO	Q7KSU2 plasmodium	215	39.5	49.4	489	2	Q81YM3_HUMAN	Q81YM3_homo sapien
143	41	51.2	480	2	Q5SNK1_9APIC	Q5SNK1 plasmodium	216	39.5	49.4	495	2	Q8C1D7_MOUSE	Q8C1D7_mus musculu
144	41	51.2	497	2	Q4PE50_USTMA	Q4PE50 uetiliago ma	217	39.5	49.4	495	2	Q6PES9_MOUSE	Q6PES9_mus musculu
145	41	51.2	513	2	Q4T2F1_TETNG	Q4T2F1 tetradodon n	218	39.5	49.4	496	2	Q6F6A5_DAUCA	Q6F6A5_daucus caro
146	41	51.2	699	2	Q9LGT8_ARATH	Q9LGT8 arabidopsis	219	39.5	49.4	516	2	Q6ZQZ6_HUMAN	Q6ZQZ6_homo sapien
147	41	51.2	711	2	Q84S65_ORYSA	Q84S65 oryza sativ	220	39.5	49.4	516	2	Q5T7W7_HUMAN	Q5T7W7_homo sapien
148	41	51.2	729	2	Q8VZK9_ARATH	Q8VZK9 arabidopsis	221	39.5	49.4	516	2	Q5RCP1_PONPY	Q5RCP1_pongo pygma
149	41	51.2	892	2	Q13486_METAN	Q13486 metarhizium	222	39.5	49.4	535	2	Q4T523_TETNG	Q4T523_tetradodon n
150	41	51.2	893	2	Q7ZAS0_9HYPO	Q7ZAS0 verticilliu	223	39	48.8	36	2	Q7QUD5_GIALA	Q7QUD5_giardia lam
151	41	51.2	894	1	N1A_BEABA	P43100 beauveria b	224	39	48.8	46	2	Q4X3H7_PLACH	Q4X3H7_plasmodium
152	41	51.2	911	2	Q51ZH4_MAGGR	Q51ZH4 magnaporthe	225	39	48.8	58	2	Q4TDS6_TETNG	Q4TDS6_tetradodon n
153	41	51.2	916	2	Q5ZC33_ORYSA	Q5ZC33 oryza sativ	226	39	48.8	87	2	Q615B7_CAEBR	Q615B7_caenorhabdi
154	41	51.2	916	2	Q8ZC37_ORYSA	Q8ZC37 oryza sativ	227	39	48.8	100	2	P88965_HHV8	P88965_human herpe
155	41	51.2	1381	2	Q4RQ84_TETNG	Q4RQ84 tetradodon n	228	39	48.8	102	2	Q9BG16_ELEMA	Q9BG16_elephas max
156	41	51.2	1428	2	Q60114_SCHPO	Q60114 schizosacch	229	39	48.8	115	2	Q9TZM6_CAEL	Q9TZM6_caenorhabdi
157	41	51.2	1513	1	MUC2_RAT	Q62635 rattus norv	230	39	48.8	119	2	Q656T0_ORYSA	Q656T0_oryza sativ
158	41	51.2	1710	2	Q5HAB4_EHRRW	Q5HAB4 ehrlichia r	231	39	48.8	120	1	YRAJ_BACSU	Q07934 bacillus su
159	40.5	50.6	78	2	Q9CXJ3_RAT	Q9CXJ3 rattus norv	232	39	48.8	130	2	Q5E336_9EUKA	Q5E336_uncultured
160	40.5	50.6	725	2	Q67QX6_SYMTH	Q67QX6 symbiobacte	233	39	48.8	130	2	Q20980_CAEL	Q20980_caenorhabdi
161	40	50.0	50	2	Q64X16_BACFR	Q64X16 bacteroides	234	39	48.8	134	2	Q970D0_SULTO	Q970D0_sulfolobus
162	40	50.0	76	2	Q76Q35_VARV	Q76Q35 variola min	235	39	48.8	134	2	Q15615_ENTHI	Q15615_entamoeba h
163	40	50.0	76	2	Q85374_VARV	Q85374 variola maj	236	39	48.8	137	2	Q8BY43_MOUSE	Q8BY43_mus musculu
164	40	50.0	121	2	Q32776_9LACT	Q32776 lactococcus	237	39	48.8	138	2	P95353_NEIGO	P95353_trypanosoma
165	40	50.0	121	2	Q87259_9LACT	Q87259 lactococcus	238	39	48.8	138	2	P95353_NEIGO	P95353_neisseria g
166	40	50.0	148	2	Q8SXC0_HCMV	Q8SXC0 human cytom	239	39	48.8	164	2	Q48341_TETNG	Q48341_tetradodon n
167	40	50.0	149	2	Q6SX69_HCMV	Q6SX69 human cytom	240	39	48.8	173	1	N06M_LATCH	Q03175_latimeria c
168	40	50.0	150	2	Q6C8B9_YARLI	Q6C8B9 yarrowia li	241	39	48.8	173	2	Q7QZ18_GIALA	Q7QZ18_giardia lam
169	40	50.0	167	2	Q56N03_VERDA	Q56N03 verticilliu	242	39	48.8	174	2	Q7SFP3_NEUCR	Q7SFP3_neurospora
170	40	50.0	167	2	Q7MZ07_PHOLL	Q7MZ07 photorhabdu	243	39	48.8	189	2	Q581W3_9TRYP	Q581W3_trypanosoma
171	40	50.0	176	2	Q8ZTA0_HUMAN	Q8ZTA0 homo sapien	244	39	48.8	192	2	Q4RXB1_TETNG	Q4RXB1_tetradodon n
172	40	50.0	235	2	Q5YD54_9PEZI	Q5YD54 collettotric	245	39	48.8	209	2	Q93991_CANAL	Q93991_candida alb
173	40	50.0	243	2	Q7TQM2_MOUSE	Q7TQM2 mus musculu	246	39	48.8	209	2	Q5A4P8_CANAL	Q5A4P8_candida alb
174	40	50.0	246	2	Q4IHJ6_GIBBE	Q4IHJ6 gibberella	247	39	48.8	209	2	Q87MW5_VIBPA	Q87MW5_vibrio para
175	40	50.0	247	2	Q62493_CAEL	Q62493 caenorhabdi	248	39	48.8	212	2	Q9A4W1_CAUCR	Q9A4W1_caulobacter
176	40	50.0	249	2	Q6OSB0_CAEBR	Q6OSB0 caenorhabdi	249	39	48.8	215	1	ERD2_ARATH	P35402_arabidopsis
177	40	50.0	250	2	Q8A7D7_BACTN	Q8A7D7 bacteroides	250	39	48.8	227	2	Q628M1_CAEBR	Q628M1_caenorhabdi

251	39	48.8	233	2	Q7V8C6	PROMM	Q7V8C6	prochloroco	324	38.5	48.1	1293	2	Q7R6A1	GIALA	Q7R6A1	giardia lam
252	39	48.8	235	2	Q4V0Z8	BACCZ	Q4V0Z8	bacillus ce	325	38.5	48.1	2531	2	Q6TXE7	RAT	Q6TXE7	rattus norv
253	39	48.8	269	2	Q7F905	ORYSA	Q7F905	oryza sativ	326	38	47.5	12	1	UTS2A	CATCO	UTS2A	catostomus
254	39	48.8	278	2	Q6CCV5	YARLI	Q6CCV5	yarrowia li	327	38	47.5	12	1	UTS2B	CATCO	UTS2B	catostomus
255	39	48.8	290	2	Q98138	HVH8	Q98138	human herpe	328	38	47.5	12	1	UTS2B	CVPCA	UTS2B	cyprinus ca
256	39	48.8	301	2	Q8ZG7	VERPE	Q8ZG7	yersinia pe	329	38	47.5	12	1	UTS2	GILMI	UTS2	gillichthys
257	39	48.8	309	2	Q82431	CABEL	Q82431	caenorhabdi	330	38	47.5	12	1	UTS2	POLSP	UTS2	poliodon sp
258	39	48.8	317	2	Q9MAU4	ANATH	Q9MAU4	arabidopsis	331	38	47.5	12	1	UTS2	SCICA	UTS2	scyllorhinu
259	39	48.8	324	2	Q45326	CABEL	Q45326	caenorhabdi	332	38	47.5	29	1	CYO12	VIOAR	CYO12	viola arven
260	39	48.8	327	2	Q8RCU3	THETN	Q8RCU3	thermoanaer	333	38	47.5	29	1	CYO12	VIOOD	CYO12	viola odora
261	39	48.8	337	2	Q9U312	CABEL	Q9U312	caenorhabdi	334	38	47.5	29	1	KAB4	OLDAP	KAB4	oldenlandia
262	39	48.8	338	2	Q4SB24	TETNG	Q4SB24	tetraodon n	335	38	47.5	29	1	KABS	OLDAP	KABS	oldenlandia
263	39	48.8	343	2	Q4O927	HVH8	Q4O927	human herpe	336	38	47.5	29	1	VARA	VIOAR	VARA	viola arven
264	39	48.8	351	2	Q9Y7F7	AKMME	Q9Y7F7	armillaria	337	38	47.5	29	1	VARC	VIOAR	VARC	viola arven
265	39	48.8	352	2	Q96FA1	HUMAN	Q96FA1	homo sapien	338	38	47.5	29	1	VARF	VIOAR	VARF	viola arven
266	39	48.8	360	2	Q6B0G7	HUMAN	Q6B0G7	homo sapien	339	38	47.5	29	1	VODM	VIOOD	VODM	viola odora
267	39	48.8	361	2	Q6OUB5	CAEBR	Q6OUB5	caenorhabdi	340	38	47.5	29	1	Q8RD20	THETN	Q8RD20	thermoanaer
268	39	48.8	362	2	Q7QE25	ANOQA	Q7QE25	anopheles g	341	38	47.5	52	2	Q4TF36	TETNG	Q4TF36	tetraodon n
269	39	48.8	390	2	Q7Q179	ANOQA	Q7Q179	anopheles g	342	38	47.5	59	2	Q4THE1	TETNG	Q4THE1	tetraodon n
270	39	48.8	431	2	Q4N5R5	THEBPA	Q4N5R5	theileria p	343	38	47.5	59	2	Q9LBZ3	STAAU	Q9LBZ3	staphylococ
271	39	48.8	432	2	Q54DY4	DICDI	Q54DY4	dictyosteli	344	38	47.5	66	2	Q8EDT1	SHEON	Q8EDT1	shewanella
272	39	48.8	435	2	Q8NJL7	ASPFU	Q8NJL7	aspergillus	345	38	47.5	78	2	UTS2	PLAFA	UTS2	platicthys
273	39	48.8	435	2	Q4WM50	ASPFU	Q4WM50	aspergillus	346	38	47.5	83	1	Q4O539	TORAC	Q4O539	nicotiana t
274	39	48.8	464	1	SYE	NEIGI	Q5F5J8	neisseria g	347	38	47.5	83	2	Q69C27	GREOV	Q69C27	pulau reovi
275	39	48.8	464	1	SYE	NEIMA	Q9JWC4	neisseria m	348	38	47.5	95	2	Q9J1B2	GREOV	Q9J1B2	nelson bay
276	39	48.8	464	1	SYE	NEIMB	Q9K1R6	neisseria m	349	38	47.5	95	2	Q8C3F8	MOUSE	Q8C3F8	mus musculu
277	39	48.8	466	1	SYE2	ANAMM	Q5PAG8	anaplasma m	350	38	47.5	101	2	Q5ZP61	9VIRU	Q5ZP61	cotesia con
278	39	48.8	470	1	SYE2	EHRRW	Q5FGW4	ehrlichia r	351	38	47.5	110	2	Q6ESG0	ORYSA	Q6ESG0	oryza sativ
279	39	48.8	470	1	SYE2	EHRRW	Q5HB98	ehrlichia r	352	38	47.5	112	2	UTS2B	MOUSE	UTS2B	mus musculu
280	39	48.8	485	1	SYE	SYNEL	Q8DL15	synecococc	353	38	47.5	113	1	Q5D8K0	SCHJA	Q5D8K0	schistosoma
281	39	48.8	485	2	Q9GNT9	9TRYPP	Q9GNT9	trypanosoma	354	38	47.5	113	2	UTS2B	RAT	UTS2B	bartonella
282	39	48.8	487	2	Q65ZL2	9MURI	Q65ZL2	mus sp. fv/	355	38	47.5	117	2	Q6G3K0	BARHE	Q6G3K0	rattus norv
283	39	48.8	490	1	SYE	BORBU	Q5I345	borrelia bu	356	38	47.5	118	1	UTS2B	RAT	UTS2B	homo sapien
284	39	48.8	490	1	SYE	BORBU	Q661P7	borrelia ga	357	38	47.5	119	1	UTS2B	HUMAN	UTS2B	homo sapien
285	39	48.8	503	2	Q9N3R8	BRAFL	Q9N3R8	branchiocto	358	38	47.5	121	1	UTS2	FIG	UTS2	mus scrofa
286	39	48.8	511	2	Q4SZ21	TETNG	Q4SZ21	tetraodon n	359	38	47.5	123	1	UTS2	MOUSE	UTS2	mus musculu
287	39	48.8	516	2	Q8ABC8	BACTN	Q8ABC8	bacteroides n	360	38	47.5	123	1	UTS2	RAT	UTS2	rattus norv
288	39	48.8	528	2	Q8BY42	DEBHA	Q8BY42	debaromyce	361	38	47.5	123	2	Q541G7	MOUSE	Q541G7	mus musculu
289	39	48.8	532	2	Q01972	CABEL	Q01972	caenorhabdi	362	38	47.5	123	2	Q5RIZ0	BRARE	Q5RIZ0	brachydanio
290	39	48.8	560	2	Q59WC7	CANAL	Q59WC7	candida alb	363	38	47.5	124	1	KAB1	OLDAP	KAB1	oldenlandia
291	39	48.8	589	2	Q4R1P1	TETNG	Q4R1P1	tetraodon n	364	38	47.5	124	1	UTS2	HUMAN	UTS2	homo sapien
292	39	48.8	600	2	Q5CSX7	CRYPV	Q5CSX7	cryptospori	365	38	47.5	124	2	Q6Q2J6	CHICK	Q6Q2J6	gallus gall
293	39	48.8	604	2	Q9VZC5	DROME	Q9VZC5	drosophila	366	38	47.5	125	1	UTS2A	CVPCA	UTS2A	cyprinus ca
294	39	48.8	641	2	Q4KLJ2	XENLA	Q4KLJ2	xenopus lae	367	38	47.5	125	1	UTS2B	BRARE	UTS2B	brachydanio
295	39	48.8	652	2	Q4TB21	TETNG	Q4TB21	tetraodon n	368	38	47.5	125	1	UTS2G	CVPCA	UTS2G	cyprinus ca
296	39	48.8	654	2	Q8YM21	ANASP	Q8YM21	anabaena sp	369	38	47.5	125	1	UTS2	MACMU	UTS2	macaca mula
297	39	48.8	656	2	Q5M7K6	XENTR	Q5M7K6	xenopus tro	370	38	47.5	125	2	Q61L82	DROME	Q61L82	drosophila
298	39	48.8	671	2	Q53H47	HUMAN	Q53H47	homo sapien	371	38	47.5	125	2	Q7S2C4	BRARE	Q7S2C4	brachydanio
299	39	48.8	699	2	Q6H464	ORYSA	Q6H464	oryza sativ	372	38	47.5	126	2	Q6Q273	CHICK	Q6Q273	gallus gall
300	39	48.8	733	2	Q86VG1	HUMAN	Q86VG1	homo sapien	373	38	47.5	127	1	UTS2	RANRI	UTS2	rana ridibu
301	39	48.8	736	2	Q8ZNB6	HUMAN	Q8ZNB6	homo sapien	374	38	47.5	127	2	Q8C5E6	MOUSE	Q8C5E6	mus musculu
302	39	48.8	738	1	CNGC7	ARATH	Q8E9N5	arabidopsis	375	38	47.5	128	2	Q6Z859	ORYSA	Q6Z859	oryza sativ
303	39	48.8	748	2	Q77066	CHOFU	Q77066	chloristoneu	376	38	47.5	129	2	Q70WH4	PLAFA	Q70WH4	platichthys
304	39	48.8	752	2	Q801W4	BRARE	Q801W4	brachydanio	377	38	47.5	129	2	Q70WH5	PLAFA	Q70WH5	platichthys
305	39	48.8	753	1	CNGC8	ARATH	Q9FXH6	arabidopsis	378	38	47.5	131	2	Q57ZJ8	9TRYPP	Q57ZJ8	trypanosoma
306	39	48.8	788	2	Q6C9B4	YARLI	Q6C9B4	yarrowia li	379	38	47.5	134	2	Q8N952	HUMAN	Q8N952	homo sapien
307	39	48.8	835	2	Q8K2R0	MOUSE	Q8K2R0	mus musculu	380	38	47.5	138	1	PA22	TRIMU	PA22	trimeresuru
308	39	48.8	844	2	Q81904	ARATH	Q81904	arabidopsis	381	38	47.5	138	1	PA22	TRIMU	PA22	trimeresuru
309	39	48.8	892	2	Q5M7X8	BRARE	Q5M7X8	brachydanio	382	38	47.5	138	2	Q6A3H8	VIPAP	Q6A3H8	vipeira aspi
310	39	48.8	895	1	POLG	CRPV	P13418	cricket par	383	38	47.5	138	2	Q6A3J6	VIPAZ	Q6A3J6	vipeira aspi
311	39	48.8	1045	2	Q9Y4F1	HUMAN	Q9Y4F1	homo sapien	384	38	47.5	146	2	Q9VYX5	DROME	Q9VYX5	drosophila
312	39	48.8	1045	2	Q5RAB8	PONPY	Q5RAB8	pongo pygma	385	38	47.5	149	2	Q6SMC6	HCMV	Q6SMC6	human cytom
313	39	48.8	1068	2	Q4QB89	LEIMA	Q4QB89	leishmania	386	38	47.5	149	2	Q6SX52	HCMV	Q6SX52	human cytom
314	39	48.8	1076	2	Q81Q29	HUMAN	Q81Q29	homo sapien	387	38	47.5	163	2	Q63096	RAT	Q63096	rattus norv
315	39	48.8	2021	2	Q8YQX0	ANASP	Q8YQX0	anabaena sp	388	38	47.5	165	2	Q8SY97	DROME	Q8SY97	drosophila
316	39	48.8	2057	2	Q9AW36	GUTH	Q9AW36	guillardia	389	38	47.5	177	2	P72773	SYNY3	P72773	synecocyst
317	39	48.8	2214	2	Q20219	CAEBL	Q20219	caenorhabdi	390	38	47.5	197	2	O42853	SCHPO	O42853	schistosacch
318	39	48.8	2258	1	POL1	BAMN	P90245	b genome po	391	38	47.5	203	2	Q4TD97	TETNG	Q4TD97	tetraodon n
319	39	48.8	4431	2	Q81J76	PLAF7	Q81J76	plasmodium	392	38	47.5	205	2	Q4THE9	TETNG	Q4THE9	tetraodon n
320	38.5	48.1	52	1	IBR2	ANACO	P27478	ananas como	393	38	47.5	207	2	Q96NL8	HUMAN	Q96NL8	homo sapien
321	38.5	48.1	65	1	SIX4	ANDAU	P21150	androctonus	394	38	47.5	207	2	Q5USN7	VIOOD	Q5USN7	viola odora
322	38.5	48.1	85	1	SCAS	MESNA	Q9UAC9	mesobuthus	395	38	47.5	209	2	Q6PDD5	MOUSE	Q6PDD5	mus musculu
323	38.5	48.1	246	2	Q7Y0Z3	ANACO	Q7Y0Z3	ananas como	396	38	47.5	210	2	Q6AY71	RAT	Q6AY71	rattus norv

397	38	47.5	219	2	Q7MTS3_PORGI	Q7mts3 porphyromon	470	38	47.5	686	2	Q6KGP3_ORYSA	Q6k6p3 oryza sativ
398	38	47.5	223	2	Q6A589_PROAC	Q6a5e9 propionibac	471	38	47.5	688	2	Q7Q7V9_ANOGA	Q7q7v9 anopheles g
399	38	47.5	223	2	Q6NTV8_XENLA	Q6ntx8 xenopus lae	472	38	47.5	695	2	Q59611_CRAGI	Q59611 crassostrea
400	38	47.5	229	2	Q4THR7_TETNG	Q4thr7 tetraodon n	473	38	47.5	698	2	Q6AV51_ORYSA	Q6av51 oryza sativ
401	38	47.5	246	2	Q7YW87_MSEPV	Q7yw87 melanoplus	474	38	47.5	732	2	Q6NQJ7_ARATH	Q6nqj7 arabidopsis
402	38	47.5	248	2	Q810P9_MOUSE	Q810p9 mus musculus	475	38	47.5	732	2	Q9SQQ3_ARATH	Q9sqq3 arabidopsis
403	38	47.5	255	2	Q91BR4_NPVST	Q91be4 spodoptera	476	38	47.5	796	2	Q4QDR7_LEIMA	Q4qdr7 leishmania
404	38	47.5	256	2	Q5C4C9_SCHJA	Q5c4c9 schistosoma	477	38	47.5	830	2	Q4HTP2_CAMUP	Q4htp2 campylobact
405	38	47.5	259	2	Q5ZP71_9VIRU	Q5zp71 cotesia con	478	38	47.5	840	2	Q60WP0_CAEBR	Q60wp0 caenorhabdi
406	38	47.5	263	2	Q7VIA2_PROMP	Q7via2 prochloroco	479	38	47.5	840	2	Q61894_CAEBL	Q61894 caenorhabdi
407	38	47.5	264	2	Q5ER64_BOOMI	Q5er64 boophilus m	480	38	47.5	941	2	Q6H964_ONCMY	Q6h964 oncorhynch
408	38	47.5	264	2	Q5ER69_BOOMI	Q5er69 boophilus m	481	38	47.5	962	2	Q4Z3E1_PLABE	Q4z3e1 plasmodium
409	38	47.5	264	2	Q5ER74_BOOMI	Q5er74 boophilus m	482	38	47.5	1442	2	Q6H062_FREDI	Q6h062 fremyella d
410	38	47.5	264	2	Q5ER75_BOOMI	Q5er75 boophilus m	483	38	47.5	1557	2	Q4H3P1_CIOIN	Q4h3p1 ciona intes
411	38	47.5	264	2	Q5ER77_BOOMI	Q5er77 boophilus m	484	38	47.5	1628	2	Q584C7_9TRYP	Q584c7 trypanosoma
412	38	47.5	264	2	Q5ER78_BOOMI	Q5er78 boophilus m	485	38	47.5	1700	2	Q4IIR0_GIBZE	Q4iir0 gibberella
413	38	47.5	264	2	Q5ER80_BOOMI	Q5er80 boophilus m	486	38	47.5	1804	2	Q6YR91_ANNAS	Q6yr91 anabaena sp
414	38	47.5	264	2	Q5ER81_BOOMI	Q5er81 boophilus m	487	38	47.5	2019	2	Q68FE0_MOUSE	Q68fe0 mus musculu
415	38	47.5	264	2	Q5ER82_BOOMI	Q5er82 boophilus m	488	38	47.5	2105	1	POLR_ASGVP	P36309 apple stem
416	38	47.5	264	2	Q5ER85_BOOMI	Q5er85 boophilus m	489	38	47.5	2207	2	Q7RTC0_PLAYO	Q7rtc0 plasmodium
417	38	47.5	264	2	Q5ER87_BOOMI	Q5er87 boophilus m	490	38	47.5	2222	2	Q619R0_CAEBR	Q619r0 caenorhabdi
418	38	47.5	264	2	Q5ER88_BOOMI	Q5er88 boophilus m	491	38	47.5	2229	2	Q19853_CAEBL	Q19853 caenorhabdi
419	38	47.5	264	2	Q5ER89_BOOMI	Q5er89 boophilus m	492	38	47.5	2233	2	Q94711_PARTE	Q94711 paramecium
420	38	47.5	264	2	Q5ER93_BOOMI	Q5er93 boophilus m	493	38	47.5	2429	2	Q4PAD1_USTWA	Q4pad1 ustilago ma
421	38	47.5	264	2	Q5XKU7_BOOMI	Q5xku7 boophilus m	494	37.5	46.9	54	2	Q92GE3_RICCN	Q92ge3 rickettsia
422	38	47.5	264	2	Q5XKU8_BOOMI	Q5xku8 boophilus m	495	37.5	46.9	95	2	Q4Y583_PLACH	Q4y583 plasmodium
423	38	47.5	264	2	Q5XKU9_BOOMI	Q5xku9 boophilus m	496	37.5	46.9	98	2	Q90427_BRABE	Q90427 brachydanio
424	38	47.5	264	2	Q5XKV0_BOOMI	Q5xkv0 boophilus m	497	37.5	46.9	140	2	Q64523_ARATH	Q64523 arabidopsis
425	38	47.5	264	2	Q5XKV1_BOOMI	Q5xkv1 boophilus m	498	37.5	46.9	192	2	Q9CWD7_MOUSE	Q9cwd7 mus musculu
426	38	47.5	264	2	Q5XKV2_BOOMI	Q5xkv2 boophilus m	499	37.5	46.9	205	2	Q9NW95_HUMAN	Q9nw95 homo sapien
427	38	47.5	264	2	Q5XKV2_BOOMI	Q5xkv2 boophilus m	500	37.5	46.9	207	2	Q5BJV9_RAT	Q5bjv9 rattus norv
428	38	47.5	268	1	Y304_ENCCU	Q8aw83 encephalito	501	37.5	46.9	209	2	Q80WB5_MOUSE	Q80wb5 mus musculu
429	38	47.5	280	2	Q8KQ88_STACA	Q8kq88 staphylococ	502	37.5	46.9	348	2	Q5DB66_SCHJA	Q5db66 schistosoma
430	38	47.5	285	2	P74637_SYNEC	P74637 synechocyst	503	37.5	46.9	406	2	Q5A135_CANAL	Q5a135 candida alb
431	38	47.5	285	2	Q8DJ11_SYNEL	Q8dj11 synechococc	504	37.5	46.9	430	2	Q6TVF3_9POXV	Q6tvf3 bovine papu
432	38	47.5	302	2	Q6SG25_9BACT	Q6sg25 uncultured	505	37.5	46.9	430	2	Q6TVT5_9POXV	Q6tv5 orf virus
433	38	47.5	319	2	Q4L120_9BURK	Q4l120 burkholderi	506	37.5	46.9	430	2	Q6TW65_9POXV	Q6tw65 orf virus
434	38	47.5	325	2	Q6IF88_HUMAN	Q6if88 homo sapien	507	37.5	46.9	500	2	Q9BRV0_HUMAN	Q9brv0 homo sapien
435	38	47.5	326	2	Q5BK10_XENTR	Q5bk10 xenopus tro	508	37.5	46.9	682	1	CNG_ICTFU	P55934 ictalurusa p
436	38	47.5	336	2	Q5GV22_XANOR	Q5gv22 xanthomonas	509	37.5	46.9	1245	2	Q4FKK3_9TRYP	Q4fkk3 trypanosoma
437	38	47.5	337	2	Q4SYW8_TETNG	Q4syw8 tetraodon n	510	37.5	46.9	1888	2	Q4Q8R2_LEIMA	Q4q8r2 leishmania
438	38	47.5	365	2	Q64Y60_BACFR	Q64y60 bacteroides	511	37	46.2	31	2	Q9DEW3_COTCO	Q9dew3 coturnix co
439	38	47.5	367	2	Q750R7_ASHGO	Q750r7 ashbya goss	512	37	46.2	31	2	Q9DFH7_9SMRG	Q9dfh7 mastacembel
440	38	47.5	379	2	Q55C29_DICDI	Q55c29 dictyosteli	513	37	46.2	31	2	Q9DFI2_BRACHD	Q9dfi2 brachydanio
441	38	47.5	386	2	Q4SL34_TETNG	Q4sl34 tetraodon n	514	37	46.2	31	2	Q9DR16_MONAL	Q9dr16 monopterus
442	38	47.5	389	2	Q50TCE_ENTHI	Q50tc8 entamoeba h	515	37	46.2	46	2	Q56BK4_9CAUD	Q56bk4 enterobacte
443	38	47.5	401	1	AURI_YEAST	Q6il122 saccharomyc	516	37	46.2	47	2	Q4ZH59_9SAUR	Q4zh59 eremias bre
444	38	47.5	426	2	Q6IL22_DROME	Q6il122 dirosophila	517	37	46.2	47	2	Q708Q9_9CAUD	Q708q9 bacterioph
445	38	47.5	429	2	Q4UDT0_THEAN	Q4udt0 theileria a	518	37	46.2	48	1	PA2V_AUSSU	P59070 austrelaps
446	38	47.5	454	2	Q5CNL2_CRYHO	Q5cnl2 cryptospori	519	37	46.2	48	2	Q697G4_9HEMI	Q697g4 neomaskelli
447	38	47.5	455	2	Q5CSW1_CRYPV	Q5csw1 cryptospori	520	37	46.2	50	2	Q7L2Q7_VIPAS	Q7l2q7 vipera aspi
448	38	47.5	461	2	Q5BN90_ACECL	Q5bn90 acetabulari	521	37	46.2	51	2	Q9DGL7_ONCMY	Q9dgl7 oncorhynch
449	38	47.5	467	2	Q7QWK3_GIALA	Q7qwk3 giardia lam	522	37	46.2	52	2	Q7L2Q5_VIPAS	Q7l2q5 vipera aspi
450	38	47.5	493	1	TNR8_RAT	P97525 rattus norv	523	37	46.2	57	1	PA2T_AUSSU	P59068 austrelaps
451	38	47.5	498	1	TNR8_MOUSE	Q60846 mus musculu	524	37	46.2	60	1	CK3_NAJHA	P01459 najia hajae a
452	38	47.5	498	2	Q57YB3_9TRYP	Q57yb3 trypanosoma	525	37	46.2	62	2	Q4XQ13_PLACH	Q4xq13 plasmodium
453	38	47.5	518	2	Q55025_TETTH	Q55029 tetrathymena	526	37	46.2	68	1	SCX2_CENGR	P60163 centruoide
454	38	47.5	529	2	Q5SCW7_HUPLU	Q5scw7 hupezia lu	527	37	46.2	68	2	Q6A3D8_VIPAP	Q6a3d8 vipera aspi
455	38	47.5	535	2	Q53111_RHOSH	Q53111 rhodobacter	528	37	46.2	71	2	Q95SV8_DROME	Q95sv8 dirosophila
456	38	47.5	538	2	Q7ROM6_GIALA	Q7rom6 giardia lam	529	37	46.2	72	2	Q4Y5H5_PLACH	Q4y5h5 plasmodium
457	38	47.5	564	2	Q6H018_FREDI	Q6h018 fremyella d	530	37	46.2	82	2	Q6BQX0_DEBHA	Q6bqx0 debaryomyce
458	38	47.5	567	2	Q4V8X2_BRABE	Q4v8x2 brachydanio	531	37	46.2	85	2	Q8CZU5_YERPE	Q8czu5 versinia pe
459	38	47.5	569	2	Q3Y0V1_BOOMI	Q3y0v1 boophilus m	532	37	46.2	89	2	Q60PP6_CAEBR	Q60pp6 caenorhabdi
460	38	47.5	574	1	SIR_BUCAI	Q44683 buchnera ap	533	37	46.2	89	2	Q9GUM4_CAEBL	Q9gum4 caenorhabdi
461	38	47.5	588	2	Q61T62_CAEBR	Q61t62 caenorhabdi	534	37	46.2	96	2	Q96CY8_HUMAN	Q96cy8 homo sapien
462	38	47.5	588	2	Q6YZP2_ORYSA	Q6yzp2 oryza sativ	535	37	46.2	106	2	Q71VT1_LISMF	Q71vt1 listeria mo
463	38	47.5	606	2	Q8Q807_9BETA	Q8q807 pongine her	536	37	46.2	106	2	Q926S8_LISIN	Q926s8 listeria mo
464	38	47.5	610	2	Q7SEF4_NEUCR	Q7sef4 neurospora	537	37	46.2	106	2	Q8Y3K5_LISMO	Q8y3k5 listeria mo
465	38	47.5	616	2	Q20852_CABEL	Q20852 caenorhabdi	538	37	46.2	108	2	Q59YU9_CANAL	Q59yu9 candida alb
466	38	47.5	630	2	Q836X7_ENTFA	Q836x7 enterococc	539	37	46.2	117	1	PA2A_PSEPO	P20258 pseudoechi
467	38	47.5	650	1	BMB6_BOOMI	P20736 boophilus m	540	37	46.2	117	1	PA2G_PSEAU	P20250 pseudoechi
468	38	47.5	650	2	Q6CMQ2_KLULA	Q6cmq2 kluyveromyc	541	37	46.2	117	2	Q6H3C5_TRIST	Q6h3c5 trimereauru
469	38	47.5	670	2	Q9SFW7_ARATH	Q9sfw7 arabidopsis	542	37	46.2	118	1	PA20_PSEAU	P20254 pseudoechi

543	37	46.2	118	1	PA21B_PSEAU	P04056 pseudechis	616	37	46.2	137	2	Q6A3D1_VIPAP	Q6A3d1 vipera aspi
544	37	46.2	118	1	PA22_ACRAN	P81237 acanthophis	617	37	46.2	137	2	Q6A3D3_VIPAP	Q6A3d3 vipera aspi
545	37	46.2	118	1	PA23_PSEAU	P20251 pseudechis	618	37	46.2	137	2	Q6A3D4_VIPAP	Q6A3d4 vipera aspi
546	37	46.2	118	1	PA25_PSEAU	P20252 pseudechis	619	37	46.2	137	2	Q6A3D5_VIPAP	Q6A3d5 vipera aspi
547	37	46.2	118	1	PA29_PSEAU	P20253 pseudechis	620	37	46.2	137	2	Q6A3D7_VIPAP	Q6A3d7 vipera aspi
548	37	46.2	118	1	PA2A_PSEAU	P20255 pseudechis	621	37	46.2	137	2	Q6A3D9_VIPAP	Q6A3d9 vipera aspi
549	37	46.2	118	1	PA2C_PSEAU	P20256 pseudechis	622	37	46.2	137	2	Q6A3E0_VIPAP	Q6A3e0 vipera aspi
550	37	46.2	118	1	PA2_BITGA	P00620 bitis gabon	623	37	46.2	137	2	Q6A3E3_VIPAP	Q6A3e3 vipera aspi
551	37	46.2	118	2	Q69Y9_HUMAN	Q69Y9 homo sapien	624	37	46.2	137	2	Q6A3E7_VIPBB	Q6A3e7 vipera beru
552	37	46.2	119	1	PA21B_ACRAN	P81236 acanthophis	625	37	46.2	137	2	Q6A3F0_VIPAP	Q6A3f0 vipera aspi
553	37	46.2	119	1	PA22_BITNA	P00621 bitis naeic	626	37	46.2	137	2	Q6A3F2_VIPAZ	Q6A3f2 vipera aspi
554	37	46.2	119	1	PA23_NOTSC	P00609 notechis ac	627	37	46.2	137	2	Q6A3F4_VIPAP	Q6A3f4 vipera aspi
555	37	46.2	120	1	PA2_CERCE	P21789 cerastes ce	628	37	46.2	137	2	Q6T7B8_BITGA	Q6t7b8 bitis gabon
556	37	46.2	121	1	PA21B_ERIMA	P42993 eristocophi	629	37	46.2	137	2	Q6YCN7_VIPBB	Q6ycn7 vipera beru
557	37	46.2	121	1	PA28_DABRP	P59071 dabola russ	630	37	46.2	137	2	Q6YCN8_VIPAS	Q6ycn8 vipera aspi
558	37	46.2	121	1	PA2_BITCA	P00622 bitis cauda	631	37	46.2	137	2	Q6YCN9_VIPAP	Q6ycn9 vipera aspi
559	37	46.2	121	1	PA2_DABRR	P81458 dabola russ	632	37	46.2	138	1	PA21B_BOTJR	P45881 bothrops ja
560	37	46.2	122	1	PA21B_BOTAS	P20474 bothrops as	633	37	46.2	138	1	PA21B_TRIFL	P06859 trimeresuru
561	37	46.2	122	1	PA21B_TRIMU	Q91506 trimeresuru	634	37	46.2	138	1	PA21B_VIPAP	Q8jfg0 vipera aspi
562	37	46.2	122	1	PA21B_VIPAP	P14420 vipera ammo	635	37	46.2	138	1	PA21B_VIPAZ	Q10754 vipera aspi
563	37	46.2	122	1	PA22_BOTIN	P84397 bothrops in	636	37	46.2	138	1	PA21_BOTIN	Q8gg87 bothrops in
564	37	46.2	122	1	PA22_VIPAZ	Q10755 vipera aspi	637	37	46.2	138	1	PA21_ECHCO	Q90z99 echis color
565	37	46.2	122	1	PA21_VIPAE	P04084 vipera ammo	638	37	46.2	138	1	PA23_ECHCO	Q910a0 echis color
566	37	46.2	122	1	PA2_CROAD	P00623 crotalus ad	639	37	46.2	138	1	PA24_DABRU	Q02471 dabola russ
567	37	46.2	122	1	PA2_VIPBB	P31854 vipera beru	640	37	46.2	138	1	PA27_DABRU	P31100 dabola russ
568	37	46.2	122	2	Q6EER5_CERGO	Q6eer5 cerrophidio	641	37	46.2	138	1	PA2A_TRIMU	Q90w39 trimeresuru
569	37	46.2	122	2	Q6EER6_SISMI	Q6eer6 sistururus m	642	37	46.2	138	1	PA2B_CRODU	P62032 crotalus du
570	37	46.2	122	2	Q6H3C6_TRIST	Q6h3c6 trimeresuru	643	37	46.2	138	1	PA2B_CROSS	P62023 crotalus sc
571	37	46.2	123	1	PA21_AGRPI	P51972 agkistrodon	644	37	46.2	138	1	PA2C_CRODU	P24027 crotalus du
572	37	46.2	123	2	Q7S1B6_AGKAC	Q7sid6 agkistrodon	645	37	46.2	138	1	PA2G5_HUMAN	P39877 homo sapien
573	37	46.2	124	1	PA21B_AGRHP	P14148 agkistrodon	646	37	46.2	138	1	PA21_VIPAP	Q8jfg1 vipera aspi
574	37	46.2	124	1	PA21B_BOTJA	P81243 bothrops ja	647	37	46.2	138	1	PA2N_TRIFL	Q805a2 trimeresuru
575	37	46.2	124	1	PA27_AGRKA	Q42194 agkistrodon	648	37	46.2	138	1	PA2_CROAT	P00624 crotalus at
576	37	46.2	124	1	PA2A_AGKCA	Q71zq4 agkistrodon	649	37	46.2	138	1	PA2_VIPAA	Q910a1 vipera ammo
577	37	46.2	124	2	Q65ZB0_9SAUR	Q65zr0 agkistrodon	650	37	46.2	138	2	Q71Q88_CROVV	Q71q88 crotalus vi
578	37	46.2	126	1	PA2A_AGRKH	Q9pfv1 agkistrodon	651	37	46.2	138	2	Q800C1_CROVV	Q800c1 crotalus vi
579	37	46.2	126	1	PA2B_AGRKH	Q9pfv0 agkistrodon	652	37	46.2	138	2	Q800C2_CROVV	Q800c2 crotalus vi
580	37	46.2	128	2	Q6A3N1_VIPAZ	Q6a3n1 vipera aspi	653	37	46.2	138	2	Q800C3_CROVV	Q800c3 crotalus vi
581	37	46.2	128	2	Q6A3N2_VIPAZ	Q6a3n2 vipera aspi	654	37	46.2	138	2	Q800C4_CROVV	Q800c4 crotalus vi
582	37	46.2	130	2	Q5TVN6_ANOAG	Q5tvn6 anopheles g	655	37	46.2	138	2	Q6A336_VIPAZ	Q6a336 vipera aspi
583	37	46.2	130	2	Q7T3T5_9SAUR	Q7t3t5 vipera russ	656	37	46.2	138	2	Q6A337_VIPAZ	Q6a337 vipera aspi
584	37	46.2	132	2	Q6A368_VIPAA	Q6a368 vipera ammo	657	37	46.2	138	2	Q6A338_VIPAZ	Q6a338 vipera aspi
585	37	46.2	136	2	Q7T3S7_ECHCA	Q6a398 vipera ammo	658	37	46.2	138	2	Q6A339_VIPAP	Q6a339 vipera aspi
586	37	46.2	137	1	PA28_VIPPA	Q9ygj7 echis carin	659	37	46.2	138	2	Q6A342_VIPAZ	Q6a342 vipera aspi
587	37	46.2	137	1	PA2G5_MOUSE	P97391 mus musculu	660	37	46.2	138	2	Q6A346_VIPAZ	Q6a346 vipera aspi
588	37	46.2	137	1	PA2G5_RAT	P51433 rattus norv	661	37	46.2	138	2	Q6A349_VIPAZ	Q6a349 vipera aspi
589	37	46.2	137	1	PA2N_VIPAA	P34180 vipera ammo	662	37	46.2	138	2	Q6A351_VIPAZ	Q6a351 vipera aspi
590	37	46.2	137	2	Q9BV58_HUMAN	Q9bv58 homo sapien	663	37	46.2	138	2	Q6A352_VIPAP	Q6a352 vipera aspi
591	37	46.2	137	2	Q5RDV6_PONPY	Q5rdv6 pongo pygma	664	37	46.2	138	2	Q6A356_VIPAP	Q6a356 vipera ammo
592	37	46.2	137	2	Q6DQ96_RAT	Q6dq96 rattus norv	665	37	46.2	138	2	Q6A3F6_VIPAP	Q6a3f6 vipera aspi
593	37	46.2	137	2	Q6GTW1_MOUSE	Q6gtw1 mus musculu	666	37	46.2	138	2	Q6A3F7_VIPAP	Q6a3f7 vipera aspi
594	37	46.2	137	2	Q6A3A0_VIPAM	Q6a3a0 vipera ammo	667	37	46.2	138	2	Q6A3G1_VIPAP	Q6a3g1 vipera aspi
595	37	46.2	137	2	Q6A3A1_VIPAM	Q6a3a1 vipera ammo	668	37	46.2	138	2	Q6A3G4_VIPAM	Q6a3g4 vipera ammo
596	37	46.2	137	2	Q6A3A3_VIPAM	Q6a3a3 vipera ammo	669	37	46.2	138	2	Q6A3G5_VIPAP	Q6a3g5 vipera ammo
597	37	46.2	137	2	Q6A3A4_VIPAE	Q6a3a4 vipera ammo	670	37	46.2	138	2	Q6A3H1_VIPAS	Q6a3h1 vipera aspi
598	37	46.2	137	2	Q6A3A5_VIPAE	Q6a3a5 vipera ammo	671	37	46.2	138	2	Q6A3H2_VIPAS	Q6a3h2 vipera aspi
599	37	46.2	137	2	Q6A3A6_VIPAE	Q6a3a6 vipera ammo	672	37	46.2	138	2	Q6A3H4_VIPAS	Q6a3h4 vipera aspi
600	37	46.2	137	2	Q6A3A7_VIPAE	Q6a3a7 vipera ammo	673	37	46.2	138	2	Q6A3H5_VIPAS	Q6a3h5 vipera aspi
601	37	46.2	137	2	Q6A3A9_VIPAA	Q6a3a9 vipera ammo	674	37	46.2	138	2	Q6A3H6_VIPAS	Q6a3h6 vipera aspi
602	37	46.2	137	2	Q6A3B0_VIPAA	Q6a3b0 vipera ammo	675	37	46.2	138	2	Q6A3H7_VIPAS	Q6a3h7 vipera aspi
603	37	46.2	137	2	Q6A3B1_VIPAA	Q6a3b1 vipera ammo	676	37	46.2	138	2	Q6A3I0_VIPAP	Q6a3i0 vipera aspi
604	37	46.2	137	2	Q6A3B2_VIPAA	Q6a3b2 vipera ammo	677	37	46.2	138	2	Q6A3I1_VIPAP	Q6a3i1 vipera aspi
605	37	46.2	137	2	Q6A3B4_VIPAS	Q6a3b4 vipera aspi	678	37	46.2	138	2	Q6A3I3_VIPAP	Q6a3i3 vipera aspi
606	37	46.2	137	2	Q6A3B5_VIPAS	Q6a3b5 vipera aspi	679	37	46.2	138	2	Q6A3I4_VIPAP	Q6a3i4 vipera aspi
607	37	46.2	137	2	Q6A3B7_VIPAP	Q6a3b7 vipera aspi	680	37	46.2	138	2	Q6A3I6_VIPAP	Q6a3i6 vipera aspi
608	37	46.2	137	2	Q6A3B8_VIPAP	Q6a3b8 vipera aspi	681	37	46.2	138	2	Q6A3I8_VIPUR	Q6a3i8 vipera ursi
609	37	46.2	137	2	Q6A3B9_VIPAP	Q6a3b9 vipera aspi	682	37	46.2	138	2	Q6A3I9_VIPBB	Q6a3i9 vipera beru
610	37	46.2	137	2	Q6A3C0_VIPAP	Q6a3c0 vipera aspi	683	37	46.2	138	2	Q6A3J0_VIPBB	Q6a3j0 vipera beru
611	37	46.2	137	2	Q6A3C2_VIPUR	Q6a3c2 vipera ursi	684	37	46.2	138	2	Q6A3J2_VIPBB	Q6a3j2 vipera beru
612	37	46.2	137	2	Q6A3C3_VIPBB	Q6a3c3 vipera beru	685	37	46.2	138	2	Q6A3J3_VIPBB	Q6a3j3 vipera beru
613	37	46.2	137	2	Q6A3C6_VIPAM	Q6a3c6 vipera ammo	686	37	46.2	138	2	Q6A3J4_VIPBB	Q6a3j4 vipera beru
614	37	46.2	137	2	Q6A3C7_VIPAM	Q6a3c7 vipera ammo	687	37	46.2	138	2	Q6A3J5_VIPAP	Q6a3j5 vipera aspi
615	37	46.2	137	2	Q6A3C9_VIPAP	Q6a3c9 vipera ammo	688	37	46.2	138	2	Q6A3K0_VIPBB	Q6a3k0 vipera beru

689	37	46.2	138	2	Q6A3K3_VIPAP	Q6a3k3 vipera aspi	762	37	46.2	209	2	Q6IUN1_9ENTR	Q6ium1 kluyvera sp
690	37	46.2	138	2	Q6A3K4_VIPAP	Q6a3k4 vipera aspi	763	37	46.2	209	2	Q6IUN7_9ENTR	Q6ium7 kluyvera sp
691	37	46.2	138	2	Q6A3K7_VIPAP	Q6a3k7 vipera aspi	764	37	46.2	209	2	Q6IUN7_9ENTR	Q6ium7 kluyvera sp
692	37	46.2	138	2	Q6A3K8_VIPAP	Q6a3k8 vipera aspi	765	37	46.2	210	1	KAB2_OLDAP	P58454 oldenlandia
693	37	46.2	138	2	Q6A3K9_VIPAP	Q6a3k9 vipera aspi	766	37	46.2	212	2	Q5IJ27_MAGGR	Q5ijj27 magnaporthes
694	37	46.2	138	2	Q6A3L0_VIPAP	Q6a3l0 vipera aspi	767	37	46.2	215	2	Q9FCM1_9ENTR	Q9fcw1 kluyvera as
695	37	46.2	138	2	Q6A3L1_VIPAP	Q6a3l1 vipera aspi	768	37	46.2	220	2	Q8VVP2_KLUCI	Q8vvp2 kluyvera ci
696	37	46.2	138	2	Q6A3M2_VIPAP	Q6a3m2 vipera aspi	769	37	46.2	224	2	Q5UJ13_9BACT	Q5uj13 uncultured
697	37	46.2	138	2	Q6A3M4_VIPAP	Q6a3m4 vipera aspi	770	37	46.2	224	2	Q5D398_9BACT	Q5d398 uncultured
698	37	46.2	138	2	Q6A3M5_VIPAP	Q6a3m5 vipera aspi	771	37	46.2	226	2	Q69GU6_HUMAN	Q69gu6 homo sapien
699	37	46.2	138	2	Q6A3M8_VIPAP	Q6a3m8 vipera ammo	772	37	46.2	228	2	Q6FIM2_CANGA	Q6fim2 candida gla
700	37	46.2	138	2	Q6A3M9_VIPAP	Q6a3m9 vipera ammo	773	37	46.2	231	2	Q8ZSE1_SALTI	Q8zse1 salmonella
701	37	46.2	138	2	Q6A3N0_VIPAM	Q6a3n0 vipera ammo	774	37	46.2	231	2	Q5LYL1_STRTI	Q5lyl1 streptococc
702	37	46.2	138	2	Q6A3N6_VIPAP	Q6a3n6 vipera aspi	775	37	46.2	231	2	Q5M374_STRT2	Q5m374 streptococc
703	37	46.2	138	2	Q6A3N8_VIPAZ	Q6a3n8 vipera aspi	776	37	46.2	240	2	Q8N114_HUMAN	Q8n114 homo sapien
704	37	46.2	138	2	Q6A3P1_VIPAP	Q6a3p1 vipera aspi	777	37	46.2	240	2	Q9MC79_BPD3	Q9mc79 bacterioph
705	37	46.2	138	2	Q6EER2_SISCT	Q6eer2 sisturus c	778	37	46.2	242	2	Q83FB2_COXBU	Q83fb2 coxiella bu
706	37	46.2	138	2	Q6EER3_SISCT	Q6eer3 sisturus c	779	37	46.2	247	2	Q4XOC9_ASPPU	Q4xoc9 aspergillus
707	37	46.2	138	2	Q6EER4_BOTSC	Q6eer4 bothriechis	780	37	46.2	254	2	Q4ICA3_GIBZE	Q4ica3 gibberella
708	37	46.2	138	2	Q6EM14_BOTJR	Q6em14 bothriops ja	781	37	46.2	256	2	Q86WX4_HUMAN	Q86wx4 homo sapien
709	37	46.2	138	2	Q6H3C9_TRIST	Q6h3c9 trimeresuru	782	37	46.2	274	2	Q86U51_HUMAN	Q86u51 homo sapien
710	37	46.2	138	2	Q6YCP0_VIPAS	Q6ycp0 vipera aspi	783	37	46.2	276	2	Q6TRW8_CHICK	Q6trw8 gallus gall
711	37	46.2	138	2	Q6YCP1_VIPAZ	Q6ycp1 vipera aspi	784	37	46.2	277	2	Q6QHY7_TRIVA	Q6qhy7 trichomonas
712	37	46.2	138	2	Q6YCP1_VIPAS	Q6ycp1 vipera aspi	785	37	46.2	280	2	Q19291_CABEL	Q19291 caenorhabdi
713	37	46.2	138	2	Q715Z8_VIPAS	Q715z8 vipera aspi	786	37	46.2	290	2	Q621G6_CABER	Q621g6 caenorhabdi
714	37	46.2	138	2	Q7T1C6_VIPAP	Q7t1c6 vipera aspi	787	37	46.2	297	2	Q5ZPB2_MORMO	Q5zpb2 morganella
715	37	46.2	138	2	Q7T1D1_VIPBB	Q7t1d1 vipera beru	788	37	46.2	297	2	Q4LAU9_KLEPN	Q4lau9 klebsiella
716	37	46.2	138	2	Q7T1D2_VIPAZ	Q7t1d2 vipera aspi	789	37	46.2	297	2	Q4SM83_TETNG	Q4sm83 tetraodon n
717	37	46.2	138	2	Q7T1D3_VIPAS	Q7t1d3 vipera aspi	790	37	46.2	311	2	Q8GPV1_PSEAE	Q8gpv1 pseudomonas
718	37	46.2	138	2	Q7T1D4_VIPAP	Q7t1d4 vipera aspi	791	37	46.2	311	2	Q892V3_CLOTE	Q892v3 clostridium
719	37	46.2	138	2	Q7T1D5_VIPBB	Q7t1d5 vipera beru	792	37	46.2	315	2	Q4XKJ2_PLACH	Q4xkj2 plasmodium
720	37	46.2	138	2	Q7T2R1_9SAUR	Q7t2r1 vipera russ	793	37	46.2	321	2	Q9PVP4_ORYLA	Q9pvp4 oryzias lat
721	37	46.2	138	2	Q7ZTA6_CROVV	Q7zta6 crotalus vi	794	37	46.2	324	2	Q6S08_EUGGR	Q6s08 euglena gra
722	37	46.2	138	2	Q7ZTA7_CROVV	Q7zta7 crotalus vi	795	37	46.2	329	2	Q8RLU9_PROMI	Q8rlu9 proteus mir
723	37	46.2	138	2	Q7ZTA8_CROVV	Q7zta8 crotalus vi	796	37	46.2	331	2	Q50N42_ENTHI	Q50n42 entamoeba h
724	37	46.2	138	2	Q7ZZQ1_9SAUR	Q7zzq1 vipera russ	797	37	46.2	331	2	Q74D10_GEOSL	Q74d10 geobacter s
725	37	46.2	138	2	Q6A358_VIPAP	Q6a358 vipera aspi	798	37	46.2	333	1	HEMH_FRATT	Q5nft3 francisella
726	37	46.2	138	2	Q6A3H0_VIPAA	Q6a3h0 vipera ammo	799	37	46.2	338	2	Q4WQ3_ASPPU	Q4wq3 aspergillus
727	37	46.2	138	2	Q6A3P3_VIPAP	Q6a3p3 vipera aspi	800	37	46.2	343	2	Q60ZN7_CABER	Q60zn7 caenorhabdi
728	37	46.2	139	1	PA24_ECHCS	P59170 echis carin	801	37	46.2	343	2	Q891V5_CLOTE	Q891v5 clostridium
729	37	46.2	139	1	PA25_ECHPL	P59172 echis pyram	802	37	46.2	350	2	Q518N3_ENTHI	Q518n3 entamoeba h
730	37	46.2	139	1	PA2C_AGRKH	Q9pve9 agkistrodon	803	37	46.2	353	2	Q6TRW9_CHICK	Q6trw9 gallus gall
731	37	46.2	139	1	PA2E_AGRKH	Q9pve2 agkistrodon	804	37	46.2	356	2	Q6TRX0_CHICK	Q6trx0 gallus gall
732	37	46.2	139	2	Q5Z8B4_ORYSA	Q5z8b4 oryza sativ	805	37	46.2	359	2	Q4IAJ2_GIBZE	Q4iaj2 gibberella
733	37	46.2	139	2	Q6H3C7_TRIST	Q6h3c7 trimeresuru	806	37	46.2	360	2	Q729F1_DESVH	Q729f1 desulfovibr
734	37	46.2	139	2	Q4QT04_BITAR	Q4qt04 bitis ariet	807	37	46.2	362	2	Q5B120_ENEMI	Q5b120 aspergillus
735	37	46.2	139	2	Q4QT02_BITAR	Q4qt02 bitis ariet	808	37	46.2	362	2	Q4SD05_TETNG	Q4sd05 tetraodon n
736	37	46.2	140	2	Q6ZQP4_HUMAN	Q6zqp4 homo sapien	809	37	46.2	370	2	Q7QEG9_ANOGA	Q7qeg9 anopheles g
737	37	46.2	144	2	Q5DNC7_9SAUR	Q5dnc7 aipysurus e	810	37	46.2	372	2	Q5CZS6_BRARE	Q5czs6 brachydanio
738	37	46.2	144	2	Q5DNC8_9SAUR	Q5dnc8 aipysurus e	811	37	46.2	372	2	Q50RC2_ENTHI	Q50rc2 entamoeba h
739	37	46.2	144	2	Q5DNC9_9SAUR	Q5dnc9 aipysurus e	812	37	46.2	378	2	Q6T9Z5_CHICK	Q6t9z5 gallus gall
740	37	46.2	144	2	Q5DND2_9SAUR	Q5dnd2 aipysurus e	813	37	46.2	387	2	Q61MP1_CABER	Q61mp1 caenorhabdi
741	37	46.2	144	2	Q5DND3_9SAUR	Q5dnd3 aipysurus e	814	37	46.2	388	2	Q4H2L5_CIOIN	Q4h2l5 ciona intes
742	37	46.2	144	2	Q5DND5_9SAUR	Q5dnd5 aipysurus e	815	37	46.2	402	2	Q7Q0Z4_ANOGA	Q7q0z4 anopheles g
743	37	46.2	144	2	Q5DND9_9SAUR	Q5dnd9 aipysurus e	816	37	46.2	407	2	Q4J0Y0_AZOVI	Q4j0y0 azotobacter
744	37	46.2	144	2	Q5DNE0_9SAUR	Q5dne0 aipysurus e	817	37	46.2	413	2	Q501W9_BRARE	Q501w9 brachydanio
745	37	46.2	144	2	Q5DNE1_9SAUR	Q5dne1 aipysurus e	818	37	46.2	415	2	Q6TRW7_CHICK	Q6trw7 gallus gall
746	37	46.2	150	2	Q6ZU01_HUMAN	Q6zu01 homo sapien	819	37	46.2	416	2	Q76L87_ORYLA	Q76l87 oryzias lat
747	37	46.2	163	2	Q4RC19_TETNG	Q4rc19 tetraodon n	820	37	46.2	417	2	Q4WQ90_ASPPU	Q4wq90 aspergillus
748	37	46.2	164	2	Q5TBT3_HUMAN	Q5tbt3 homo sapien	821	37	46.2	423	2	Q24742_BACFO	Q24742 bacteroides
749	37	46.2	169	2	Q6QXC4_GVAS	Q6qxc4 agrotis aeg	822	37	46.2	440	2	Q5UW75_BRARE	Q5uuw75 brachydanio
750	37	46.2	174	2	Q6ZBB1_HUMAN	Q6zbb1 homo sapien	823	37	46.2	440	2	Q4RUF2_TETNG	Q4ruf2 tetraodon n
751	37	46.2	181	2	Q6SG40_HUMAN	Q6sg40 homo sapien	824	37	46.2	449	1	CCA_METJA	Q59511 methanococc
752	37	46.2	190	2	Q5BWX2_SCHJA	Q5bwx2 schistosoma	825	37	46.2	449	2	Q6YHU8_ORENI	Q6yhu8 oreochromis
753	37	46.2	192	2	Q17893_CABEL	Q17893 caenorhabdi	826	37	46.2	450	2	Q5PBD8_ANAMM	Q5pbd8 anaplasm m
754	37	46.2	193	2	Q7PQ13_ANOGA	Q7pq13 anopheles g	827	37	46.2	474	2	Q8M8V6_9ERIC	Q8m8v6 tetramerist
755	37	46.2	201	2	Q5DBP8_SCHJA	Q5dbp8 schistosoma	828	37	46.2	476	2	Q8M941_9ERIC	Q8m941 pelliciera
756	37	46.2	202	2	Q8BJP3_MOUSE	Q8bjp3 m mus muscu	829	37	46.2	486	2	Q96SC8_HUMAN	Q96sc8 homo sapien
757	37	46.2	207	2	Q4GXZ2_ECOLI	Q4gxz2 escherichia	830	37	46.2	494	2	Q33840_CABER	Q33840 caenorhabdi
758	37	46.2	208	1	YEAF_SCHPO	O14080 schizosacch	831	37	46.2	496	2	Q614H2_CABER	Q614h2 caenorhabdi
759	37	46.2	209	2	Q96MW8_HUMAN	Q96mw8 homo sapien	832	37	46.2	497	2	Q5ZKL3_CHICK	Q5zkl3 gallus gall
760	37	46.2	209	2	Q6IUN9_9ENTR	Q6ium9 kluyvera sp	833	37	46.2	498	2	Q6NVW2_HUMAN	Q6nvw2 homo sapien
761	37	46.2	209	2	Q6IUN5_9ENTR	Q6ium5 kluyvera sp	834	37	46.2	499	2	Q4IDC5_GIBZE	Q4idc5 gibberella

835	37	46.2	503	2	054274_9STAP	054274	staphylococ	908	37	46.2	998	2	075M88_HUMAN	Q75M88	homo sapien
836	37	46.2	504	2	Q6M9B7_9ERIC	Q6M9B7	kluyveravia	909	37	46.2	1015	1	PARP1_BOVIN	P18493	bos taurus
837	37	46.2	520	2	Q6CUP8_KLULA	Q6CUP8	kluyveromyc	910	37	46.2	1060	1	Q4MZ12_THEPA	Q4MZ12	theileria p
838	37	46.2	521	2	Q6MXR1_SERMA	Q6MXR1	serriatia ma	911	37	46.2	1091	2	Q8T5G5_SCHUA	Q8T5G5	schistosoma
839	37	46.2	524	2	Q52AR3_MAGGR	Q52AR3	magnaporthe	912	37	46.2	1271	2	Q75B00_ASHGO	Q75B00	ashbya goss
840	37	46.2	525	2	Q4WM43_ASFFU	Q4WM43	aspergillus	913	37	46.2	1340	2	Q8NDA2_HUMAN	Q8NDA2	homo sapien
841	37	46.2	525	2	Q8NUL1_ASFFU	Q8NUL1	aspergillus	914	37	46.2	1360	1	GLI1_XENLA	Q1690	xenopus lae
842	37	46.2	525	2	Q61FA0_CABBR	Q61FA0	caenorhabdi	915	37	46.2	1411	2	Q5BGG2_EMENI	Q5BGG2	aspergillus
843	37	46.2	531	2	Q8CFP8_MOUSE	Q8CFP8	mus musculus	916	37	46.2	1519	2	Q6QI93_RAT	Q6QI93	rattus norv
844	37	46.2	534	2	Q8JY38_XENLA	Q8JY38	mus musculus	917	37	46.2	1594	2	Q4Y7T6_PLACH	Q4Y7T6	plasmodium
845	37	46.2	536	2	Q6UKM0_BACFO	Q6UKM0	bacteroides	918	37	46.2	1628	2	Q7RN68_PLAYO	Q7RN68	plasmodium
846	37	46.2	558	2	Q43071_SCHPO	Q43071	schizosach	919	37	46.2	1644	2	Q4PQ9_9HEPC	Q4PQ9	hepatitis c
847	37	46.2	574	2	Q4H3P8_CIOIN	Q4H3P8	ciona intes	920	37	46.2	1644	2	Q4PQ8_9HEPC	Q4PQ8	hepatitis c
848	37	46.2	596	2	Q4HYF5_GIBZE	Q4HYF5	gibberella	921	37	46.2	1644	2	Q4PQ7_9HEPC	Q4PQ7	hepatitis c
849	37	46.2	598	2	Q4WDW7_ASFFU	Q4WDW7	aspergillus	922	37	46.2	1644	2	Q4PQ6_9HEPC	Q4PQ6	hepatitis c
850	37	46.2	618	2	Q510G7_ENTHI	Q510G7	entamoeba h	923	37	46.2	1776	1	POLR_OYVU	P20127	ononis yell
851	37	46.2	622	2	Q7PLX6_CHRVO	Q7PLX6	chromobacte	924	37	46.2	1798	2	Q4S8D9_TETNG	Q4S8D9	tetradon n
852	37	46.2	662	2	Q4T103_TETNG	Q4T103	tetradon n	925	37	46.2	1835	2	Q9QCX3_9VIRU	Q9QCX3	chayote mos
853	37	46.2	677	2	Q5A23_TETNG	Q5A23	tetradon n	926	37	46.2	1932	2	Q91260_PHMV	Q91260	physalis mo
854	37	46.2	681	2	Q5POL0_AZOSE	Q5POL0	azoarcus sp	927	37	46.2	1946	2	Q8YTN2_ANASP	Q8YTN2	anabaena sp
855	37	46.2	699	2	Q8MY74_9BILA	Q8MY74	pychodera	928	37	46.2	1968	2	Q5CTM9_CRYPV	Q5CTM9	cryptospori
856	37	46.2	713	1	SNF6_CABEL	SNF6	caenorhabdi	929	37	46.2	2053	2	Q5XL62_TETTH	Q5XL62	tetrahymena
857	37	46.2	723	2	Q9M0R2_ARATH	Q9M0R2	arabidopsis	930	37	46.2	2063	2	Q58128_9TRYP	Q58128	trypanosoma
858	37	46.2	736	2	Q28482_MACPA	Q28482	macaca fasc	931	37	46.2	2155	1	TECTA_HUMAN	Q5443	homo sapien
859	37	46.2	769	2	Q51IM2_ENTHI	Q51IM2	entamoeba h	932	37	46.2	2155	1	TECTA_MOUSE	Q08523	mus musculus
860	37	46.2	870	2	Q9P942_HANAN	Q9P942	hansenula a	933	37	46.2	2258	2	Q55459_9POTY	Q55459	barley mild
861	37	46.2	871	2	Q5BFW1_EMENI	Q5BFW1	aspergillus	934	37	46.2	2258	2	Q93128_9POTY	Q93128	barley mild
862	37	46.2	890	2	Q7QF48_ANOGA	Q7QF48	anopheles g	935	37	46.2	2258	2	Q65654_9POTY	Q65654	barley mild
863	37	46.2	899	2	Q5K8J9_CRYNE	Q5K8J9	cryptococc	936	37	46.2	2258	2	Q68VH7_9POTY	Q68VH7	barley mild
864	37	46.2	913	2	Q5UZY1_RAT	Q5UZY1	rattus norv	937	37	46.2	2258	2	Q68VH8_9POTY	Q68VH8	barley mild
865	37	46.2	920	2	Q5K8K0_CRYNE	Q5K8K0	cryptococc	938	37	46.2	2258	2	Q68VH9_9POTY	Q68VH9	barley mild
866	37	46.2	929	2	Q8J259_TUBBO	Q8J259	tuber borch	939	37	46.2	2258	2	Q9WAA3_9POTY	Q9WAA3	barley mild
867	37	46.2	949	2	Q6EKI8_HUMAN	Q6EKI8	homo sapien	940	37	46.2	2475	2	Q501R6_XENTR	Q501R6	xenopus tro
868	37	46.2	949	2	Q6EKI9_HUMAN	Q6EKI9	homo sapien	941	37	46.2	2481	1	FINC_XENLA	Q91740	xenopus lae
869	37	46.2	949	2	Q6EKJ0_HUMAN	Q6EKJ0	homo sapien	942	37	46.2	2481	2	Q6GQ45_XENLA	Q6GQ45	xenopus lae
870	37	46.2	949	2	Q6GUP8_HUMAN	Q6GUP8	homo sapien	943	36.5	45.6	37	2	Q88361_MOUSE	Q88361	mus musculus
871	37	46.2	956	2	Q56SY0_9AVES	Q56SY0	harpactes e	944	36.5	45.6	75	2	Q57K84_SALCH	Q57K84	salmonella
872	37	46.2	957	2	Q75M85_HUMAN	Q75M85	homo sapien	945	36.5	45.6	123	2	P87282_YEAST	P87282	saccharomyc
873	37	46.2	957	2	Q56SM1_APAVI	Q56SM1	apaloderna	946	36.5	45.6	124	2	Q5LBB8_BACFN	Q5LBB8	bacteroides
874	37	46.2	957	2	Q56SX2_EUPNE	Q56SX2	euplotes	947	36.5	45.6	124	2	Q64RU6_BACFR	Q64RU6	bacteroides
875	37	46.2	957	2	Q56SX3_PHAPA	Q56SX3	pharomachru	948	36.5	45.6	149	2	Q4S237_TETNG	Q4S237	tetradon n
876	37	46.2	957	2	Q56SX4_PHAPA	Q56SX4	pharomachru	949	36.5	45.6	161	2	Q48242_9NEOP	Q48242	dennyus som
877	37	46.2	957	2	Q56SX5_PHAHA	Q56SX5	pharomachru	950	36.5	45.6	172	2	Q50TB6_ENTHI	Q50TB6	entamoeba h
878	37	46.2	957	2	Q56SX6_9AVES	Q56SX6	priotelus r	951	36.5	45.6	178	2	Q5Y800_PETHY	Q5Y800	petunia hyb
879	37	46.2	957	2	Q56SX7_PRITE	Q56SX7	priotelus t	952	36.5	45.6	204	2	Q5PPU8_XENLA	Q5PPU8	xenopus lae
880	37	46.2	957	2	Q56SX8_PRITE	Q56SX8	priotelus t	953	36.5	45.6	205	2	Q96H48_HUMAN	Q96H48	homo sapien
881	37	46.2	957	2	Q56SX9_HARDI	Q56SX9	harpactes d	954	36.5	45.6	205	2	Q9V7F5_DROME	Q9V7F5	drosophila
882	37	46.2	957	2	Q56SY1_9AVES	Q56SY1	harpactes o	955	36.5	45.6	257	2	Q7RJU5_PLAYO	Q7RJU5	plasmodium
883	37	46.2	957	2	Q56SY2_9AVES	Q56SY2	harpactes d	956	36.5	45.6	257	2	Q4RIY0_TETNG	Q4RIY0	tetradon n
884	37	46.2	957	2	Q56SY3_HARAR	Q56SY3	harpactes a	957	36.5	45.6	262	2	Q23092_ARATH	Q23092	arabidopsis
885	37	46.2	957	2	Q56SY4_9AVES	Q56SY4	harpactes o	958	36.5	45.6	266	2	Q9R1G6_MOUSE	Q9R1G6	mus musculus
886	37	46.2	957	2	Q56SY5_TROME	Q56SY5	trogon mela	959	36.5	45.6	269	2	Q9UIK8_HUMAN	Q9UIK8	homo sapien
887	37	46.2	957	2	Q56SY6_TROVI	Q56SY6	trogon viri	960	36.5	45.6	270	2	Q5AQD4_EMENI	Q5AQD4	aspergillus
888	37	46.2	957	2	Q56SY7_9AVES	Q56SY7	trogon surr	961	36.5	45.6	277	2	Q8RST7_ERWCH	Q8RST7	erwinia chr
889	37	46.2	957	2	Q56SY8_TROCO	Q56SY8	trogon viol	962	36.5	45.6	335	2	Q8D6H1_VIBVU	Q8D6H1	vibrio vuln
890	37	46.2	957	2	Q56SY9_TROCO	Q56SY9	trogon curu	963	36.5	45.6	343	2	Q01575_CABEL	Q01575	caenorhabdi
891	37	46.2	957	2	Q56SZ0_TROEL	Q56SZ0	trogon eleg	964	36.5	45.6	350	2	Q5ZNU1_9VIRU	Q5ZNU1	cotesia con
892	37	46.2	957	2	Q56SZ1_TRORU	Q56SZ1	trogon rufu	965	36.5	45.6	413	2	Q91ML8_LSDV	Q91ML8	lumpy skin
893	37	46.2	957	2	Q56SZ2_TROCM	Q56SZ2	trogon comp	966	36.5	45.6	524	2	Q7QDR8_ANOGA	Q7QDR8	anopheles g
894	37	46.2	957	2	Q56SZ3_TROML	Q56SZ3	trogon mela	967	36.5	45.6	581	2	Q98Q22_MYCFU	Q98Q22	mycoplasma
895	37	46.2	957	2	Q56SZ4_9AVES	Q56SZ4	trogon mass	968	36.5	45.6	708	2	Q8NF27_HUMAN	Q8NF27	homo sapien
896	37	46.2	957	2	Q56SZ5_TROPE	Q56SZ5	trogon pers	969	36.5	45.6	814	2	Q5CR06_CRYPV	Q5CR06	cryptospori
897	37	46.2	957	2	Q56SZ6_TROMX	Q56SZ6	trogon mexi	970	36.5	45.6	840	2	Q6PAJ3_MOUSE	Q6PAJ3	mus musculus
898	37	46.2	957	2	Q56SZ7_TROCO	Q56SZ7	trogon coll	971	36.5	45.6	898	2	Q68EU9_XENLA	Q68EU9	xenopus lae
899	37	46.2	957	2	Q56SZ8_9AVES	Q56SZ8	trogon aura	972	36.5	45.6	917	2	Q75VX8_HUMAN	Q75VX8	homo sapien
900	37	46.2	965	2	Q4H3T4_CIOIN	Q4H3T4	ciona intes	973	36.5	45.6	1083	2	Q76698_CABEL	Q76698	caenorhabdi
901	37	46.2	976	2	Q8MWP9_SCHJA	Q8MWP9	schistosoma	974	36.5	45.6	1200	2	Q8BY74_MOUSE	Q8BY74	mus musculus
902	37	46.2	977	2	Q75M87_HUMAN	Q75M87	homo sapien	975	36.5	45.6	1487	2	Q15843_LEIMA	Q15843	leishmania
903	37	46.2	978	2	Q75M86_HUMAN	Q75M86	homo sapien	976	36.5	45.6	2548	2	Q5DU37_MOUSE	Q5DU37	mus musculus
904	37	46.2	979	2	Q80SX4_RAT	Q80SX4	rattus norv	977	36	45.0	28	2	Q4XQ74_PLACH	Q4XQ74	plasmodium
905	37	46.2	990	2	Q5AV89_EMENI	Q5AV89	aspergillus	978	36	45.0	37	2	Q7QP33_STRPN	Q7QP33	streptococc
906	37	46.2	998	1	GTFF21_HUMAN	P78347	h general t	979	36	45.0	40	2	Q8CKA1_YERPE	Q8CKA1	yersinia pe
907	37	46.2	998	1	GTFF21_MOUSE	Q98828	mus musculus	980	36	45.0	43	2	Q8FTJ4_ECOL6	Q8FTJ4	escherichia

981 36 45.0 46 2 Q4X3D8 PLASMODIUM
 982 36 45.0 53 2 Q5VRD7 ORYZA SATIV
 983 36 45.0 55 2 Q5VSB5 ORYZA SATIV
 984 36 45.0 55 2 Q5VSB6 ORYZA SATIV
 985 36 45.0 60 1 CX1 NAJMO
 986 36 45.0 60 1 CX1 NAJPA
 987 36 45.0 60 1 CX2 NAJHA
 988 36 45.0 60 1 CX2 NAJMO
 989 36 45.0 60 1 CX2 NAJNI
 990 36 45.0 60 1 CX3 NAJMO
 991 36 45.0 60 1 CX3 NAJNI
 992 36 45.0 60 1 CX4 NAJHA
 993 36 45.0 60 1 CX5 NAJHA
 994 36 45.0 60 1 CX5 NAJHA
 995 36 45.0 60 1 CX6 NAJHA
 996 36 45.0 60 1 CX7 NAJHA
 997 36 45.0 60 1 CX8 NAJHA
 998 36 45.0 62 1 SXK8 CENNO
 999 36 45.0 64 2 Q6V4V1 CENNO
 1000 36 45.0 66 1 SXK1_CENII

ALIGNMENTS

RESULT 1
 Q8T6U9 BOMMO PRELIMINARY; PRT; 405 AA.
 ID Q8T6U9 BOMMO PRELIMINARY; PRT; 405 AA.
 AC Q8T6U9;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE AKH receptor.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditryaia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21902048; PubMed=11904407; DOI=10.1073/pnas.052556499;
 RA Staubli F., Jorgensen T.J.D., Cazzamali G., Williamson M., Lenz C.,
 RA Sondergaard L., Roepstorff P., Grimmelikhuijzen C.J.P.;
 RT Molecular identification of the insect adipokinetic hormone
 receptors.;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:3446-3451(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; AP403542; AAL95712.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004968; F:gonadotropin-releasing hormone receptor act. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR001658; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00529; GNADOTRPHINR.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; UNKNOWN_1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
 DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 405 AA; 46200 MW; D413F25EA4155AB3 CRC64;

Query Match 62.5%; Score 50; DB 2; Length 405;
 Best Local Similarity 85.7%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
 DB 279 YYCYCLW 285

RESULT 2

Q7MNB7 VIBVY PRELIMINARY; PRT; 507 AA.
 ID Q7MNB7 VIBVY PRELIMINARY; PRT; 507 AA.
 AC Q7MNB7;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein VV0800.
 GN OrderedLocustNames=VV0800;
 OS Vibrio vulnificus (strain YJ016).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=196600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14655965; DOI=10.1101/gr.1295503;
 RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
 RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
 RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-P.;
 RT Comparative genome analysis of Vibrio vulnificus, a marine
 pathogen.;
 RL Genome Res. 13:2577-2587(2003).
 DR EMBL; BA000037; BAC93564.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 507 AA; 58254 MW; PFFC4E282CC756EA CRC64;

Query Match 60.0%; Score 48; DB 2; Length 507;
 Best Local Similarity 85.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKC 10
 DB 394 YCFWKC 400

RESULT 3

Q83861 GREOV PRELIMINARY; PRT; 1132 AA.
 ID Q83861 GREOV PRELIMINARY; PRT; 1132 AA.
 AC Q83861;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE 130KD protein.
 OS Nilaparvata lugens reovirus.
 OC Viruses; dsRNA viruses; Reoviridae; Fijivirus.
 OX NCBI_TaxID=33724;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Izumo;
 RX MEDLINE=96145144; PubMed=8558122;
 RA Nakashima N., Koizumi M., Watanabe H., Hiroaki N.;
 RT Complete nucleotide sequence of the Nilaparvata lugens reovirus: a
 putative member of the genus Fijivirus.;
 RL J. Gen. Virol. 77:139-146(1996).
 DR EMBL; D49696; BAA08545.1; -; Genomic RNA.
 SQ SEQUENCE 1132 AA; 130041 MW; 6E8F5714B8EA0576 CRC64;

Query Match 60.0%; Score 48; DB 2; Length 1132;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYCYCFWKT 9
 DB 292 YYCYCLYRT 300

RESULT 4

Q4LEW9 PHYPA PRELIMINARY; PRT; 891 AA.
 ID Q4LEW9 PHYPA PRELIMINARY; PRT; 891 AA.
 AC Q4LEW9;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

```

DE Pyridine nucleotide-dependent nitrate reductase.
GN Name=Nial1;
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RT Uesaka K., Yoshikawa A., Tsuchimoto R., Omata T.;
RT "Molecular cloning and characterization of nitrate and nitrite
RT reductases in the moss Physcomitrella patens.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB187568; BAE06056.1; -; mRNA.
SQ SEQUENCE 891 AA; 99540 MW; AA015B577F0689BB CRC64;

Query Match 58.8%; Score 47; DB 2; Length 891;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFWK 8
|:|:|:|:|
Db 417 YWCWCFWQ 424

RESULT 5
Q4LEW8_PHYPA
ID Q4LEW8_PHYPA PRELIMINARY; PRT; 892 AA.
AC Q4LEW8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Pyridine nucleotide-dependent nitrate reductase.
GN Name=Nial1;
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RT Uesaka K., Yoshikawa A., Tsuchimoto R., Omata T.;
RT "Molecular cloning and characterization of nitrate and nitrite
RT reductases in the moss Physcomitrella patens.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB187569; BAE06057.1; -; mRNA.
SQ SEQUENCE 892 AA; 99811 MW; DCFD844650A7A7E5 CRC64;

Query Match 58.8%; Score 47; DB 2; Length 892;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFWK 8
|:|:|:|:|
Db 422 YWCWCFWQ 429

RESULT 6
Q22426_CABEL
ID Q22426_CABEL PRELIMINARY; PRT; 1302 AA.
AC Q22426;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Twik family of potassium channels protein 2.
GN Name=twk-2; ORFNames=TI2C9.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;

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RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: U41104; AAK18976.2; -; Genomic DNA.
DR Ensembl: T12C9.3; Caenorhabditis elegans.
DR WormBase; WBGene00006657; twk-2.
DR WormPep; T12C9.3; CE36894.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005560; DUF326.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF03860; DUF326; 3.
KW Complete proteome; Ionic channel.
SQ SEQUENCE 1302 AA; 148653 MW; DA737D251C81548A CRC64;

Query Match 58.8%; Score 47; DB 2; Length 1302;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTCT 11
|:|:|:|:|
Db 815 YSFWKTCT 822

RESULT 7
Q5QIV6_9SOLA
ID Q5QIV6_9SOLA PRELIMINARY; PRT; 449 AA.
AC Q5QIV6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Nitrate reductase (Fragment).
OS Nicotiana attenuata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=49451;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Root;
RA Schittko U., Baldwin I.T.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY460335; AAS19200.1; -; mRNA.
DR GO; GO:0030151; F:molybdenum ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008335; Euk Mb oxred.
DR InterPro; IPR005066; Mo-co dimer.
DR InterPro; IPR00572; Oxidored molyb.
DR Pfam; PF03404; Mo-co dimer; 1.
DR Pfam; PF00174; Oxidored molyb; 1.
DR PRINTS; PR00407; EUMOPTERIN.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
FT NON TER 449
SQ SEQUENCE 449 AA; 51008 MW; OFFDIAA6EB3468EC CRC64;

Query Match 57.5%; Score 46; DB 2; Length 449;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
|:|:|:|:|
Db 420 YWCWCFW 426

RESULT 8
P29291_AGRGI
ID P29291_AGRGI PRELIMINARY; PRT; 487 AA.
AC P29291;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nitrate reductase (EC 1.6.6.1) (Fragment).
 GN Name=agnr2;
 OS Agrostemma githago (Corn cockle) (Purple cockle).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllales; Caryophyllaceae; Agrostemma.
 OX NCBI_TaxID=39848;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA White R., Kende H.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA White R.J.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U64309; AAC39554.1; -, mRNA.
 DR HSSP; P17571; 2CND.
 DR GO; GO:0016491; P:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR001834; Cyt B5 reductase.
 DR InterPro; IPR008335; Euk_Mb_oxred.
 DR InterPro; IPR008333; FAD_binding_6.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR005066; Mo-co dimer.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00173; Cyt-b5; 1.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF03404; Mo-co dimer; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTOCHROME_B5.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00410; PHEHYDRXLASE.
 DR PRODOM; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Oxidoreductase.
 FT NON_TER 1
 SQ SEQUENCE 487 AA; 55167 MW; 7363CCB94EE00EC7 CRC64;
 Query Match 57.5%; Score 46; DB 2; Length 487;
 Best Local Similarity 71.4%; Pred. No. 98;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYCYCFW 7
 Db 2 YWCWCFW 8
 RESULT 9
 ID P92922_AGRGI PRELIMINARY; PRT; 497 AA.
 AC P92922;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAR-2004 (TrEMBLrel. 03, Last sequence update)
 DE Nitrate reductase (EC 1.6.6.1) (Fragment).
 GN Name=agnr3;
 OS Agrostemma githago (Corn cockle) (Purple cockle).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllales; Caryophyllaceae; Agrostemma.
 OX NCBI_TaxID=39848;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA White R., Kende H.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RA White R.J.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U64310; AAB39555.1; -, mRNA.
 DR HSSP; P17571; 2CND.
 DR GO; GO:0016491; P:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR001834; Cyt B5 reductase.
 DR InterPro; IPR008335; Euk_Mb_oxred.
 DR InterPro; IPR008333; FAD_binding_6.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR005066; Mo-co dimer.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR InterPro; IPR001221; Phe hydroxylase.
 DR Pfam; PF00173; Cyt-b5; 1.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF03404; Mo-co dimer; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTOCHROME_B5.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00410; PHEHYDRXLASE.
 DR PRODOM; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Oxidoreductase.
 FT NON_TER 1
 SQ SEQUENCE 497 AA; 56187 MW; 1696BAP8080646C4 CRC64;
 Query Match 57.5%; Score 46; DB 2; Length 497;
 Best Local Similarity 71.4%; Pred. No. 1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYCYCFW 7
 Db 12 YWCWCFW 18
 RESULT 10
 ID Q43265_MAIZE PRELIMINARY; PRT; 501 AA.
 AC Q43265;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nitrate reductase (EC 1.6.6.1) (Fragment).
 GN Name=NARIS;
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Scutellum;
 EX MEDLINE=90267474; PubMed=2189408;
 RA Hyde G.E., Campbell W.H.;
 RT "High-level expression in Escherichia coli of the catalytically active flavin domain of corn leaf NADH:nitrate reductase and its comparison to human NADH:cytochrome B5 reductase."
 RL Biochem. Biophys. Res. Commun. 168:1285-1291(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Scutellum;
 EX MEDLINE=92084635; PubMed=1748631;
 RA Hyde G.E., Crawford N.M., Campbell W.H.;
 RT "The sequence of squash NADH:nitrate reductase and its relationship to the sequences of other flavoprotein oxidoreductases. A family of flavoprotein pyridine nucleotide cytochrome reductases."
 RL J. Biol. Chem. 266:23542-23547(1991).
 DR EMBL; M77792; AAA33483.1; -, mRNA.
 DR PIR; S51160; S51160.

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DR HSP, P17571; 2CND.
DR SMR; Q43265; 243-501.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001199; Cyt_B5_reductase.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR008335; Euk_Mb_oxred.
DR InterPro; IPR008333; FAD binding 6.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR005066; Mo-co dimer.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00173; Cyt-b5; 1.
DR Pfam; PF00970; FAD binding 6; 1.
DR Pfam; PF03404; Mo-co dimer; 1.
DR Pfam; PF00175; NAD binding 1; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 501 AA; 56055 MW; 683C8FEP227499AE CRC64;

Query Match 57.5%; Score 46; DB 2; Length 501;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 16 YWCWCFW 22

RESULT 11
NIAI MAIZE STANDARD; PRT; 621 AA.
AC P17571;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitrate reductase [NADH] (SC 1.7.1.1) (NR) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN N1
RC STRAIN=cv. W64 X W128E; TISSUE=Leaf;
RA Gowri G., Campbell W.H.;
RT "cDNA clones for corn leaf NADH: nitrate reductase and chloroplast
RT NAD(P) (+): Glyceraldehyde-3-phosphate dehydrogenase.";
RL Plant Physiol. 90:792-798(1989).
RN N2
RC SEQUENCE REVISION TO 389-390; 405-406 AND 414-417, AND
RC CHARACTERIZATION
RC STRAIN=cv. W64 X W128E; TISSUE=Leaf;
RX MEDLINE=90267474; PubMed=2189408;
RA Hyde G.E., Campbell W.H.;
RT "High-level expression in Escherichia coli of the catalytically active
RT flavin domain of corn leaf NADH:nitrate reductase and its comparison
RT to human NADH:cytochrome B5 reductase.";
RL Biochem. Biophys. Res. Commun. 168:1285-1291(1990).
RN N3
RC SECONDARY STRUCTURE OF FAD DOMAIN.
RX MEDLINE=92084635; PubMed=1748631;
RA Hyde G.E., Crawford N.M., Campbell W.H.;
RT "The sequence of squash NADH:nitrate reductase and its relationship to
RT the sequences of other flavoprotein oxidoreductases. A family of
RT flavoprotein pyridine nucleotide cytochrome reductases.";
RL J. Biol. Chem. 266:23542-23547(1991).

[4] MUTAGENESIS OF CYS-593.
RX MEDLINE=94245686; PubMed=8188655;
RA Dwivedi U.N., Shiraishi N., Campbell W.H.;
RT "Identification of an 'essential' cysteine of nitrate reductase via
RT mutagenesis of its recombinant cytochrome b reductase domain.";
RL J. Biol. Chem. 269:13785-13791(1994).
[5]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF FAD DOMAIN.
RX MEDLINE=95111952; PubMed=7812715;
RA Lu G., Campbell W.H., Schneider G., Lindqvist Y.;
RT "Crystal structure of the FAD-containing fragment of corn nitrate
RT reductase at 2.5-A resolution: relationship to other flavoprotein
RT reductases.";
RL Structure 2:809-821(1994).
[6]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 232-501.
RX MEDLINE=95280311; PubMed=7760334;
RA Lu G., Lindqvist Y., Schneider G., Dwivedi U., Campbell W.H.;
RT "Structural studies on corn nitrate reductase: refined structure of
RT the cytochrome b reductase fragment at 2.5 A, its ADP complex and an
RT active-site mutant and modeling of the cytochrome b domain.";
RL J. Mol. Biol. 248:931-948(1995).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Binds 1 FAD.
CC -1- COFACTOR: Binds 1 heme group (called cytochrome b-557).
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Belongs to the nitrate reductase family.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
EMBL; M27821; AAA03202.1; ALT_SEQ; mRNA.
PDB; 1CNE; X-ray; @=352-621.
PDB; 1CNF; X-ray; @=352-621.
PDB; 2CND; X-ray; @=352-621.
SMR; P17571; 363-621.
Gramene; P17571; -.
MaizeDB; 25899; -.
InterPro; IPR001199; Cyt_B5_reductase.
InterPro; IPR001834; Cyt_B5_reductase.
InterPro; IPR008335; Euk_Mb_oxred.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR005066; Mo-co dimer.
InterPro; IPR008333; Oxred_FAD bd.
InterPro; IPR001433; Oxred_FAD_NAD bd.
InterPro; IPR000572; Oxred_molyb_bd.
Pfam; PF00173; Cyt-b5; 1.
Pfam; PF00970; FAD binding 6; 1.
Pfam; PF03404; Mo-co dimer; 1.
Pfam; PF00175; NAD binding 1; 1.
PRINTS; PR00406; CYTB5RDTASE.
PRINTS; PR00363; CYTOCHROME B5.
PRINTS; PR00407; EUMOPTERIN.
PRINTS; PR00371; FPNCR.
ProDom; PD000612; Cyt_B5; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS0255; CYTOCHROME_B5_2; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
3D-structure; FAD; Flavoprotein; Heme; Iron; Metal-binding;
Molybdenum; Multigene family; NAD; Nitrate assimilation;
Oxidoreductase.
DOMAIN 249 Cytochrome b5 heme-binding.
METAL 284 Iron (heme axial ligand) (By similarity).
METAL 307 Iron (heme axial ligand) (By similarity).
SITE 593 Necessary for efficient electron

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Transfer.
Interchain (Potential).
C->S: Reduction of activity.

FT DISULFID 138 138
FT MUTAGEN 593 593
FT NON_TER 1
FT STRAND 364 375
FT TURN 376 377
FT STRAND 378 384
FT TURN 388 389
FT TURN 396 397
FT STRAND 399 406
FT TURN 407 408
FT STRAND 409 415
FT TURN 421 422
FT STRAND 426 432
FT STRAND 439 439
FT TURN 440 441
FT STRAND 442 442
FT TURN 443 444
FT HELIX 447 454
FT TURN 457 458
FT STRAND 460 467
FT STRAND 470 471
FT TURN 478 480
FT STRAND 481 482
FT STRAND 483 485
FT STRAND 489 495
FT HELIX 496 498
FT HELIX 499 511
FT TURN 512 515
FT STRAND 519 526
FT HELIX 529 531
FT TURN 533 534
FT HELIX 535 544
FT TURN 546 548
FT STRAND 549 555
FT HELIX 561 563
FT STRAND 568 569
FT HELIX 574 580
FT STRAND 588 593
FT HELIX 596 600
FT TURN 601 603
FT HELIX 604 608
FT TURN 609 611
FT HELIX 614 617
FT STRAND 618 621
SQ SEQUENCE 621 AA; ACC27684ED0FF5D3 CRC64;

Query Match 57.5%; Score 46; DB 1; Length 621;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
DB 136 YWCWCFW 142

RESULT 12

ID P92920 AGRGI PRELIMINARY; PRT; 629 AA.
AC P92920;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nitrate reductase (EC 1.6.6.1) (Fragment).
GN Name=agnrl;
OS Agrostemma githago (Corn cockle) (Purple cockle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Agrostemma.
OX NCBI_TaxID=39848;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA White R., Kende H.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA White R.J.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64308; AAB39553.1; -, mRNA.
DR HSP; P17571; 2CND.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001199; Cyt_B5_reductase.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR008335; Euk_Mb_oxred.
DR InterPro; IPR008333; FAD binding 6.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR005066; Mo-co_dimer.
DR InterPro; IPR005072; Oxidored_molyb.
DR InterPro; IPR001433; Oxred_FAD_NAD(P).
DR Pfam; PF00173; Cyt-b5; 1.
DR Pfam; PF00970; FAD binding 6; 1.
DR Pfam; PF03404; Mo-Go dimer; 1.
DR Pfam; PF00175; NAD binding 1; 1.
DR Pfam; PF00174; Oxidored_molyb; 1.
DR PRINTS; PR00406; CYTBSRDTASE.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRINTS; PR00407; HUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Oxidoreductase.

FT NON_TER 1

SQ SEQUENCE 629 AA; 71360 MW; A1238871F58A98B7 CRC64;
Query Match 57.5%; Score 46; DB 2; Length 629;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
DB 144 YWCWCFW 150

RESULT 13

Q8LT14 SOLTU PRELIMINARY; PRT; 750 AA.
AC Q8LT14;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nitrate reductase (Fragment).
GN Name=8NRS;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yamamoto A., Katou S., Yoshioka H., Doke N., Kawakita K.;
RT "Nitrate reductase, a nitric oxide-producing enzyme: induction by
pathogen signals.";
RL J. Gen. Plant Pathol. 69:218-229(2003).
DR EMBL; AB062142; BAB93533.1; -, mRNA.
DR HSP; P17571; 2CND.
DR GO; GO:0030151; P:molybdenum ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0042128; P:nitrate assimilation; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR008335; Euk_Mb_oxred.
DR InterPro; IPR008333; FAD binding 6.
DR InterPro; IPR001709; FPN_cyt_redctse.

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DR InterPro; IPR005066; Mo-co dimer.
DR InterPro; IPR012137; Nitr_rd_NADH.
DR InterPro; IPR000572; Oxidored molyb.
DR InterPro; IPR01433; Oxred FAD/NAD(P).
DR InterPro; IPR01221; Phe_hydroxylase.
DR Pfam; PF00173; Cyt_b5; 1.
DR Pfam; PF00970; FAD binding 6; 1.
DR Pfam; PF03404; Mo-co dimer; 1.
DR PIRSF; PIRSF00233; Nitr_rd_NADH; 1.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD00612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
FT NON_TER 1
SQ SEQUENCE 750 AA; 84201 MW; 38014D6568219ED CRC64;

Query Match 57.5%; Score 46; DB 2; Length 750;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 264 YWCWCFW 270

RESULT 14
O48930 SOYBN PRELIMINARY; PRT; 875 AA.
AC O48930;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nitrate reductase (Fragment).
GN Name=BCNR-A;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96123229; PubMed=8534848;
RA Wu S., Lu Q., Kriz A.L., Harper J.E.;
RT "Identification of cDNA clones corresponding to two inducible nitrate
reductase genes in soybean; analysis in wild-type and nrl mutant.";
PL Plant Mol. Biol. 29:491-506(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chyna B., Smarrelli J.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF022780; AAB93560.1; -; mRNA.
DR HSSP; P17571; 2CND.
DR SMR; O48930; 622-875.
DR GO; GO:0030151; F:molybdenum ion binding; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0042128; P:nitrate assimilation; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR01834; Cyt_B5_reductase.
DR InterPro; IPR008335; Euk_Mb_oxred.
DR InterPro; IPR008333; FAD binding 6.
DR InterPro; IPR01709; FPN_cyt_redtase.
DR InterPro; IPR005066; Mo-Co dimer.
DR InterPro; IPR012137; Nitr_rd_NADH.
DR InterPro; IPR000572; Oxidored molyb.
DR InterPro; IPR01433; Oxred FAD/NAD(P).

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DR InterPro; IPR001221; Phe_hydroxylase.
DR Pfam; PF00173; Cyt_b5; 1.
DR Pfam; PF00970; FAD binding 6; 1.
DR Pfam; PF03404; Mo-co dimer; 1.
DR PIRSF; PIRSF00233; Nitr_rd_NADH; 1.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD00612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
FT NON_TER 1
SQ SEQUENCE 875 AA; 98406 MW; 8E9F2A29F55AC005 CRC64;

Query Match 57.5%; Score 46; DB 2; Length 875;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 392 YWCWCFW 398

RESULT 15
NIAL_PHAVU STANDARD; PRT; 881 AA.
AC P39865;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR-1).
GN Name=NIAL; Synonym=NRI;
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Saxa; TISSUE=Shoot;
RA Hoff T., Stummann B.M., Henningsen K.W.;
RT "Cloning and expression of a gene encoding a root specific nitrate
reductase in bean (Phaseolus vulgaris).";
PL Physiol. Plantarum 82:197-204(1991).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Binds 1 FAD.
CC -1- COFACTOR: Binds 1 heme group (called cytochrome b-557).
CC -1- COPACTOR: Binds 1 molybdenum ion.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: Belongs to the nitrate reductase family.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; X53603; CAA37672.1; -; Genomic_DNA.
DR PIR; S25445; S25445.
DR HSSP; P17571; 2CND.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR01834; Cyt_B5_reductase.
DR InterPro; IPR008335; Euk_Mb_oxred.

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DR InterPro; IPR001709; FPN cvt reductase.
DR InterPro; IPR005066; Mo-Co dimer.
DR InterPro; IPR012137; Nitr rd NADH.
DR InterPro; IPR008333; Oxred_FAD_bd.
DR InterPro; IPR001433; Oxred_FAD_NAD_bd.
DR InterPro; IPR000572; Oxred_molyb_bd.
DR Pfam; PF00173; Cyt-b5; 1.
DR Pfam; PF00970; FAD binding_6; 1.
DR Pfam; PF03404; Mo-Co dimer; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF00174; Oxidored molyb; 1.
DR PIRSF; PIRSF000233; Nitr rd NADH; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD000612; Cyt B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW FAD; Flavoprotein; Heme; Iron; Metal-binding; Molybdenum;
KW Multigene family; NAD; Nitrate assimilation; Oxidoreductase.
FT DOMAIN 515 590 Cytochrome b5 heme-binding.
FT METAL 167 167 Molybdenum-pterin (Potential).
FT METAL 221 221 Molybdenum-pterin (Potential).
FT METAL 550 550 Iron (heme axial ligand) (By similarity).
FT METAL 573 573 Iron (heme axial ligand) (By similarity).
FT DISULFID 406 406 Interchain (Potential).
SQ SEQUENCE 881 AA; 99223 MW; A212A1288B4E5661 CRC64;

Query Match 57.5%; Score 46; DB 1; Length 881;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
Db 404 YWCWCFW 410
|:|:|

RESULT 16
ID NIA1 SOYBN STANDARD; PRT; 886 AA.
AC P54233;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Inducible nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR).
GN Name=INR1;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Williams; TISSUE=Leaf;
RX MEDLINE=96123229; PubMed=8534848;
RA Wu S., Lu Q., Kriz A.L., Harper J.S.;
RT "Identification of cDNA clones corresponding to two inducible nitrate
reductase genes in soybean: analysis in wild-type and nri mutant.";
RL Plant Mol. Biol. 29:491-506(1995).
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: Binds 1 FAD.
CC -!- COFACTOR: Binds 1 heme group (called cytochrome b-557).
CC -!- COFACTOR: Binds 1 molybdenum ion.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the nitrate reductase family.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; L23854; AAA96727.1; -; mRNA.
CC PIR; A59223; A59223.
CC HSSP; P17571; 2CND.
CC SWR; P54233; 632-886.
CC InterPro; IPR001199; Cyt B5.
CC InterPro; IPR001834; Cyt B5_reductase.
CC InterPro; IPR008335; Euk Mb_oxred.
CC InterPro; IPR001709; FPN cvt reductase.
CC InterPro; IPR005066; Mo-Co dimer.
CC InterPro; IPR012137; Nitr rd NADH.
CC InterPro; IPR008333; Oxred_FAD_bd.
CC InterPro; IPR001433; Oxred_FAD_NAD_bd.
CC Pfam; PF00173; Cyt-b5; 1.
CC Pfam; PF00970; FAD binding_6; 1.
CC Pfam; PF03404; Mo-Co dimer; 1.
CC Pfam; PF00175; NAD binding_1; 1.
CC Pfam; PF00174; Oxidored molyb; 1.
CC PIRSF; PIRSF000233; Nitr rd NADH; 1.
CC PRINTS; PR00406; CYTB5RDTASE.
CC PRINTS; PR00363; CYTOCHROME B5.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRINTS; PR00371; FPNCR.
CC PRODOM; PD000612; Cyt B5; 1.
CC PROSITE; PS00191; CYTOCHROME B5_1; 1.
CC PROSITE; PS0255; CYTOCHROME B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW FAD; Flavoprotein; Heme; Iron; Metal-binding; Molybdenum;
KW Multigene family; NAD; Nitrate assimilation; Oxidoreductase.
FT DOMAIN 513 588 Cytochrome b5 heme-binding.
FT METAL 165 165 Molybdenum-pterin (Potential).
FT METAL 219 219 Molybdenum-pterin (Potential).
FT METAL 548 548 Iron (heme axial ligand) (By similarity).
FT METAL 571 571 Iron (heme axial ligand) (By similarity).
FT DISULFID 404 404 Interchain (Potential).
SQ SEQUENCE 886 AA; 99799 MW; C18C73BDE3DE0614 CRC64;

Query Match 57.5%; Score 46; DB 1; Length 886;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
Db 402 YWCWCFW 408
|:|:|

RESULT 17
ID NIA3 MAIZE STANDARD; PRT; 889 AA.
AC P49102;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitrate reductase [NADH] 3 (EC 1.7.1.1) (NR).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. B73; TISSUE=Seedling;
RA Campbell W.H., Redinbaugh M.G., Ingemarsson B., Dougherty E.S.,
RA Campbell E.R.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -----

```


CC -1- COPACTOR: Binds 1 FAD per subunit (By similarity).
 CC -1- COPACTOR: Binds 1 heme group per subunit (By similarity).
 CC -1- COPACTOR: Binds 1 molybdenum-pterin group per subunit (By similarity).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SIMILARITY: Belongs to the nitrate reductase family.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: U20450; AAA62316.1; -; Genomic_DNA.
 DR PIR: T02240; T02240.
 DR HSSP: P17571; 2CND.
 DR SMR: P49102; 632-889.
 DR Gramene; P49102; -.
 DR MaizDB; 30041; -.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR001834; Cyt B5 reductase.
 DR InterPro; IPR008335; Euk Mb oxred.
 DR InterPro; IPR001709; FPN cyt redctse.
 DR InterPro; IPR005066; Mo-co dimer.
 DR InterPro; IPR012137; Nitr rd NADH.
 DR InterPro; IPR008333; Oxred FAD bd.
 DR InterPro; IPR001433; Oxred FAD NAD bd.
 DR InterPro; IPR005072; Oxred molyb bd.
 DR Pfam; PF00173; Cyt-b5; 1.
 DR Pfam; PF00970; FAD-binding_6; 1.
 DR Pfam; PF03404; Mo-co dimer; 1.
 DR Pfam; PF00175; NAD-binding_1; 1.
 DR Pfam; PF00174; Oxidored molyb; 1.
 DR PIRSF; PIRSF00233; Nitr rd NADH; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTOCHROME5.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR ProDom; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW FAD; Flavoprotein; Heme; Iron; Metal-binding; Molybdenum;
 KW Multigene family; NAD; Nitrate assimilation; Oxidoreductase.
 FT DOMAIN 520 595 Cytochrome b5 heme-binding.
 FT METAL 181 181 Molybdenum-pterin (Potential).
 FT METAL 235 235 Molybdenum-pterin (Potential).
 FT METAL 555 555 Iron (heme axial ligand) (By similarity).
 FT METAL 578 578 Iron (heme axial ligand) (By similarity).
 FT DISULFID 404 404 Interchain (Potential).
 SQ SEQUENCE 889 AA; 98811 MW; 3614A8BB44B822F5 CRC64;
 Query Match 57.5%; Score 46; DB 1; Length 889;
 Best Local Similarity 71.4%; Pred. NO. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 YVCYCFW 7
 Db 418 YWCWCFW 424
 |.:|||
 RESULT 18
 Q6ZHH7 ORYSA PRELIMINARY; PRT; 889 AA.
 AC Q6ZHH7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DR Putative nitrate reductase.
 GN Name=QJ133_F08.4;
 OS Oryza sativa (japonica cultivar-group).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004058; BAB16843.1; -; Genomic_DNA.
 DR HSSP; P00173; IAQA.
 DR Gramene; Q6ZHH7; -.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR001834; Cyt B5 reductase.
 DR InterPro; IPR008335; Euk Mb oxred.
 DR InterPro; IPR008333; FAD-binding_6.
 DR InterPro; IPR001709; FPN cyt redctse.
 DR InterPro; IPR005066; Mo-co dimer.
 DR InterPro; IPR012137; Nitr rd NADH.
 DR InterPro; IPR005072; Oxidored molyb.
 DR InterPro; IPR001433; Oxred FAD/NAD(P).
 DR InterPro; IPR001221; Phe hydroxylase.
 DR Pfam; PF00173; Cyt-b5; 1.
 DR Pfam; PF00970; FAD-binding_6; 1.
 DR Pfam; PF03404; Mo-co dimer; 1.
 DR Pfam; PF00175; NAD-binding_1; 1.
 DR Pfam; PF00174; Oxidored molyb; 1.
 DR PIRSF; PIRSF00233; Nitr rd NADH; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTOCHROME5.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR ProDom; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 DR SEQUENCE 889 AA; 98639 MW; 940048FFEC2F6300 CRC64;
 Query Match 57.5%; Score 46; DB 2; Length 889;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 YVCYCFW 7
 Db 402 YWCWCFW 408
 |.:|||
 RESULT 19
 NIA2 PHAVU
 ID NIA2 PHAVU STANDARD; PRT; 890 AA.
 AC P39866;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR-2).
 GN Name=NIA2; Synonyms=NR2;
 OS Phaseolus vulgaris (Kidney bean) (French bean).
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 CC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 CC Phaseolus.
 OX NCBI_TaxID=3885;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=cv. Saxa;
 RA Jensen P.S., Hoff T., Stummann B.M., Henningsen K.W.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: Binds 1 FAD.
 CC -1- COFACTOR: Binds 1 heme group (called cytochrome b-557).

```

CC -|- COPACTOR: Binds 1 molybdenum ion.
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SIMILARITY: Belongs to the nitrate reductase family.
CC -|- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U01029; AAA95940.1; -, Unassigned_DNA.
CC PIR; T11805; T11805.
CC HSSP; P17571; 2CND.
CC InterPro; IPR001199; Cyt_B5_reductase.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR008335; Euk_Mb_oxred.
CC InterPro; IPR001709; FPN_cyt_redctse.
CC InterPro; IPR005066; Mo-Co_dimer.
CC InterPro; IPR012137; Nitr_rd_NADH.
CC InterPro; IPR008333; Oxred_FAD_bd.
CC InterPro; IPR001433; Oxred_FAD_NAD_bd.
CC Pfam; PF00173; Cyt-b5; 1.
CC Pfam; PF00970; FAD_binding_6; 1.
CC Pfam; PF03404; Mo-Co_dimer; 1.
CC Pfam; PF00175; NAD_Binding_1; 1.
CC Pfam; PF00174; Oxidored_molyb; 1.
CC PIRSF; PIRSF000233; Nitr_rd_NADH; 1.
CC PRINTS; PR00406; CYTB5RDTASE.
CC PRINTS; PR00363; CYTOCHROMEBS.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRINTS; PR00371; FPNCR.
CC PRODOM; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS0255; CYTOCHROME_B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW PAD; Flavoprotein; Heme; Iron; Metal-binding; Molybdenum;
KW Multigene family; NAD; Nitrate assimilation; Oxidoreductase.
FT DOMAIN 513 588 Cytochrome b5 heme-binding.
FT METAL 165 165 Molybdenum-pterin (Potential).
FT METAL 219 219 Molybdenum-pterin (Potential).
FT METAL 548 548 Iron (heme axial ligand) (By similarity).
FT METAL 571 571 Iron (heme axial ligand) (By similarity).
FT DISULFID 404 404 Interchain (Potential).
SQ SEQUENCE 890 AA; 99995 MW; FC03B96F0139DE1E CRC64;

Query Match 57.5%; Score 46; DB 1; Length 890;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
Db 402 YWCWCFW 408
|:|:|:|:|

RESULT 20
Q9SYRO_SOYBN PRELIMINARY; PRT; 890 AA.
AC Q9SYRO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Nitrate reductase (Fragment).
GN Name=nrt2;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabiales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OC NCBI_TaxID=3847;
RN [1]
CC NUCLEOTIDE SEQUENCE.

```

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RA Smarrelli J., Chaveriat J.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF055369; AAD19790.1; -, Genomic_DNA.
DR HSSP; P17571; 2CND.
DR SMR; Q9SYRO; 636-890.
DR GO; GO:0030151; F:molybdenum ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0042128; P:nitrate assimilation; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR008335; Euk_Mb_oxred.
DR InterPro; IPR008333; FAD_binding_6.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR005066; Mo-Co_dimer.
DR InterPro; IPR012137; Nitr_rd_NADH.
DR InterPro; IPR008333; Oxred_FAD_bd.
DR InterPro; IPR001433; Oxred_FAD_NAD(P).
DR InterPro; IPR001221; Phe_hydroxylase.
DR Pfam; PF00173; Cyt-b5; 1.
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF03404; Mo-Co_dimer; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF00174; Oxidored_molyb; 1.
DR PIRSF; PIRSF000233; Nitr_rd_NADH; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PRINTS; PR00410; PHEHYDRILASE.
DR PRODOM; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
FT NON TER 890 890
SQ SEQUENCE 890 AA; 100077 MW; D05AF4B67C9F93 CRC64;

Query Match 57.5%; Score 46; DB 2; Length 890;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
Db 406 YWCWCFW 412
|:|:|:|:|

RESULT 21
NIA7_HORVU
ID NIA7_HORVU STANDARD; PRT; 891 AA.
AC P27968;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitrate reductase [NAD(P)H] (BC 1.7.1.2).
GN Name=NAR-7;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
CC NUCLEOTIDE SEQUENCE.
RC STRAIN=sv. Himalaya;
RX MEDLINE=91375416; PubMed=1896007; DOI=10.1007/BF00260624;
RA Miyazaki J., Juricek M., Angelis K., Schnorr K.M., Kleinhofs A.,
RA Warner R.L.;
RT "Characterization and sequence of a novel nitrate reductase from
RT barley.";
RL Mol. Gen. Genet. 228:329-334(1991).
CC -|- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -|- CATALYTIC ACTIVITY: Nitrite + NAD(P)(+) + H(2)O = nitrate +
CC NAD(P)H.

```

CC	-1-	COPACTOR:	Binds 1 FAD per subunit.
CC	-1-	COPACTOR:	Binds 1 heme group per subunit.
CC	-1-	COPACTOR:	Binds 1 molybdenum-pterin group per subunit.
CC	-1-	SUBUNIT:	Homodimer.
CC	-1-	INDUCTION:	By nitrate.
CC	-1-	SIMILARITY:	Belongs to the nitrate reductase family.
CC	-1-	SIMILARITY:	Contains 1 cytochrome b5 heme-binding domain.
CC	-----		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.		
CC	-----		
EMBL;	XG0173;	CAA42739.1;	-; Genomic_DNA.
PIR;	S16895;	RDBHNP.	
HSSP;	P17571;	2CND.	
Gramene;	27968;	--	
InterPro;	IPR001199;	Cyt_B5.	
InterPro;	IPR001834;	Cyt_B5_reductase.	
InterPro;	IPR008335;	Euk_Mb_oxred.	
InterPro;	IPR001709;	FEN_cyt_redctase.	
InterPro;	IPR005066;	Mo-co dimer.	
InterPro;	IPR012137;	Nitr_rd_NADH.	
InterPro;	IPR008333;	Oxred_FAD_bd.	
InterPro;	IPR001433;	Oxred_FAD_NAD_bd.	
InterPro;	IPR000572;	Oxred_molyb_bd.	
pfam;	PF00173;	Cyt_b5; 1.	
pfam;	PF00970;	FAD binding 6; 1.	
pfam;	PF03404;	Mo-co dimer; 1.	
pfam;	PF00175;	NAD binding 1; 1.	
pfam;	PF00174;	Oxidored_molyb; 1.	
PfirsP;	PfirsP000233;	Nitr_rd_NADH; 1.	
PRINTS;	PR00406;	CYTBSRD7ASE.	
PRINTS;	PR00363;	CYTOCHROMEBS.	
PRINTS;	PR00407;	EUMOPTERIN.	
PRINTS;	PR00371;	FPNCR.	
ProdDom;	PD000612;	Cyt_B5; 1.	
PROSITE;	PS00191;	CYTOCHROME B5_1; 1.	
PROSITE;	PS02555;	CYTOCHROME B5_2; 1.	
PROSITE;	PS00559;	MOLYBDOPTERIN_EUK; 1.	
FAD;	Flavoprotein;	Heme; Iron; Metal-binding; Molybdenum; Multigene family; NAD; NADP; Nitrate assimilation; Oxidoreductase.	
DOMAIN	515	590	Cytochrome b5 heme-binding.
METAL	168	168	Molybdenum-pterin (potential).
METAL	221	221	Molybdenum-pterin (potential).
METAL	550	550	Iron (heme axial ligand) (By similarity).
METAL	573	573	Iron (heme axial ligand) (By similarity).
DISULFID	406	406	Interchain (potential).
SEQUENCE	891 AA;	98630 MW;	AA47EC52FCIEFD13 CRC64;
Query Match		57.5%;	Score 46; DB 1; Length 891;
Best Local Similarity		71.4%;	Pred. No. 1.7e+02;
Matches	5;	Conservative	2; Mismatches 0; Indels 0; Gaps 0;
QY	1	YYCYCFW 7	
		:	
Db	404	YWCWCFW 410	
RESULT 22			
NIA BETVE	ID	NIA BETVE	STANDARD; PRT; 898 AA.
AC	P27783;		
DT	01-AUG-1992	(Rel. 23, Created)	
DT	01-AUG-1992	(Rel. 23, Last sequence update)	
DT	13-SEP-2005	(Rel. 48, Last annotation update)	
DE	Nitrate reductase [NAD(P)H]	(EC 1.7.1.2) (NR).	
GN	Name=NIAL;		
OS	Betula verrucosa (White birch)	(Betula pendula).	
OC	Eukaryota;	Viridiplantae;	Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta;	Magnoliophyta;	eudicotyledons; core eudicotyledons;
OC	rosids;	eurosid I;	Fagales; Betulaceae; Betula.

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RESULT 23
NIA_LOTJA          STANDARD;          PRT;          900 AA.
ID  NIA_LOTJA
AC  P39669;
DT  01-FEB-1995 (Rel. 31, Created)
DT  01-FEB-1995 (Rel. 31, Last sequence update)
DT  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
GN  Name=NIA;
OS  Lotus japonicus.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC  rosoids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
OX  NCBI_TaxID=34305;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=cv. Gifu / B-129;
RA  Waterhouse R.N., Smyth A.J., Prosser I.M., Forde B.G., Clarkson D.T.;
RL  Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC  - FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC  step of nitrate assimilation in plants, fungi and bacteria.
CC  - CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC  - COPACTOR: Binds 1 FAD.
CC  - COPACTOR: Binds 1 heme group (called cytochrome b-557).
CC  - COPACTOR: Binds 1 molybdenum ion.
CC  - SIMILARITY: Homodimer (By similarity).
CC  - SIMILARITY: Belongs to the nitrate reductase family.
CC  - SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  EMBL; X80670; CAA56696.1; -; Genomic DNA.
DR  PIR; S47029; 847029.
DR  HSSP; P17571; 2CND.
DR  SMR; P39869; 646-900.
DR  InterPro; IPR001199; Cyt_B5.
DR  InterPro; IPR001834; Cyt_B5_reductase.
DR  InterPro; IPR008335; Euk_Mb_oxrd.
DR  InterPro; IPR001709; FPN_cyt_redctse.
DR  InterPro; IPR005066; Mo-Co_dimer.
DR  InterPro; IPR012137; Nitr_rd_NADH.
DR  InterPro; IPR008333; Oxrd_FAD_bd.
DR  InterPro; IPR001433; Oxrd_FAD_NAD_bd.
DR  InterPro; IPR000572; Oxrd_molyb_bd.
DR  Pfam; PF00173; Cyt-b5; 1.
DR  Pfam; PF00970; FAD_binding_6; 1.
DR  Pfam; PF03404; Mo-co_dimer; 1.
DR  Pfam; PF00175; NAD_binding_1; 1.
DR  Pfam; PF00174; Oxidored_molyb; 1.
DR  PIRSF; PIRSF000233; Nitr_rd_NADH; 1.
DR  PRINTS; PR00406; CYTB5RD7ASE.
DR  PRINTS; PR00363; CYTOCHROME_B5.
DR  PRINTS; PR00407; EUMOPTERIN.
DR  ProDom; P000612; Cyt_B5; 1.
DR  PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR  PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR  PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW  FAD; Flavoprotein; Heme; Iron; Metal-binding; Molybdenum; NAD;
KW  Nitrate assimilation; Oxidoreductase.
FT  DOMAIN 521 596 Cytochrome b5 heme-binding.
FT  METAL 172 172 Molybdenum-pterin (Potential).
FT  METAL 226 226 Molybdenum-pterin (Potential).
FT  METAL 556 556 Iron (heme axial ligand) (By similarity).
FT  METAL 579 579 Iron (heme axial ligand) (By similarity).
FT  DISULFID 411 411 Interchain (Potential).
SQ  SEQUENCE 900 AA; 101420 MW; 547C25388DD13535 CRC64;

Query Match          57.5%; Score 46; DB 1; Length 900;

Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YYCYCFW 7
Db 409 YMCWCFW 415
|:|:|
|:|:|

RESULT 24
NIAI_TOBAC          STANDARD;          PRT;          904 AA.
ID  NIAI_TOBAC
AC  P11605;
DT  01-OCT-1989 (Rel. 12, Created)
DT  01-OCT-1989 (Rel. 12, Last sequence update)
DT  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR1).
GN  Name=NIAI;
OS  Nicotiana tabacum (Common tobacco).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC  asterids; lamids; Solanales; Solanaceae; Nicotiana.
OX  NCBI_TaxID=4097;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=cv. Xanthi; TISSUE=Leaf;
RA  Vaucheret H., Kronenberger J., Rouze P., Caboche M.;
RL  Plant Mol. Biol. 12:597-600(1989).
CC  - FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC  step of nitrate assimilation in plants, fungi and bacteria.
CC  - CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC  - COPACTOR: Binds 1 FAD per subunit.
CC  - COPACTOR: Binds 1 heme group per subunit.
CC  - COPACTOR: Binds 1 molybdenum-pterin group per subunit.
CC  - ENZYME REGULATION: Regulated by the nitrogen source and controlled
CC  by the circadian rhythm.
CC  - SUBUNIT: Homodimer.
CC  - SIMILARITY: Belongs to the nitrate reductase family.
CC  - SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  EMBL; X14058; CAA32216.1; -; Genomic DNA.
DR  PIR; S04838; RDNTNT.
DR  HSSP; P17571; 2CND.
DR  InterPro; IPR001199; Cyt_B5.
DR  InterPro; IPR001834; Cyt_B5_reductase.
DR  InterPro; IPR008335; Euk_Mb_oxrd.
DR  InterPro; IPR001709; FPN_cyt_redctse.
DR  InterPro; IPR005066; Mo-Co_dimer.
DR  InterPro; IPR012137; Nitr_rd_NADH.
DR  InterPro; IPR008333; Oxrd_FAD_bd.
DR  InterPro; IPR001433; Oxrd_FAD_NAD_bd.
DR  InterPro; IPR000572; Oxrd_molyb_bd.
DR  Pfam; PF00173; Cyt-b5; 1.
DR  Pfam; PF00970; FAD_binding_6; 1.
DR  Pfam; PF03404; Mo-co_dimer; 1.
DR  Pfam; PF00175; NAD_binding_1; 1.
DR  Pfam; PF00174; Oxidored_molyb; 1.
DR  PIRSF; PIRSF000233; Nitr_rd_NADH; 1.
DR  PRINTS; PR00406; CYTB5RD7ASE.
DR  PRINTS; PR00363; CYTOCHROME_B5.
DR  PRINTS; PR00407; EUMOPTERIN.
DR  ProDom; P000612; Cyt_B5; 1.
DR  PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR  PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR  PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.

```

KW FAD; Flavoprotein; Heme; Iron; Metal-binding; Molybdenum;
 KW Multigene family; NAD; Nitrate assimilation; Oxidoreductase.
 FT DOMAIN 531 606 Cytochrome b5 heme-binding.
 FT METAL 183 183 Molybdenum-pterin (Potential).
 FT METAL 237 237 Molybdenum-pterin (Potential).
 FT METAL 566 566 Iron (heme axial ligand) (By similarity).
 FT METAL 589 589 Iron (heme axial ligand) (By similarity).
 FT DISULFID 422 422 Interchain (Potential).
 SQ SEQUENCE 904 AA; 101908 MW; 856428DA723EE154 CRC64;
 Query Match 57.5%; Score 46; DB 1; Length 904;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYCYCFW 7
 Db 420 YMCWCFW 426
 ID NIA2 TOBAC STANDARD; PRT; 904 AA.
 AC P08509;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR2).
 GN Name=NIA2;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=cv. Xanthi; TISSUE=Leaf;
 RA Vaucheret H., Kronenberger J., Rouze P., Caboche M.;
 RT "Complete nucleotide sequence of the two homeologous tobacco nitrate
 reductase genes."
 RL Plant Mol. Biol. 12:597-600(1989).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 171-724.
 RA Calza R., Huttner E., Vincentz M., Rouze P., Galangau F.,
 RA Vaucheret H., Cherel I., Meyer C., Kronenberger J., Caboche M.;
 RT "Cloning of DNA fragments complementary to tobacco nitrate reductase
 mRNA and encoding epitopes common to the nitrate reductases from
 higher plants."
 RL Mol. Genet. 209:552-562(1987).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: Binds 1 FAD per subunit.
 CC -1- COFACTOR: Binds 1 heme group per subunit.
 CC -1- COFACTOR: Binds 1 molybdenum-pterin group per subunit.
 CC -1- ENZYME REGULATION: Regulated by the nitrogen source and controlled
 by the circadian rhythm.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: Belongs to the nitrate reductase family.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL; X14059; CAA32217.1; -; Genomic_DNA.
 DR EMBL; X06134; CAA29497.1; -; mRNA.
 DR PIR; S04839; RDNTNS.
 DR HSSP; P17571; 2CND.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR008335; Euk_Mb_oxred.

DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR005066; Mo-co_dimer.
 DR InterPro; IPR012137; Nitr_rd_NADH.
 DR InterPro; IPR008333; Oxred_FAD_bd.
 DR InterPro; IPR001433; Oxred_FAD_NAD_bd.
 DR InterPro; IPR000572; Oxred_molyb_bd.
 DR Pfam; PF00173; Cyt-b5; 1.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF03404; Mo-co_dimer; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR Pfam; PF00174; Oxidored_molyb; 1.
 DR PIRSF; PIRSF000233; Nitr_rd_NADH; 1.
 DR PRINTS; PR00406; CYTBSRDTASE.
 DR PRINTS; PR00363; CYTOCHROMEBS.
 DR PRINTS; PR00407; KUOPTERIN.
 DR PRINTS; PR00371; PFNCR.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS00255; CYTOCHROME_B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 KW FAD; Flavoprotein; Heme; Iron; Metal-binding; Molybdenum;
 KW Multigene family; NAD; Nitrate assimilation; Oxidoreductase.
 FT DOMAIN 531 606 Cytochrome b5 heme-binding.
 FT METAL 183 183 Molybdenum-pterin (Potential).
 FT METAL 237 237 Iron (heme axial ligand) (By similarity).
 FT METAL 566 566 Iron (heme axial ligand) (By similarity).
 FT METAL 589 589 Iron (heme axial ligand) (By similarity).
 FT DISULFID 422 422 Interchain (Potential).
 SQ SEQUENCE 904 AA; 101958 MW; 75196875A3561D69 CRC64;
 Query Match 57.5%; Score 46; DB 1; Length 904;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYCYCFW 7
 Db 420 YMCWCFW 426
 ID Q93XS1 PRUPE PRELIMINARY; PRT; 906 AA.
 AC Q93XS1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nitrate reductase.
 GN Name=PpNri;
 OS Prunus persica (Peach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids;
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=3760;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Root;
 RA Nakamura Y., Masuda K., Umekiya Y.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB061670; BAB55002.1; -; mRNA.
 DR HSSP; P17571; 2CND.
 DR GO; GO:0030151; F:molybdenum ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0042128; P:nitrate assimilation; IEA.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR008335; Euk_Mb_oxred.
 DR InterPro; IPR008333; FAD_binding_6.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR005066; Mo-co_dimer.
 DR InterPro; IPR012137; Nitr_rd_NADH.
 DR InterPro; IPR000572; Oxidored_molyb.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).

Pfam; PF00173; Cyt-b5; 1.
DR InterPro; IPR00970; FAD binding_6; 1.
DR Pfam; PF03404; Mo-co dimer; 1.
DR InterPro; IPR008333; Oxred_FAD bd.
DR Pfam; PF00175; NAD binding_1; 1.
DR InterPro; IPR001433; Oxred_FAD_NAD bd.
DR Pfam; PF00174; Oxidored molyb; 1.
DR PIRSF; PIRSF000233; Nitrd_NADH; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS0559; MOLYBDOPTERIN_EUK; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
SQ SEQUENCE 906 AA; 101743 MW; D264335BFCABE13E3 CRC64;

Query Match 57.5%; Score 46; DB 2; Length 906;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
|.:|:|

Db 414 YWCWCFW 420

RESULT 27
NIA_PETH STANDARD; PRT; 909 AA.

ID ID NIA_PETH STANDARD; PRT; 909 AA.
AC P36859;
CT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
GN Name=NIA;
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asteride; lamids; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]

NUCLEOTIDE SEQUENCE.
RP STRAIN=cv. TLRU13; TISSUE=Leaf;
RC MEDLINE=93292981; PubMed=8514183; DOI=10.1016/0378-1119(93)90557-J;
RX Salanoubat M., Ha D.B.D.;
RT "Analysis of the petunia nitrate reductase apoenzyme-encoding gene: a first step for sequence modification analysis.";
RL Gene 128:147-154(1993).

-|- FUNCTION: Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.
CC -|- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -|- COFACTOR: Binds 1 FAD per subunit.
CC -|- COPACTOR: Binds 1 heme group per subunit.
CC -|- ENZYME REGULATION: Regulated by the nitrogen source and controlled by the circadian rhythm.
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- DEVELOPMENTAL STAGE: Maximum expression 2 hours after sunrise. Low expression found 2 hours before and 8 hours after sunrise.
CC -|- SIMILARITY: Belongs to the nitrate reductase family.
CC -|- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.

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EMBL; LI3691; AAA33713.1; -, Genomic_DNA.
DR HSSP; P17571; 2CND.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR008335; Euk Mb Oxred.
DR InterPro; IPR001709; FPN cyt redctse.

```

DR Pfam; PF00173; Cyt-b5; 1.
DR Pfam; PF00970; FAD-binding_6; 1.
DR Pfam; PF03404; Mo-co dimer; 1.
DR Pfam; PF00175; NAD-binding_1; 1.
DR Pfam; PF00174; Oxidored molyb; 1.
DR PIRSF; PIRSF000233; Nitr_rd_NADH; 1.
DR PRINTS; PR00406; CYTB5REDTASE.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
SQ SEQUENCE 910 AA; 101520 MW; 680C504DD9D3AAD5 CRC64;

Query Match 57.5%; Score 46; DB 2; Length 910;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 425 YWCWCFW 431

RESULT 29
NIA_LYCES STANDARD; PRT; 911 AA.
AC P17570;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
GN Name=NIA;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Manapal; TISSUE=Leaf;
RX MEDLINE=90185211; PubMed=2628174; DOI=10.1016/0378-1119(89)90430-7;
RA Daniel-Vedele P., Dorbe M.P., Caboche M., Rouze P.;
RT "Cloning and analysis of the tomato nitrate reductase-encoding gene:
RT protein domain structure and amino acid homologies in higher plants.";
RL Gene 85:371-380(1989).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COPACTOR: Binds 1 FAD.
CC -1- COPACTOR: Binds 1 heme group (called cytochrome b-557).
CC -1- SUBUNIT: Homodimer.
CC -1- COPACTOR: Binds 1 molybdenum ion.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X14060; CRA32218.1; -; Genomic_DNA.
DR PIR; JQ0373; RDTONH.
DR HSSP; P17571; 2CND.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR008335; Euk_Mb_oxred.
DR InterPro; IPR001709; FPN_cyt_redtase.
DR InterPro; IPR005066; Mo-co_dimer.
DR InterPro; IPR012137; Nitr_rd_NADH.

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DR InterPro; IPR008333; Oxred_FAD_bd.
DR InterPro; IPR001433; Oxred_FAD_NAD_bd.
DR Pfam; PF00173; Cyt-b5; 1.
DR Pfam; PF00970; FAD-binding_6; 1.
DR Pfam; PF03404; Mo-Co dimer; 1.
DR Pfam; PF00175; NAD-binding_1; 1.
DR Pfam; PF00174; Oxidored molyb; 1.
DR PIRSF; PIRSF000233; Nitr_rd_NADH; 1.
DR PRINTS; PR00406; CYTB5REDTASE.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW FAD; Flavoprotein; Heme; Iron; Metal-binding; Molybdenum; NAD;
KW Nitrate assimilation; Oxidoreductase.
FT DOMAIN 536 611 Cytochrome b5 heme-binding.
FT METAL 188 188 Molybdenum-pterin (Potential).
FT METAL 242 242 Molybdenum-pterin (Potential).
FT METAL 571 571 Iron (heme axial ligand) (By similarity).
FT METAL 594 594 Iron (heme axial ligand) (By similarity).
FT DISULFID 427 427 Interchain (Potential).
SQ SEQUENCE 911 AA; 102453 MW; DE8736181F02A0D5 CRC64;

Query Match 57.5%; Score 46; DB 1; Length 911;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 425 YWCWCFW 431

RESULT 30
O04926 SOLTU PRELIMINARY; PRT; 911 AA.
AC O04926;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NADH nitrate reductase (EC 1.6.6.3).
GN Name=StnR3;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Desiree;
RA Harris N., Foster J.M., Kumar A., Davies H.V., Wray J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U95317; AAB52786.1; -; mRNA.
DR HSSP; P17571; 2CND.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR008335; Euk_Mb_oxred.
DR InterPro; IPR008333; FAD-binding_6.
DR InterPro; IPR001709; FPN_cyt_redtase.
DR InterPro; IPR005066; Mo-co_dimer.
DR InterPro; IPR012137; Nitr_rd_NADH.
DR InterPro; IPR000572; Oxidored molyb.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00173; Cyt-b5; 1.
DR Pfam; PF00970; FAD-binding_6; 1.
DR Pfam; PF03404; Mo-Co dimer; 1.
DR Pfam; PF00175; NAD-binding_1; 1.

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DR Pfam; PF00174; Oxidored molyb; 1.
 DR PIRSF; PIRSF00233; Nitr rd NADH; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTOCHROMEBS.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00410; PHEHYDRXLASE.
 DR PRODOM; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 911 AA; 102609 MW; 2357AD1E4459EB6F CRC64;
 Query Match 57.5%; Score 46; DB 2; Length 911;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
 |:|:|:|
 Db 425 YWCWCFW 431

RESULT 31
 O24390_SOLTU PRELIMINARY; PRT; 911 AA.
 ID O24390; SOLTU PRELIMINARY; PRT; 911 AA.
 AC O24390;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE NADH nitrate reductase (EC 1.6.6.3).
 GN Name=stNR2;
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20407511; PubMed=10948229; DOI=10.1093/jxbbot/51.347.1017;
 RA Harris N., Foster J.M., Kumar A., Davies H.V., Gebhardt C., Wray J.L.;
 RT "Two cDNAs representing alleles of the nitrate reductase gene of
 potato (Solanum tuberosum L. cv. Desiree): sequence analysis, genomic
 organization and expression."
 RL J. Exp. Bot. 51:1017-1026(2000).
 DR EMBL; U76701; AAB18965.1; -; mRNA.
 DR HSSP; P17571; 2CND.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR001834; Cyt B5_reductase.
 DR InterPro; IPR008335; Suk_Mb_oxred.
 DR InterPro; IPR008333; FAD binding_6.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR005066; Mo-co_dimer.
 DR InterPro; IPR012137; Nitr rd NADH.
 DR InterPro; IPR000572; Oxidored_molyb.
 DR InterPro; IPR001433; Oxred FAD/NAD(P).
 DR InterPro; IPR001221; Phe hydroxylase.
 DR Pfam; PF00173; Cyt-b5; 1.
 DR Pfam; PF00970; FAD binding_6; 1.
 DR InterPro; IPR001834; Cyt B5_reductase.
 DR InterPro; IPR008335; Suk_Mb_oxred.
 DR InterPro; IPR008333; FAD binding_6.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR005066; Mo-co_dimer.
 DR InterPro; IPR012137; Nitr rd NADH.
 DR InterPro; IPR000572; Oxidored_molyb.
 DR InterPro; IPR001433; Oxred FAD/NAD(P).
 DR InterPro; IPR001221; Phe hydroxylase.
 DR Pfam; PF00173; Cyt-b5; 1.
 DR Pfam; PF00970; FAD binding_6; 1.
 DR Pfam; PF03404; Mo-co_dimer_1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR Pfam; PF00174; Oxidored molyb; 1.
 DR PIRSF; PIRSF00233; Nitr rd NADH; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTOCHROMEBS.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00410; PHEHYDRXLASE.
 DR PRODOM; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.

DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 911 AA; 102596 MW; C9BC63A1AD25640E CRC64;
 Query Match 57.5%; Score 46; DB 2; Length 911;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
 |:|:|:|
 Db 425 YWCWCFW 431

RESULT 32
 Q8LTI3_SOLTU PRELIMINARY; PRT; 911 AA.
 ID Q8LTI3_SOLTU PRELIMINARY; PRT; 911 AA.
 AC Q8LTI3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nitrate reductase.
 GN Name=stNR6;
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX Yamamoto A., Katou S., Yoshioka H., Doke N., Kawakita K.;
 RT "Nitrate reductase, a nitric oxide-producing enzyme: induction by
 pathogen signals."
 RL J. Gen. Plant Pathol. 69:218-229(2003).
 DR EMBL; AB062143; BAB93334.1; -; mRNA.
 DR HSSP; P17571; 2CND.
 DR GO; GO:0030151; F:molybdenum ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0042128; P:nitrate assimilation; IEA.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR001834; Cyt B5_reductase.
 DR InterPro; IPR008335; Suk_Mb_oxred.
 DR InterPro; IPR008333; FAD binding_6.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR005066; Mo-co_dimer.
 DR InterPro; IPR012137; Nitr rd NADH.
 DR InterPro; IPR000572; Oxidored_molyb.
 DR InterPro; IPR001433; Oxred FAD/NAD(P).
 DR InterPro; IPR001221; Phe hydroxylase.
 DR Pfam; PF00173; Cyt-b5; 1.
 DR Pfam; PF00970; FAD binding_6; 1.
 DR Pfam; PF03404; Mo-co_dimer_1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR Pfam; PF00174; Oxidored molyb; 1.
 DR PIRSF; PIRSF00233; Nitr rd NADH; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTOCHROMEBS.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00410; PHEHYDRXLASE.
 DR PRODOM; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 SQ SEQUENCE 911 AA; 102467 MW; C00F0B9ABA94BDB CRC64;
 Query Match 57.5%; Score 46; DB 2; Length 911;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYCYCFW 7
 |:|:|:|
 Db 425 YWCWCFW 431


```

FT DISULFID 425 425 Interchain (Potential).
FT NON TER 1
SQ SEQUENCE 912 AA; 101467 MW; 47AB9CSB303190CC CRC64;

Query Match 57.5%; Score 46; DB 1; Length 912;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 423 YWCWCFW 429

RESULT 34
Q9FUC2_RICCO
ID Q9FUC2_RICCO PRELIMINARY; PRT; 914 AA.
AC Q9FUC2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nitrate reductase.
GN Name=NIA;
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaceae;
OC Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tsai C.-B., Eckert M., Kaldenhoff R., Kaiser W.M.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF314093; AAG30576.1; -; mRNA.
DR HSSP; P17571; 2CND.
DR SMR; Q9FUC2; 653-914.
DR GO; GO:0030151; F:molybdenum ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0042128; P:nitrate assimilation; IEA.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR001834; Cyt B5_reductase.
DR InterPro; IPR008335; Euk Mb Oxred.
DR InterPro; IPR008333; FAD binding 6.
DR InterPro; IPR001709; FPN_cyt reductse.
DR InterPro; IPR005066; Mo-co dimer.
DR InterPro; IPR012137; Nitr rd NADH.
DR InterPro; IPR000572; Oxidored molyb.
DR InterPro; IPR001433; Oxred FAD/NAD(P).
DR Pfam; PF00173; Cyt-b5; 1.
DR Pfam; PF00970; FAD binding 6; 1.
DR Pfam; PF03404; Mo-co dimer; 1.
DR Pfam; PF00175; NAD binding 1; 1.
DR Pfam; PF00174; Oxidored molyb; 1.
DR PIRSF; PIRSF000233; Nitr rd NADH; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD000612; Cyt B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS00255; CYTOCHROME B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
SQ SEQUENCE 914 AA; 102838 MW; C77CE3DEDA9ED78F CRC64;

Query Match 57.5%; Score 46; DB 2; Length 914;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 423 YWCWCFW 429

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RESULT 33
NIA2_HORVU
ID NIA2_HORVU STANDARD; PRT; 912 AA.
AC P27969.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitrate reductase (NADH) (SC 1.7.1.1) (NR) (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Steptoe; TISSUE=Leaf;
RX MEDLINE=91326031; PubMed=1865878; DOI=10.1007/BF00273931;
RA Schnorr K.M., Juricek M., Huang C., Culley D., Kleinhofs A.;
RT "Analysis of barley nitrate reductase cDNA and genomic clones.";
RL Mol. Gen. Genet. 227:411-416(1991).
CC -|- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -|- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -|- COFACTOR: Binds 1 FAD per subunit.
CC -|- COFACTOR: Binds 1 heme group per subunit.
CC -|- COFACTOR: Binds 1 molybdenum-pterin group per subunit.
CC -|- SUBUNIT: Homodimer.
CC -|- SIMILARITY: Belongs to the nitrate reductase family.
CC -|- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X57844; CAA40975.1; -; mRNA.
DR PIR; S17454; RDBHNS.
DR HSSP; P17571; 2CND.
DR SMR; P27969; 653-912.
DR Gramene; P27969; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR001834; Cyt B5_reductase.
DR InterPro; IPR008335; Euk Mb Oxred.
DR InterPro; IPR001709; FPN_cyt reductse.
DR InterPro; IPR005066; Mo-co dimer.
DR InterPro; IPR012137; Nitr rd NADH.
DR InterPro; IPR008333; Oxred FAD bd.
DR InterPro; IPR001433; Oxred FAD NAD bd.
DR InterPro; IPR000572; Oxred_molyb_bd.
DR Pfam; PF00173; Cyt-b5; 1.
DR Pfam; PF00970; FAD binding 6; 1.
DR Pfam; PF03404; Mo-co dimer; 1.
DR Pfam; PF00175; NAD binding 1; 1.
DR Pfam; PF00174; Oxidored molyb; 1.
DR PIRSF; PIRSF000233; Nitr rd NADH; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD000612; Cyt B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS00255; CYTOCHROME B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Multigene family; NAD; Nitrate assimilation; Molybdenum;
KW FAD; Flavoprotein; Heme; Iron; Metal-binding; Oxidoreductase.
FT DOMAIN 535 610 Cytochrome b5 heme-binding.
FT METAL 186 186 Molybdenum-pterin (Potential).
FT METAL 240 240 Molybdenum-pterin (Potential).
FT METAL 570 570 Iron (heme axial ligand) (By similarity).
FT METAL 593 593 Iron (heme axial ligand) (By similarity).

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RESULT 37
NIA_CUCMA
ID NIA_CUCMA STANDARD; PRT; 918 AA.
AC P17569;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3661;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Crawford N.M., Campbell W.H., Davis R.;
RA "Nitrate reductase from squash: cDNA cloning and nitrate regulation.";
RA Proc. Natl. Acad. Sci. U.S.A. 83:8073-8076(1986).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Seedling;
RX MEDLINE=92084635; PubMed=1748631;
RA Hyde G.E., Crawford N.M., Campbell W.H.;
RT "The sequence of squash NADH:nitrate reductase and its relationship to
RT the sequences of other flavoprotein oxidoreductases. A family of
RT flavoprotein pyridine nucleotide cytochrome reductases.";
RL J. Biol. Chem. 266:23542-23547(1991).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COPACTOR: Binds 1 FAD per subunit.
CC -1- COPACTOR: Binds 1 heme group per subunit.
CC -1- COPACTOR: Binds 1 molybdenum-pterin group per subunit.
CC -1- SUBUNIT: Homodimer.
CC -1- INDUCTION: By nitrate.
CC -1- SIMILARITY: Belongs to the nitrate reductase family.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
-----
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-----
EMBL; M33154; AAA33114.1; -; mRNA.
PIR; A41667; A41667.
HSSP; P17571; 2CND.
InterPro; IPR001199; Cyt B5.
InterPro; IPR001834; Cyt B5 reductase.
InterPro; IPR008335; Euk Mb oxred.
InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR005066; Mo-Co dimer.
InterPro; IPR012137; Nitr_rdn_NADH.
InterPro; IPR008333; Oxred FAD bd.
InterPro; IPR001433; Oxred FAD NAD bd.
InterPro; IPR000572; Oxred_molyb_bd.
Pfam; PF00173; Cyt-b5; 1.
Pfam; PF00970; FAD_binding_6; 1.
Pfam; PF03404; Mo-co_dimer; 1.
Pfam; PF00175; NAD_binding_1; 1.
Pfam; PF00174; Oxidored_molyb; 1.
PIRSP; PIRSF00233; Nitr_rdn_NADH; 1.
PRINTS; PR00406; CYTB5RDASE.
PRINTS; PR00363; CYTOCHROMEBS.
PRINTS; PR00407; EUMOPTERIN.
PRINTS; PR00371; FPNCR.
ProDom; PD000612; Cyt B5; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS0255; CYTOCHROME_B5_2; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW FAD; Flavoprotein; Heme; Iron; Metal-binding; Molybdenum; NAD;
KW Nitrate assimilation; Oxidoreductase.

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FT DOMAIN 543 618 Cytochrome b5 heme-binding.
FT METAL 195 195 Molybdenum-pterin (Potential).
FT METAL 249 249 Molybdenum-pterin (Potential).
FT METAL 578 578 Iron (heme axial ligand) (By similarity).
FT METAL 601 601 Iron (heme axial ligand) (By similarity).
FT DISULPID 434 434 Interchain (Potential).
SQ SEQUENCE 918 AA; 103384 MW; A2CAPDDADEN1B2D1 CRC64;

Query Match 57.5%; Score 46; DB 1; Length 918;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 432 YMCWCFW 438

RESULT 38
NIA_CICIN
ID NIA_CICIN STANDARD; PRT; 920 AA.
AC P43101;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
GN Name=NIA;
OS Cichorium intybus (Chicory).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
OC Cichorieae; Cichorium.
OX NCBI_TaxID=13427;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Witloof; TISSUE=Leaf, and Root;
RX MEDLINE=97141273; PubMed=8987617; DOI=10.1007/BF00196644;
RA Palms B., Goupil P., de Almeida Engler J., Van der Straeten D.,
RA Van Montagu M., Rambour S.;
RT "Evidence for the nitrate-dependent spatial regulation of the nitrate
RT reductase gene in chicory roots.";
RL Planta 200:20-27(1996).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COPACTOR: Binds 1 FAD per subunit.
CC -1- COPACTOR: Binds 1 heme group per subunit.
CC -1- COPACTOR: Binds 1 molybdenum-pterin group per subunit.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- TISSUE SPECIFICITY: In cortical cells of roots grown at low
CC nitrate concentrations, in vascular tissues of roots at high
CC nitrate concentrations and in root apex under both conditions.
CC -1- SIMILARITY: Belongs to the nitrate reductase family.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
-----
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use as long as its content is in no way modified and this statement is not
removed.
-----
EMBL; X84103; CAA58909.1; -; Genomic_DNA.
EMBL; X84102; CAA58908.1; -; mRNA.
PIR; S52301; S52301.
HSSP; P17571; 2CND.
SMR; P43101; 665-920.
InterPro; IPR001199; Cyt B5.
InterPro; IPR001834; Cyt B5 reductase.
InterPro; IPR008335; Euk Mb oxred.
InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR005066; Mo-Co dimer.
InterPro; IPR012137; Nitr_rdn_NADH.
InterPro; IPR008333; Oxred FAD bd.
InterPro; IPR001433; Oxred FAD NAD bd.

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DR InterPro; IPR000572; Oxred_molyb_bd.
DR Pfam; PF00173; Cyt-b5; 1.
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF03404; Mo-co_dimer; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF00174; Oxidored_molyb; 1.
DR PIRSF; PIRSF00233; Nitr_rd_NADH; 1.
DR PRINTS; PR00406; CYTESRDTASE.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_2; 1.
DR PROSITE; PS02055; CYTOCHROME_B5_1; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW FAD; Flavoprotein; Heme; Iron; Metal-binding; Molybdenum; NAD;
KW Nitrate assimilation; Oxidoreductase.
FT DOMAIN 534 609 Cytochrome b5 heme-binding.
FT METAL 185 185 Molybdenum-pterin (Potential).
FT METAL 239 239 Molybdenum-pterin (Potential).
FT METAL 569 569 Iron (heme axial ligand) (By similarity).
FT METAL 592 592 Iron (heme axial ligand) (By similarity).
FT DISULFID 424 424 Interchain (Potential).
SQ SEQUENCE 920 AA; 103520 MW; FE1E332CC9A4D58 CRC64;

Query Match 57.5%; Score 46; DB 1; Length 920;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVCYCFW 7
|:|:|:|
Db 422 YWCRCFW 428

RESULT 39
ID IL04_HCMVA STANDARD; PRT; 152 AA.
AC P17146; Q7M6P4;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Early glycoprotein GP48 precursor.
GN Name=UL4;
OS Human cytomegalovirus (strain AD169) (HHV-5) (Human herpesvirus 5).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horenell T., Hutchison C.A. III, Kourazides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169."
RT Curr. Top. Microbiol. Immunol. 154:125-169(1990).
RN [2]
RP GENOME REANNOTATION.
RX MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;
RA Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,
RA Alexander D.J., McGeoch D.J., Hayward G.S.;
RA "The human cytomegalovirus genome revisited: comparison with the
RT chimpanzee cytomegalovirus genome."
RL J. Gen. Virol. 84:17-28(2003).
RN [3]
RP ERRATUM.
RA Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,
RA Alexander D.J., McGeoch D.J., Hayward G.S.;
RL J. Gen. Virol. 84:1053-1053(2003).
CC -1- FUNCTION: Since gp48 was found in the virion, it is considered an
CC early structural protein.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- PTM: N-glycosylated and possibly O-glycosylated.
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CC -1- SIMILARITY: Belongs to the RL11 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X17403; CAA35437.1; -; Genomic DNA.
DR EMBL; BK000394; DAA00144.1; -; Genomic DNA.
DR PIR; S09767; VGBEY9.
DR InterPro; IPR003599; Ig.
DR SMART; SM00409; IG; 1.
KW Early protein; Glycoprotein; Membrane; Signal.
FT SIGNAL 1 25
FT CHAIN 26 152
FT CARBOHYD 48 48 Early glycoprotein GP48.
FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 61 61 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 69 69 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 112 112 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 152 AA; 17750 MW; CE39A2C0836F7145 CRC64;

Query Match 56.2%; Score 45; DB 1; Length 152;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YVCYCFWTKCT 11
|:|:|:|
Db 19 YVCYCFGTCS 28

RESULT 40
ID Q4TAAL_TETNG PRELIMINARY; PRT; 261 AA.
AC Q4TAAL;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF7392, whole genome shotgun sequence.
GN ORNames=GSTNG0004030001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Berradinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01007392; CAF90181.1; -; Genomic DNA.
SQ SEQUENCE 261 AA; 28630 MW; 7B2C73F63C4C2FDC CRC64;

Query Match 56.2%; Score 45; DB 2; Length 261;
Best Local Similarity 83.3%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YCYCFW 7
Db 31 FCYCFW 36

RESULT 41
ID Q9FH41 ARATH PRELIMINARY; PRT; 262 AA.
AC Q9FH41
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K2N11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones."
RL DNA Rep. 7:31-63 (2000).
DR EMBL; AB022213; BAB11198.1; -; Genomic DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001706; Ribosomal_L35.
DR ProDom; PD003417; Ribosomal_L35; 1.
SQ SEQUENCE 262 AA; 30321 MW; 50F164E1055AE35B CRC64;

Query Match 56.2%; Score 45; DB 2; Length 262;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCF 6
Db 257 YYCYCF 262

RESULT 42
Q96615 CAEL
ID Q96615 CAEL PRELIMINARY; PRT; 334 AA.
AC Q96615
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serpentine receptor, class h protein 33.
GN Name=srh-33; ORFNames=M02H5.9;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for

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RT investigating biology."
RL Science 282:2012-2018 (1998).
DR EMBL; AC006675; AAK84559.1; -; Genomic DNA.
DR Ensembl; M02H5.9; Caenorhabditis elegans.
DR WormBase; WBGene0005256; M02H5.9.
DR WormPep; M02H5.9; CE25956.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003003; 7TM chemrecept2.
DR InterPro; IPR000168; Nm7TM_chemrecept.
DR Pfam; PF01604; 7tm_5; 1.
KW Complete proteome; Receptor.
SQ SEQUENCE 334 AA; 38574 MW; 3FB75103857A17CE CRC64;

Query Match 56.2%; Score 45; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YCYCFWKC 10
Db 53 YLHCFWITC 61

RESULT 43
Q4N4M4 THEPA
ID Q4N4M4 THEPA PRELIMINARY; PRT; 342 AA.
AC Q4N4M4
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TP02_0616;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angioli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Fraser C.M., Nene V.;
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
RT lymphocytes."
RL Science 309:134-137 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angioli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T.R., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AAGK01000002; EAN32899.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 342 AA; 39492 MW; 909B60B58F9A9PB9 CRC64;

Query Match 56.2%; Score 45; DB 2; Length 342;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 YCYCFW 7
Db      186 FCYCFW 191

RESULT 44
Q8P124_XANAC
ID      Q8P124_XANAC PRELIMINARY; PRT; 843 AA.
AC      Q8P124;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Beta-hexosaminidase.
GN      Name=ahA;
OS      Xanthomonas axonopodis (pv. citri).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC      Xanthomonadaceae; Xanthomonas.
OX      NCBI_TaxID=92829;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      STRAIN=306 / ATCC 13902 / XV 101;
RX      MEDLINE=2202145; PubMed=12024217; DOI=10.1038/417459a;
RA      da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA      Quaggio R.B., Monteliro-Vitorello C.B., Van Sluys M.A.,
RA      Almeida N.F., Jr., Alves L.M.C. do Amaral A.M., Bertolini M.C.,
RA      Camargo L.E.A., Camarotte G., Camavan F., Cardozo J., Chambergo F.,
RA      Clepina L.P., Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA      El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA      Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA      Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA      Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA      Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA      Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA      Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA      Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA      Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,
RA      Setubal J.C., Kitajima J.P.;
RA      "Comparison of the genomes of two Xanthomonas pathogens with differing
RT      host specificities."
RL      Nature 417:459-463(2002).
RL      EMBL; AE011950; AAM37919.1; -; Genomic_DNA.
DR      HSSP; O85361; 1HP4.
DR      GO; GO:0004563; P:beta-N-acetylhexosaminidase activity; IEA.
DR      GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR      InterPro; IPR001540; P:carbohydrate metabolism; IEA.
DR      Pfam; PF00728; Glyco_hydro_20; 1.
DR      PRINTS; PR00738; GLYDRLASE20.
KW      Complete proteome.
SQ      SEQUENCE 843 AA; 90454 MW; D68C6D4D02809F7C CRC64;

Query Match 56.2%; Score 45; DB 2; Length 843;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 CYCFWKTCT 11
Db      12 CYCAWLPT 20

RESULT 45
Q60PD2_CABER
ID      Q60PD2_CABER PRELIMINARY; PRT; 2869 AA.
AC      Q60PD2;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      Hypothetical protein CBG222297.
GN      Name=CBG222297;
OS      Caenorhabditis briggsae.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC      Rhabditidae; Pelodidae; Caenorhabditidae.
OX      NCBI_TaxID=6238;

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[1]
RN      NUCLEOTIDE SEQUENCE.
RP      The C. briggsae Sequencing Consortium;
RL      Submitted (Sep-2003) to the EMBL/GenBank/DBJ databases.
CC      -1- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
DR      EMBL; CAAC01000129; CAB74540.1; -; Genomic_DNA.
DR      GO; GO:0000785; C:chromatin; IEA.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0003682; F:chromatin binding; IEA.
DR      GO; GO:0004386; F:helicase activity; IEA.
DR      GO; GO:0016787; F:hydrolase activity; IEA.
DR      GO; GO:0006333; P:chromatin assembly or disassembly; IEA.
DR      GO; GO:0016568; P:chromatin modification; IEA.
DR      GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR      InterPro; IPR006576; BRK.
DR      InterPro; IPR000953; Chromo.
DR      InterPro; IPR011545; DEAD/DEAH_N.
DR      InterPro; IPR011137; Glyco_hydro_11.
DR      InterPro; IPR001650; Helicase_C.
DR      InterPro; IPR001005; Myb_DNA_Binding.
DR      InterPro; IPR000330; SNF2_N.
DR      Pfam; PF00385; Chromo; 1.
DR      Pfam; PF00271; Helicase_C; 1.
DR      Pfam; PF00176; SNF2_N; 1.
DR      Pfam; PF07533; TCH; 1.
DR      SMART; SM00592; BRK; 1.
DR      SMART; SM00298; CHROMO; 2.
DR      SMART; SM00487; DEXDC; 1.
DR      SMART; SM00490; HELICC; 1.
DR      SMART; SM00717; SANT; 1.
DR      PROSITE; PS00013; CHROMO_2; 2.
DR      PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; UNKNOWN_1.
KW      Hypothetical protein.
SQ      SEQUENCE 2869 AA; 318194 MW; 443632EE77DD83A9 CRC64;

Query Match 56.2%; Score 45; DB 2; Length 2869;
Best Local Similarity 75.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 YCYCFWKT 9
Db      995 YCHCDWKT 1002

RESULT 46
Q8BKAS_MOUSE
ID      Q8BKAS_MOUSE PRELIMINARY; PRT; 227 AA.
AC      Q8BKAS;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched
DE      library, clone:R130309A10 product:hypothetical General substrate
DE      transporters/Cellular retinoid-hydro-binding protein (CRL)/Triple
DE      function domain (TRIO) containing protein, full insert sequence.
GN      Name=A330019N05Rik;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      STRAIN=C57BL/6J; TISSUE=EyeBall;
RX      MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA      Carninci P., Hayashizaki Y.;
RA      "High-efficiency full-length cDNA cloning.";
RL      Meth. Enzymol. 303:19-44(1999).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.

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084491_CHLTR
ID 084491_CHLTR PRELIMINARY; PRT; 332 AA.
AC
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein C7484.
GN OrderedLocustNames=C7484;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=D / UW-3 / Cx;
RX MEDLINE=99000809; PubMed=9784136; DOI=10.1126/science.282.5389.754;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
DR EMBL; AB001322; AAC68084.1; -; Genomic_DNA.
DR PIR; B71508; B71508.
DR GO; GO:0005488; F.binding; IEA.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like helical.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 332 AA; 38648 MW; CF612B774DF7489B CRC64;

Query Match 55.0%; Score 44; DB 2; Length 332;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YYCYCFWK 8
Db 150 FSCFCFWK 157

RESULT 49
Q9PJQ7_CHLMU
ID Q9PJQ7_CHLMU PRELIMINARY; PRT; 332 AA.
AC
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=TC0771;
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MoPn / N199;
RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
RA Shirai M., Ishikawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CML029 from USA."
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AB001645; AAD18741.1; -; Genomic DNA.
DR EMBL; AE002176; AAF38027.1; -; Genomic DNA.
DR EMBL; AE017159; AAP98555.1; -; Genomic DNA.
DR EMBL; BA000008; BAA98809.1; -; Genomic_DNA.
DR PIR; D72057; D72057.
DR PIR; G86565; G86565.
DR TIGR; CP0145; -.
DR GO; GO:0005488; F.binding; IEA.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like helical.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 332 AA; 38623 MW; 9E53D9E1F22DA6C7 CRC64;

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Query Match 55.0%; Score 44; DB 2; Length 332;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YYCYCFWK 8
Db 150 FSCFCFWK 157

RESULT 50
Q9Z7V2_CHLPN
ID Q9Z7V2_CHLPN PRELIMINARY; PRT; 334 AA.
AC
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein CP0602 (Hypothetical protein CP0145)
DE Hypothetical protein CP0602.
GN OrderedLocustNames=CP0145, CPJ0602, CPN0602, CPB0626;
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388; DOI=10.1038/7716;
RA Kalman S., Mitchell W.P., Marathe R., Lammel C.J., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.,
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."
RT Nat. Genet. 21:385-389(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TW-183;
RX Geng M.M., Schuhmacher A., Muehldorfer I., Bensach K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
RA Shirai M., Ishikawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CML029 from USA."
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AB001645; AAD18741.1; -; Genomic DNA.
DR EMBL; AE002176; AAF38027.1; -; Genomic DNA.
DR EMBL; AE017159; AAP98555.1; -; Genomic DNA.
DR EMBL; BA000008; BAA98809.1; -; Genomic_DNA.
DR PIR; D72057; D72057.
DR PIR; G86565; G86565.
DR TIGR; CP0145; -.
DR GO; GO:0005488; F.binding; IEA.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like helical.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 334 AA; 38801 MW; E71BE23883932911 CRC64;

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Query Match 55.0%; Score 44; DB 2; Length 334;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 1 YVCYCFWK 8
Db 151 PSCPCFWK 158

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Job time : 101.333 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:05:44 ; Search time 14.6667 Seconds
(without alignments)
62.007 Million cell updates/sec

Title: US-10-796-158-7

Perfect score: 80

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Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA.*

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2: /cgm2_6/ptodata/1/iaa/6-COMB.pep.*

3: /cgm2_6/ptodata/1/iaa/H-COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	53	66.2	8	2	US-09-734-583B-4
3	53	66.2	9	2	US-08-586-670A-16
4	50	62.5	8	2	US-09-484-318-1
5	50	62.5	8	2	US-09-484-318-8
6	50	62.5	8	2	US-09-484-319-1
7	50	62.5	8	2	US-09-484-319-8
8	50	62.5	8	2	US-09-484-320-1
9	50	62.5	8	2	US-09-484-320-8
10	50	62.5	8	2	US-09-484-321-1
11	50	62.5	8	2	US-09-484-321-8
12	50	62.5	8	2	US-09-484-323-1
13	50	62.5	8	2	US-09-484-323-8
14	50	62.5	8	2	US-09-325-769-1
15	50	62.5	8	2	US-09-325-769-2
16	50	62.5	8	2	US-09-636-170-1
17	50	62.5	8	2	US-09-636-170-8
18	50	62.5	8	2	US-09-637-518-1
19	50	62.5	8	2	US-09-637-518-8
20	50	62.5	8	2	US-09-528-200-159
21	50	62.5	109	2	US-09-270-767-60353
22	48	60.0	8	2	US-09-528-200-156
23	45	56.2	6	2	US-09-734-583B-2
24	45	56.2	8	2	US-09-528-200-157
25	44	55.0	237	2	US-09-252-991A-29558
26	44	55.0	338	2	US-09-198-452A-642
27	44	55.0	338	2	US-09-438-185A-604

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30	43	53.8	8	2	US-09-852-870A-2	Sequence 2, Appli
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32	42	52.5	7	2	US-09-657-276-640	Sequence 640, App
33	42	52.5	8	1	US-08-286-748B-7	Sequence 7, Appli
34	42	52.5	8	2	US-08-586-670A-13	Sequence 13, Appli
35	42	52.5	8	2	US-08-586-670A-14	Sequence 14, Appli
36	42	52.5	9	2	US-08-586-670A-11	Sequence 11, Appli
37	42	52.5	9	2	US-08-586-670A-15	Sequence 15, Appli
38	42	52.5	12	1	US-08-752-852A-103	Sequence 103, App
39	42	52.5	109	2	US-09-905-243-67	Sequence 67, Appli
40	42	52.5	146	2	US-09-270-767-43249	Sequence 43249, A
41	41.5	51.9	34	2	US-08-985-526-15	Sequence 15, Appli
42	41	51.2	12	1	US-08-752-852A-108	Sequence 108, App
43	41	51.2	15	1	US-08-685-589A-201	Sequence 201, App
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46	41	51.2	61	2	US-09-248-796A-23474	Sequence 23474, A
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53	41	51.2	109	1	US-09-196-522-266	Sequence 266, App
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59	41	51.2	177	2	US-09-484-577A-52	Sequence 52, Appli
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61	41	51.2	234	2	US-09-770-916-4	Sequence 4, Appli
62	41	51.2	236	1	US-08-792-824-3	Sequence 3, Appli
63	41	51.2	236	1	US-08-792-824-9	Sequence 9, Appli
64	41	51.2	236	1	US-08-792-824-12	Sequence 12, Appli
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82	40	50.0	8	2	US-09-623-548A-198	Sequence 198, App
83	40	50.0	8	2	US-09-657-276-197	Sequence 197, App
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104	40	50.0	128	2	US-08-569-147-78	Sequence 78, Appl	177	38	47.5	103	2	US-09-477-071-4	Sequence 4, Appli
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107	40	50.0	211	2	US-09-543-681A-6708	Sequence 6708, Ap	179	38	47.5	124	2	US-09-990-444-266	Sequence 266, App
108	40	50.0	475	2	US-09-270-767-45548	Sequence 45548, A	180	38	47.5	124	2	US-09-997-333-266	Sequence 266, App
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111	39	48.8	8	2	US-08-384-061-5	Sequence 5, Appli	183	38	47.5	134	2	US-09-027-381-2	Sequence 2, Appli
112	39	48.8	18	1	US-08-852-870A-5	Sequence 5, Appli	184	38	47.5	139	2	US-09-477-071-2	Sequence 2, Appli
113	39	48.8	18	1	US-08-752-852A-133	Sequence 133, App	185	38	47.5	139	2	US-09-949-016-7521	Sequence 7521, Ap
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119	39	48.8	106	2	US-09-205-231-84	Sequence 84, Appl	191	38	47.5	401	2	US-08-492-459-29	Sequence 29, Appl
120	39	48.8	106	2	US-09-205-231-86	Sequence 86, Appl	192	38	47.5	401	2	US-08-423-752-6	Sequence 6, Appli
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126	39	48.8	125	2	US-09-205-231-55	Sequence 55, Appl	198	38	47.5	401	2	US-08-716-873-43	Sequence 43, Appl
127	39	48.8	125	2	US-09-205-231-57	Sequence 57, Appl	199	38	47.5	401	2	US-08-716-873-43	Sequence 43, Appl
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129	39	48.8	126	2	US-09-205-231-27	Sequence 27, Appl	201	38	47.5	401	2	US-09-368-431-20	Sequence 20, Appl
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131	39	48.8	271	1	US-08-400-115-4	Sequence 4, Appli	203	38	47.5	401	2	US-09-368-431-42	Sequence 42, Appl
132	39	48.8	280	2	US-09-949-016-9417	Sequence 9417, Ap	204	38	47.5	401	2	US-09-368-431-43	Sequence 43, Appl
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134	39	48.8	290	2	US-08-793-624-27	Sequence 27, Appl	206	38	47.5	401	2	US-09-414-006-8	Sequence 8, Appli
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139	38.5	48.1	85	2	US-09-599-632-38	Sequence 38, Appl	211	38	47.5	401	2	US-09-951-217-6	Sequence 6, Appli
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141	38	47.5	6	1	US-08-465-764-3	Sequence 3, Appli	213	38	47.5	401	2	US-09-951-217-22	Sequence 22, Appl
142	38	47.5	6	1	US-08-470-932-2	Sequence 2, Appli	214	38	47.5	401	2	US-09-951-217-42	Sequence 42, Appl
143	38	47.5	6	1	US-08-467-025-2	Sequence 2, Appli	215	38	47.5	401	2	US-09-951-217-43	Sequence 43, Appl
144	38	47.5	6	1	US-08-347-397-3	Sequence 3, Appli	216	38	47.5	446	2	US-09-134-000C-3434	Sequence 3434, Ap
145	38	47.5	6	2	US-08-931-095-22	Sequence 22, Appl	217	38	47.5	465	2	US-09-270-767-37268	Sequence 37268, A
146	38	47.5	6	2	US-08-931-095-23	Sequence 23, Appl	218	38	47.5	465	2	US-09-270-767-52485	Sequence 52485, A
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149	38	47.5	8	2	US-09-384-061-9	Sequence 9, Appli	221	38	47.5	549	2	US-08-461-004A-61	Sequence 61, Appl
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153	38	47.5	9	2	US-08-931-095-17	Sequence 17, Appl	225	38	47.5	650	1	US-08-325-071-59	Sequence 59, Appl
154	38	47.5	9	2	US-08-931-095-24	Sequence 24, Appl	226	38	47.5	650	1	US-08-325-071-63	Sequence 63, Appl
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156	38	47.5	11	2	US-09-058-725B-5	Sequence 5, Appli	228	38	47.5	650	2	US-08-461-004A-56	Sequence 56, Appl
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162	38	47.5	12	2	US-09-623-548A-99	Sequence 99, Appl	234	38	47.5	2254	1	US-08-286-819A-28	Sequence 28, Appl
163	38	47.5	12	2	US-10-360-101-98	Sequence 98, Appl	235	38	47.5	2254	2	US-08-980-357-28	Sequence 28, Appl
164	38	47.5	12	2	US-09-657-276-99	Sequence 99, Appl	236	38	47.5	2254	2	US-09-357-375-28	Sequence 28, Appl
165	38	47.5	13	2	US-09-623-548A-100	Sequence 100, App	237	37.5	46.9	7	2	US-09-734-583B-5	Sequence 5, Appli
166	38	47.5	13	2	US-09-657-276-100	Sequence 100, App	238	37.5	46.9	170	2	US-09-358-383C-27	Sequence 27, Appl
167	38	47.5	14	1	US-08-685-589A-195	Sequence 195, App	239	37.5	46.9	428	2	US-09-248-796A-15900	Sequence 15900, A
168	38	47.5	15	1	US-08-685-589A-183	Sequence 183, App	240	37	46.2	6	1	US-08-282-980B-8	Sequence 8, Appli
169	38	47.5	15	1	US-08-685-589A-187	Sequence 187, App	241	37	46.2	6	2	US-08-931-095-5	Sequence 5, Appli
170	38	47.5	15	1	US-08-685-589A-188	Sequence 188, App	242	37	46.2	6	2	US-09-528-200-195	Sequence 195, App
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172	38	47.5	15	1	US-08-685-589A-241	Sequence 241, App	244	37	46.2	8	1	US-08-287-957-13	Sequence 13, Appl
173	38	47.5	30	2	US-08-895-474-10	Sequence 10, Appl	245	37	46.2	8	1	US-08-287-957-15	Sequence 15, Appl
							246	37	46.2	8	1	US-08-287-957-22	Sequence 22, Appl

247	37	46.2	8	1	US-08-287-957-23	Sequence 23, Appl	320	37	46.2	342	2	US-09-136-073-2	Sequence 2, Appl
248	37	46.2	8	1	US-08-287-957-24	Sequence 24, Appl	321	37	46.2	342	2	US-09-457-024A-2	Sequence 2, Appl
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252	37	46.2	9	1	US-08-287-957-21	Sequence 21, Appl	325	37	46.2	619	2	US-09-543-581A-5503	Sequence 5503, Ap
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262	37	46.2	10	1	US-08-287-957-38	Sequence 38, Appl	335	36	45.0	13	1	US-08-752-852A-12	Sequence 12, Appl
263	37	46.2	10	1	US-08-752-852A-96	Sequence 96, Appl	336	36	45.0	15	1	US-08-685-589A-184	Sequence 184, App
264	37	46.2	10	2	US-08-893-749-15	Sequence 15, Appl	337	36	45.0	15	1	US-08-752-852A-10	Sequence 10, Appl
265	37	46.2	11	2	US-08-893-749-17	Sequence 17, Appl	338	36	45.0	15	1	US-08-752-852A-11	Sequence 11, Appl
266	37	46.2	11	2	US-08-893-749-18	Sequence 18, Appl	339	36	45.0	15	1	US-08-752-852A-16	Sequence 16, Appl
267	37	46.2	11	2	US-08-893-749-19	Sequence 19, Appl	340	36	45.0	15	1	US-08-752-852A-17	Sequence 17, Appl
268	37	46.2	11	2	US-08-893-749-34	Sequence 34, Appl	341	36	45.0	15	1	US-08-752-852A-19	Sequence 19, Appl
269	37	46.2	11	2	US-08-586-670A-4	Sequence 4, Appl	342	36	45.0	53	2	US-09-270-767-40917	Sequence 40917, A
270	37	46.2	11	2	US-08-586-670A-8	Sequence 8, Appl	343	36	45.0	53	2	US-09-270-767-56133	Sequence 56133, A
271	37	46.2	12	1	US-08-752-852A-89	Sequence 89, Appl	344	36	45.0	67	2	US-09-248-796A-23577	Sequence 23577, A
272	37	46.2	12	1	US-08-752-852A-104	Sequence 104, App	345	36	45.0	78	2	US-09-270-767-37667	Sequence 37667, A
273	37	46.2	12	1	US-08-752-852A-109	Sequence 109, App	346	36	45.0	78	2	US-09-270-767-52884	Sequence 52884, A
274	37	46.2	13	1	US-08-685-589A-169	Sequence 169, App	347	36	45.0	82	2	US-09-107-433-4060	Sequence 4060, Ap
275	37	46.2	13	1	US-08-752-852A-4	Sequence 4, Appl	348	36	45.0	107	4	PCT-US94-07659-8	Sequence 8, Appl
276	37	46.2	13	1	US-08-752-852A-184	Sequence 184, App	349	36	45.0	109	2	US-09-107-532A-4585	Sequence 4585, Ap
277	37	46.2	28	2	US-09-270-767-34912	Sequence 34912, A	350	36	45.0	111	2	US-09-270-767-34228	Sequence 34228, A
278	37	46.2	28	2	US-09-270-767-50129	Sequence 50129, A	351	36	45.0	111	2	US-09-270-767-49445	Sequence 49445, A
279	37	46.2	32	2	US-09-270-767-58110	Sequence 58110, A	352	36	45.0	114	2	US-09-270-767-34608	Sequence 34608, A
280	37	46.2	32	2	US-09-270-767-42796	Sequence 42796, A	353	36	45.0	114	2	US-09-270-767-49825	Sequence 49825, A
281	37	46.2	72	2	US-09-270-767-37581	Sequence 37581, A	354	36	45.0	119	2	US-09-640-211A-2221	Sequence 2221, Ap
282	37	46.2	72	2	US-09-270-767-52798	Sequence 52798, A	355	36	45.0	124	2	US-09-231-077D-10	Sequence 10, Appl
283	37	46.2	77	2	US-09-107-532A-7019	Sequence 7019, Ap	356	36	45.0	127	2	US-08-933-983-7	Sequence 7, Appl
284	37	46.2	79	2	US-09-543-681A-5859	Sequence 5859, Ap	357	36	45.0	202	2	US-09-252-991A-28110	Sequence 28110, A
285	37	46.2	82	2	US-09-248-796A-23873	Sequence 23873, A	358	36	45.0	234	4	PCT-US94-07659-4	Sequence 4, Appl
286	37	46.2	96	2	US-09-270-767-33811	Sequence 33811, A	359	36	45.0	239	2	US-09-134-001C-4165	Sequence 4165, Ap
287	37	46.2	96	2	US-09-270-767-49028	Sequence 49028, A	360	36	45.0	422	2	US-09-634-238-227	Sequence 227, App
288	37	46.2	106	2	US-10-153-334-5	Sequence 5, Appl	361	36	45.0	443	2	US-09-583-110-4200	Sequence 4200, Ap
289	37	46.2	108	2	US-09-107-532A-6130	Sequence 6130, Ap	362	36	45.0	443	2	US-09-107-433-3180	Sequence 3180, Ap
290	37	46.2	108	2	US-09-649-063-12	Sequence 12, Appl	363	36	45.0	470	2	US-10-001-189-65	Sequence 65, Appl
291	37	46.2	114	2	US-08-537-871A-19	Sequence 19, Appl	364	36	45.0	478	2	US-09-270-767-43204	Sequence 43204, A
292	37	46.2	117	1	US-08-888-497-44	Sequence 44, Appl	365	36	45.0	527	2	US-08-369-822C-25	Sequence 25, Appl
293	37	46.2	117	2	US-09-362-230-44	Sequence 44, Appl	366	36	45.0	527	2	US-08-582-776C-40	Sequence 40, Appl
294	37	46.2	117	4	PCT-US94-07926-44	Sequence 44, Appl	367	36	45.0	527	2	US-08-434-831B-37	Sequence 37, Appl
295	37	46.2	118	1	US-08-888-497-40	Sequence 40, Appl	368	36	45.0	530	2	US-09-949-016-6085	Sequence 6085, Ap
296	37	46.2	118	2	US-09-090-602-4	Sequence 4, Appl	369	36	45.0	554	2	US-09-949-016-8532	Sequence 8532, Ap
297	37	46.2	118	2	US-09-097-094-5	Sequence 5, Appl	370	36	45.0	554	2	US-09-949-016-8533	Sequence 8533, Ap
298	37	46.2	118	2	US-09-362-230-40	Sequence 40, Appl	371	36	45.0	554	2	US-09-949-016-9420	Sequence 9420, Ap
299	37	46.2	118	4	PCT-US94-07926-40	Sequence 40, Appl	372	36	45.0	554	2	US-09-949-016-9421	Sequence 9421, Ap
300	37	46.2	122	1	US-07-734-534A-1	Sequence 1, Appl	373	36	45.0	613	2	US-09-949-016-7583	Sequence 7583, Ap
301	37	46.2	135	2	US-08-537-871A-33	Sequence 33, Appl	374	36	45.0	672	2	US-09-270-767-46165	Sequence 46165, A
302	37	46.2	137	1	US-08-888-497-30	Sequence 30, Appl	375	36	45.0	1013	2	US-08-860-886-2	Sequence 2, Appl
303	37	46.2	137	2	US-09-247-155-109	Sequence 109, App	376	36	45.0	1014	2	US-09-078-347A-3	Sequence 3, Appl
304	37	46.2	137	2	US-09-362-230-30	Sequence 30, Appl	377	36	45.0	1014	2	US-09-596-248D-25	Sequence 25, Appl
305	37	46.2	137	2	US-09-903-190-109	Sequence 109, App	378	36	45.0	1014	2	US-09-296-662-35	Sequence 35, Appl
306	37	46.2	137	4	PCT-US94-07926-30	Sequence 30, Appl	379	36	45.0	1063	2	US-09-596-248D-47	Sequence 47, Appl
307	37	46.2	138	1	US-08-888-497-32	Sequence 32, Appl	380	36	45.0	3011	1	US-08-453-552-2	Sequence 2, Appl
308	37	46.2	138	2	US-09-362-230-32	Sequence 32, Appl	381	36	45.0	3011	1	US-08-710-637-2	Sequence 2, Appl
309	37	46.2	138	2	US-09-975-456B-9	Sequence 9, Appl	382	36	45.0	3011	4	PCT-US93-00907-2	Sequence 2, Appl
310	37	46.2	138	4	PCT-US94-07926-32	Sequence 32, Appl	383	36	45.0	3165	1	US-08-459-146-3	Sequence 3, Appl
311	37	46.2	155	2	US-09-148-545-164	Sequence 164, App	384	36	45.0	3165	1	US-08-459-065-3	Sequence 3, Appl
312	37	46.2	155	2	US-09-148-545-225	Sequence 225, App	385	35.5	44.4	91	2	US-09-621-976-6759	Sequence 6759, Ap
313	37	46.2	155	2	US-09-621-011-164	Sequence 164, App	386	35.5	44.4	262	2	US-09-808-387-30	Sequence 30, Appl
314	37	46.2	155	2	US-09-621-011-225	Sequence 225, App	387	35.5	44.4	288	2	US-09-813-918-3	Sequence 3, Appl
315	37	46.2	164	2	US-09-621-976-5560	Sequence 5560, Ap	388	35.5	44.4	288	2	US-10-060-311-3	Sequence 3, Appl
316	37	46.2	182	2	US-09-949-016-10306	Sequence 10306, A	389	35.5	44.4	288	2	US-10-778-300-3	Sequence 3, Appl
317	37	46.2	199	2	US-09-252-991A-29327	Sequence 29327, A	390	35.5	44.4	332	2	US-09-107-532A-3752	Sequence 3752, Ap
318	37	46.2	248	2	US-09-649-063-23	Sequence 23, Appl	391	35.5	44.4	369	2	US-09-489-039A-9093	Sequence 9093, Ap
319	37	46.2	312	2	US-09-252-991A-18251	Sequence 18251, A	392	35.5	44.4	454	2	US-09-813-918-2	Sequence 2, Appl

393	35.5	44.4	454	2	US-10-060-311-2	Sequence 2, Appli	466	35	43.8	319	2	US-08-311-731A-322	Sequence 322, App
394	35.5	44.4	454	2	US-10-778-300-2	Sequence 2, Appli	467	35	43.8	331	2	US-09-543-681A-6087	Sequence 6087, Ap
395	35.5	44.4	1724	1	US-08-477-451-15	Sequence 15, Appl	468	35	43.8	360	2	US-09-826-509-471	Sequence 471, App
396	35	43.8	8	2	US-08-467-472C-10	Sequence 10, Appl	469	35	43.8	373	2	US-09-039-198A-14	Sequence 14, Appl
397	35	43.8	8	2	US-08-467-472C-11	Sequence 11, Appl	470	35	43.8	373	2	US-09-039-198A-15	Sequence 15, Appl
398	35	43.8	8	2	US-09-384-061-10	Sequence 10, Appl	471	35	43.8	373	2	US-08-877-599-14	Sequence 14, Appl
399	35	43.8	8	2	US-09-384-061-11	Sequence 11, Appl	472	35	43.8	373	2	US-08-877-599-15	Sequence 15, Appl
400	35	43.8	8	2	US-09-623-548A-200	Sequence 200, App	473	35	43.8	373	2	US-09-267-574-14	Sequence 14, Appl
401	35	43.8	8	2	US-09-657-276-200	Sequence 200, App	474	35	43.8	373	2	US-09-267-574-15	Sequence 15, Appl
402	35	43.8	10	2	US-09-852-870A-10	Sequence 10, Appl	475	35	43.8	379	2	US-09-492-709A-355	Sequence 355, App
403	35	43.8	10	2	US-09-852-870A-11	Sequence 11, Appl	476	35	43.8	387	1	US-08-486-839-6	Sequence 6, Appli
404	35	43.8	12	1	US-08-752-852A-40	Sequence 40, Appl	477	35	43.8	387	2	US-09-151-011-6	Sequence 6, Appli
405	35	43.8	14	1	US-08-752-852A-112	Sequence 112, App	478	35	43.8	387	2	US-09-343-623-6	Sequence 6, Appli
406	35	43.8	26	2	US-09-042-353-283	Sequence 283, App	479	35	43.8	387	2	US-09-977-827-6	Sequence 6, Appli
407	35	43.8	131	2	US-08-758-417A-131	Sequence 131, App	480	35	43.8	435	2	US-09-248-796A-15235	Sequence 15235, A
408	35	43.8	27	2	US-09-471-276-1406	Sequence 1406, Ap	481	35	43.8	434	2	US-09-949-016-7968	Sequence 7968, Ap
409	35	43.8	60	2	US-09-673-395A-353	Sequence 353, App	482	35	43.8	447	2	US-09-234-332-11	Sequence 11, Appl
410	35	43.8	77	2	US-09-248-796A-21016	Sequence 21016, A	483	35	43.8	466	1	US-08-486-839-4	Sequence 4, Appli
411	35	43.8	85	2	US-09-252-991A-18572	Sequence 18572, A	484	35	43.8	466	2	US-09-151-011-4	Sequence 4, Appli
412	35	43.8	92	1	US-07-728-215-39	Sequence 39, Appl	485	35	43.8	466	2	US-09-039-198A-2	Sequence 2, Appli
413	35	43.8	92	2	US-08-938-085A-39	Sequence 39, Appl	486	35	43.8	466	2	US-09-039-198A-4	Sequence 4, Appli
414	35	43.8	92	2	US-10-072-844-39	Sequence 39, Appl	487	35	43.8	466	2	US-09-343-623-4	Sequence 4, Appli
415	35	43.8	92	2	US-10-072-844-39	Sequence 39, Appl	488	35	43.8	466	2	US-08-877-599-2	Sequence 2, Appli
416	35	43.8	92	2	US-10-072-841A-39	Sequence 39, Appl	489	35	43.8	466	2	US-08-877-599-4	Sequence 4, Appli
417	35	43.8	92	2	US-09-621-976-5458	Sequence 5458, Ap	490	35	43.8	466	2	US-09-267-574-2	Sequence 2, Appli
418	35	43.8	92	2	US-10-219-631A-39	Sequence 39, Appl	491	35	43.8	466	2	US-09-267-574-4	Sequence 4, Appli
419	35	43.8	107	2	US-08-933-983-76	Sequence 76, Appl	492	35	43.8	466	2	US-09-977-827-4	Sequence 4, Appli
420	35	43.8	113	2	US-09-543-681A-8228	Sequence 8228, Ap	493	35	43.8	501	2	US-09-342-325C-44	Sequence 44, Appl
421	35	43.8	115	2	US-09-107-532A-6806	Sequence 6806, Ap	494	35	43.8	501	2	US-10-244-367-44	Sequence 44, Appl
422	35	43.8	121	2	US-09-673-395A-583	Sequence 583, App	495	35	43.8	503	2	US-09-902-540-11174	Sequence 11174, A
423	35	43.8	126	2	US-09-840-459-72	Sequence 72, Appl	496	35	43.8	718	1	US-08-444-792-4	Sequence 4, Appli
424	35	43.8	126	2	US-09-497-625A-72	Sequence 72, Appl	497	35	43.8	718	1	US-08-445-042-4	Sequence 4, Appli
425	35	43.8	127	2	US-08-933-983-5	Sequence 5, Appli	498	35	43.8	749	2	US-09-949-016-8645	Sequence 8645, Ap
426	35	43.8	127	2	US-08-933-983-9	Sequence 9, Appli	499	35	43.8	749	2	US-09-949-016-8646	Sequence 8646, Ap
427	35	43.8	127	2	US-08-933-983-17	Sequence 17, Appl	500	35	43.8	749	2	US-09-949-016-8647	Sequence 8647, Ap
428	35	43.8	138	2	US-09-673-395A-631	Sequence 631, App	501	35	43.8	749	2	US-09-949-016-8648	Sequence 8648, Ap
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431	35	43.8	141	2	US-09-270-767-32033	Sequence 32033, A	504	35	43.8	766	2	US-09-949-016-11357	Sequence 11357, A
432	35	43.8	150	2	US-09-270-767-47250	Sequence 47250, A	505	35	43.8	766	2	US-09-949-016-11358	Sequence 11358, A
433	35	43.8	150	2	US-09-270-767-32187	Sequence 32187, A	506	35	43.8	784	2	US-09-949-016-9467	Sequence 9467, Ap
434	35	43.8	152	2	US-09-673-395A-489	Sequence 489, App	507	35	43.8	788	1	US-07-728-215-32	Sequence 32, Appl
435	35	43.8	160	2	US-09-270-767-47404	Sequence 47404, A	508	35	43.8	788	2	US-08-938-085A-32	Sequence 32, Appl
436	35	43.8	160	2	US-09-270-767-47404	Sequence 47404, A	509	35	43.8	788	2	US-09-409-648-3	Sequence 3, Appli
437	35	43.8	176	2	US-09-270-767-43906	Sequence 43906, A	510	35	43.8	788	2	US-09-409-648-4	Sequence 4, Appli
438	35	43.8	179	2	US-09-342-325C-53	Sequence 53, Appl	511	35	43.8	788	2	US-10-072-844-32	Sequence 32, Appl
439	35	43.8	179	2	US-09-342-325C-54	Sequence 54, Appl	512	35	43.8	788	2	US-10-072-844-32	Sequence 32, Appl
440	35	43.8	179	2	US-10-244-367-53	Sequence 53, Appl	513	35	43.8	788	2	US-10-072-841A-32	Sequence 32, Appl
441	35	43.8	179	2	US-10-244-367-54	Sequence 54, Appl	514	35	43.8	788	2	US-09-054-272-8	Sequence 8, Appli
442	35	43.8	180	2	US-09-342-325C-51	Sequence 51, Appl	515	35	43.8	788	2	US-09-054-272-44	Sequence 44, Appl
443	35	43.8	180	2	US-09-342-325C-56	Sequence 56, Appl	516	35	43.8	788	2	US-10-219-631A-32	Sequence 32, Appl
444	35	43.8	180	2	US-10-244-367-51	Sequence 51, Appl	517	35	43.8	788	2	US-09-949-016-5901	Sequence 5901, Ap
445	35	43.8	180	2	US-10-244-367-56	Sequence 56, Appl	518	35	43.8	1050	2	US-09-954-987B-175	Sequence 175, App
446	35	43.8	184	2	US-09-673-395A-630	Sequence 630, App	519	35	43.8	1088	2	US-09-949-016-8011	Sequence 8011, Ap
447	35	43.8	187	2	US-09-252-991A-29971	Sequence 29971, A	520	35	43.8	1088	2	US-08-726-214-14	Sequence 14, Appl
448	35	43.8	197	2	US-09-252-991A-28579	Sequence 28579, A	521	35	43.8	1258	2	US-09-538-092-886	Sequence 886, App
449	35	43.8	199	2	US-09-528-760A-2	Sequence 2, Appli	522	35	43.8	1971	2	US-09-914-272A-1	Sequence 1, Appli
450	35	43.8	199	2	US-09-951-843-2	Sequence 2, Appli	523	35	43.8	1971	2	US-10-638-333-1	Sequence 1, Appli
451	35	43.8	199	2	US-10-358-619-2	Sequence 2, Appli	524	35	43.8	1971	2	US-10-747-133A-1	Sequence 1, Appli
452	35	43.8	224	2	US-09-456-090A-48	Sequence 48, Appl	525	35	43.8	3712	2	US-10-037-417-48	Sequence 48, Appl
453	35	43.8	224	2	US-09-453-234-48	Sequence 48, Appl	526	35	43.8	3712	2	US-10-037-417-51	Sequence 51, Appl
454	35	43.8	227	2	US-09-270-767-40613	Sequence 40613, A	527	35	43.8	5179	2	US-09-538-092-1258	Sequence 1258, Ap
455	35	43.8	227	2	US-09-270-767-55829	Sequence 55829, A	528	35	43.8	5179	2	US-10-158-847-102	Sequence 102, App
456	35	43.8	233	2	US-09-252-991A-32770	Sequence 32770, A	529	34.5	43.1	13	2	US-10-158-825-102	Sequence 102, App
457	35	43.8	252	2	US-09-489-039A-9195	Sequence 9195, App	530	34.5	43.1	57	2	US-09-275-252A-38	Sequence 38, Appl
458	35	43.8	260	2	US-09-538-092-950	Sequence 950, App	531	34.5	43.1	82	2	US-09-599-632-6	Sequence 6, Appli
459	35	43.8	264	2	US-09-270-767-39321	Sequence 39321, A	532	34.5	43.1	84	2	US-09-270-767-37706	Sequence 37706, A
460	35	43.8	264	2	US-09-270-767-54538	Sequence 54538, A	533	34.5	43.1	84	2	US-09-270-767-52923	Sequence 2, Appli
461	35	43.8	264	2	US-09-949-016-10789	Sequence 10789, A	534	34.5	43.1	85	2	US-09-599-632-2	Sequence 2, Appli
462	35	43.8	268	2	US-09-934-551-4	Sequence 4, Appli	535	34.5	43.1	161	2	US-09-949-016-7596	Sequence 7596, Ap
463	35	43.8	268	2	US-10-224-414-4	Sequence 4, Appli	536	34.5	43.1	229	2	US-09-966-880A-36	Sequence 36, Appl
464	35	43.8	290	2	US-09-252-991A-21030	Sequence 21030, A	537	34.5	43.1	261	2	US-09-275-252A-18	Sequence 18, Appl
465	35	43.8	301	2	US-09-252-991A-27597	Sequence 27597, A	538	34.5	43.1	270	2	US-09-270-767-44386	Sequence 44386, A

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540	34	42.5	8	1	US-08-287-957-96	Sequence 96, Appl	613	34	42.5	236	2	US-09-270-767-60936	Sequence 60936, A
541	34	42.5	8	1	US-08-287-957-99	Sequence 99, Appl	614	34	42.5	240	2	US-09-270-767-65733	Sequence 65733, A
542	34	42.5	8	1	US-08-676-263-6	Sequence 6, Appli	615	34	42.5	286	2	US-09-270-767-33755	Sequence 33755, A
543	34	42.5	8	2	US-08-467-472C-7	Sequence 7, Appli	616	34	42.5	286	2	US-09-270-767-48792	Sequence 48792, A
544	34	42.5	8	2	US-08-586-670A-10	Sequence 10, Appl	617	34	42.5	288	2	US-09-270-767-38330	Sequence 38330, A
545	34	42.5	8	2	US-09-384-061-7	Sequence 7, Appli	618	34	42.5	288	2	US-09-270-767-53547	Sequence 53547, A
546	34	42.5	8	2	US-08-852-870A-7	Sequence 7, Appli	619	34	42.5	318	2	US-09-270-767-43008	Sequence 43008, A
547	34	42.5	9	1	US-08-676-263-7	Sequence 7, Appli	620	34	42.5	319	2	US-09-328-352-7642	Sequence 7642, Ap
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551	34	42.5	9	2	US-09-042-107-316	Sequence 316, App	624	34	42.5	340	2	US-09-270-767-58348	Sequence 58348, A
552	34	42.5	9	2	US-08-722-250D-316	Sequence 316, App	625	34	42.5	345	2	US-08-985-492-10	Sequence 10, Appl
553	34	42.5	9	2	US-08-676-475A-316	Sequence 316, App	626	34	42.5	353	2	US-08-985-492-4	Sequence 4, Appli
554	34	42.5	9	2	US-10-607-595-316	Sequence 316, App	627	34	42.5	354	2	US-08-985-492-6	Sequence 6, Appli
555	34	42.5	35	2	US-09-471-276-911	Sequence 911, App	628	34	42.5	354	2	US-09-999-833A-178	Sequence 178, App
556	34	42.5	44	2	US-09-716-129-75	Sequence 75, Appl	629	34	42.5	354	2	US-10-020-445A-178	Sequence 178, App
557	34	42.5	47	2	US-09-471-276-1525	Sequence 1525, Ap	630	34	42.5	359	2	US-09-270-767-60194	Sequence 60194, A
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559	34	42.5	50	2	US-09-136-218-22	Sequence 22, Appl	632	34	42.5	371	2	US-08-457-918-7	Sequence 7, Appli
560	34	42.5	50	2	US-09-896-720-22	Sequence 22, Appl	633	34	42.5	371	2	US-10-157-408-7	Sequence 7, Appli
561	34	42.5	59	2	US-08-905-223-317	Sequence 317, App	634	34	42.5	384	2	US-09-489-039A-13229	Sequence 13229, A
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563	34	42.5	61	2	US-08-513-999C-6864	Sequence 6864, Ap	636	34	42.5	388	2	US-09-949-016-8467	Sequence 8467, Ap
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571	34	42.5	68	2	US-09-270-767-43845	Sequence 43845, A	644	34	42.5	477	2	US-09-270-767-43020	Sequence 43020, A
572	34	42.5	68	2	US-09-270-767-59246	Sequence 59246, A	645	34	42.5	498	1	US-08-660-963-12	Sequence 12, Appl
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574	34	42.5	77	2	US-09-270-767-49941	Sequence 49941, A	647	34	42.5	520	2	US-09-270-767-45430	Sequence 45430, A
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576	34	42.5	99	2	US-09-248-796A-21392	Sequence 21392, A	649	34	42.5	534	2	US-09-252-991A-20181	Sequence 20181, A
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588	34	42.5	156	2	US-09-605-703B-1350	Sequence 1350, Ap	661	34	42.5	1055	2	US-09-855-722-2	Sequence 2, Appli
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592	34	42.5	181	2	US-09-198-452A-1156	Sequence 1156, Ap	665	34	42.5	1238	2	US-09-214-278-5	Sequence 5, Appli
593	34	42.5	183	2	US-09-252-991A-24251	Sequence 24251, A	666	34	42.5	1238	2	US-09-855-722-5	Sequence 5, Appli
594	34	42.5	191	2	US-09-270-767-33624	Sequence 33624, A	667	34	42.5	1248	2	US-08-882-046-6	Sequence 6, Appli
595	34	42.5	191	2	US-09-270-767-48841	Sequence 48841, A	668	34	42.5	1248	2	US-09-566-047-6	Sequence 6, Appli
596	34	42.5	192	2	US-09-252-991A-27382	Sequence 27382, A	669	34	42.5	1257	2	US-08-611-729A-8	Sequence 8, Appli
597	34	42.5	193	2	US-09-252-991A-21712	Sequence 21712, A	670	34	42.5	1257	2	US-09-195-524-8	Sequence 8, Appli
598	34	42.5	196	2	US-09-252-991A-23657	Sequence 23657, A	671	34	42.5	1257	2	US-09-310-685-6	Sequence 6, Appli
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603	34	42.5	208	2	US-09-270-767-51584	Sequence 51584, A	676	34	42.5	2231	1	US-08-153-799-16	Sequence 16, Appl
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605	34	42.5	210	2	US-10-062-548-75	Sequence 75, Appl	678	34	42.5	2324	4	FCT-US95-09819-1	Sequence 1, Appli
606	34	42.5	214	2	US-09-328-352-6025	Sequence 6025, Ap	679	34	42.5	2355	2	US-10-360-101-235	Sequence 235, App
607	34	42.5	217	2	US-09-484-577A-34	Sequence 34, Appl	680	34	42.5	2386	1	US-09-016-366A-12	Sequence 12, Appl
608	34	42.5	221	2	US-09-252-991A-32018	Sequence 32018, A	681	34	42.5	2386	1	US-09-961-403-1	Sequence 1, Appli
609	34	42.5	221	2	US-09-248-796A-16852	Sequence 16852, A	682	34	42.5	2446	1	US-08-551-356-2	Sequence 2, Appli
610	34	42.5	226	2	US-09-252-991A-20432	Sequence 20432, A	683	34	42.5	2446	1	FCT-US93-12687-2	Sequence 2, Appli
611	34	42.5	232	2	US-09-270-767-39931	Sequence 39931, A	684	34	42.5	3177	1	US-08-477-451-4	Sequence 4, Appli

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686	33.5	41.9	13	2	US-10-158-825-103	Sequence 103, App	759	33	41.2	112	2	US-09-248-796A-27870	Sequence 27870, A
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688	33.5	41.9	24	1	US-08-484-631-126	Sequence 126, App	761	33	41.2	117	2	US-09-270-767-51348	Sequence 51348, A
689	33.5	41.9	24	1	US-08-827-570-126	Sequence 126, App	762	33	41.2	118	2	US-09-270-767-35845	Sequence 35845, A
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695	33.5	41.9	374	2	US-09-270-767-36720	Sequence 36720, A	768	33	41.2	148	2	US-09-248-796A-15527	Sequence 15527, A
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709	33	41.2	6	2	US-08-488-446-175	Sequence 175, App	782	33	41.2	222	2	US-09-270-767-48080	Sequence 48080, A
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722	33	41.2	15	2	US-08-984-294-13	Sequence 13, Appl	795	33	41.2	248	2	US-09-380-419C-4	Sequence 4, Appli
723	33	41.2	18	1	US-07-876-883-13	Sequence 13, Appl	796	33	41.2	250	2	US-09-270-767-45176	Sequence 45176, A
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725	33	41.2	18	2	US-08-984-294-6	Sequence 6, Appli	798	33	41.2	254	2	US-08-686-968C-7	Sequence 7, Appli
726	33	41.2	18	2	US-08-984-294-7	Sequence 7, Appli	799	33	41.2	254	2	US-08-478-316-16	Sequence 16, Appl
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731	33	41.2	51	2	US-10-178-213-296	Sequence 296, App	804	33	41.2	254	2	US-09-019-793A-16	Sequence 16, Appl
732	33	41.2	58	2	US-09-513-999C-5955	Sequence 5955, Ap	805	33	41.2	254	2	US-09-019-793A-17	Sequence 17, Appl
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734	33	41.2	58	2	US-10-178-213-331	Sequence 231, App	807	33	41.2	254	2	US-09-019-793A-19	Sequence 19, Appl
735	33	41.2	58	2	US-10-178-213-334	Sequence 234, App	808	33	41.2	254	2	US-09-019-793A-22	Sequence 22, Appl
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737	33	41.2	64	2	US-09-270-767-60882	Sequence 60882, A	810	33	41.2	254	2	US-09-601-326-16	Sequence 16, Appl
738	33	41.2	65	2	US-09-248-796A-24662	Sequence 24662, A	811	33	41.2	254	2	US-09-601-326-17	Sequence 17, Appl
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740	33	41.2	70	2	US-09-270-767-34746	Sequence 34746, A	813	33	41.2	254	2	US-09-601-326-19	Sequence 19, Appl
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743	33	41.2	77	2	US-09-673-395A-412	Sequence 412, App	816	33	41.2	254	4	PCT-US95-10904-69	Sequence 2, Appli
744	33	41.2	77	2	US-09-270-767-60668	Sequence 60668, A	817	33	41.2	261	2	US-10-003-759-2	Sequence 2, Appli
745	33	41.2	80	2	US-09-248-796A-26646	Sequence 26646, A	818	33	41.2	274	2	US-09-270-767-45379	Sequence 45379, A
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748	33	41.2	84	2	US-09-599-632-24	Sequence 24, Appl	821	33	41.2	311	2	US-09-380-419C-3	Sequence 3, Appli
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750	33	41.2	86	2	US-10-178-213-330	Sequence 230, App	823	33	41.2	325	2	US-09-107-532A-5774	Sequence 5774, Ap
751	33	41.2	86	2	US-10-178-213-333	Sequence 233, App	824	33	41.2	332	1	US-08-671-525B-8	Sequence 8, Appli
752	33	41.2	91	2	US-09-248-796A-24992	Sequence 24992, A	825	33	41.2	332	1	US-08-672-109B-8	Sequence 8, Appli
753	33	41.2	92	2	US-09-205-258-551	Sequence 551, App	826	33	41.2	332	1	US-08-842-045-8	Sequence 8, Appli
754	33	41.2	92	2	US-10-004-860-551	Sequence 551, App	827	33	41.2	332	1	US-08-842-238-8	Sequence 8, Appli
755	33	41.2	99	2	US-10-290-579A-216	Sequence 216, App	828	33	41.2	332	1	US-08-662-560-2	Sequence 2, Appli
756	33	41.2	100	2	US-10-104-047-2364	Sequence 2364, Ap	829	33	41.2	332	1	US-08-780-749A-2	Sequence 2, Appli
757	33	41.2	105	2	US-09-621-976-5035	Sequence 5035, Ap	830	33	41.2	332	1	US-08-780-749A-6	Sequence 6, Appli

831	33	41.2	332	2	US-08-706-281A-16	Sequence 16, Appl	904	33	41.2	525	2	US-09-949-016-9648	Sequence 9648, Ap
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833	33	41.2	332	2	US-09-097-231-16	Sequence 16, Appl	906	33	41.2	575	2	US-09-328-352-6465	Sequence 6465, Ap
834	33	41.2	332	2	US-08-870-511-2	Sequence 2, Appl	907	33	41.2	587	2	US-09-815-923-4	Sequence 4, Appl
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842	33	41.2	332	2	US-09-831-206-2	Sequence 2, Appl	915	33	41.2	819	1	US-08-424-268-20	Sequence 20, Appl
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845	33	41.2	351	2	US-09-232-200-55	Sequence 55, Appl	918	33	41.2	915	2	US-09-905-125A-34	Sequence 34, Appl
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872	33	41.2	387	1	US-08-429-964-7	Sequence 7, Appl	945	33	41.2	1032	2	US-09-115-954-8	Sequence 8, Appl
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878	33	41.2	436	2	US-09-999-833A-442	Sequence 442, App	951	33	41.2	3088	2	US-09-562-702A-8	Sequence 8, Appl
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ALIGNMENTS

RESULT 1
US-09-528-200-158
; Sequence 158, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHIA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSTIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR FILING DATE: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-528-200-158

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Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 PCFWKTKT 8

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; Sequence 4, Application US/09734583B
; Patent No. 6930088

; GENERAL INFORMATION:
; APPLICANT: Hornik, Vered
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOG
; FILE REFERENCE: 87534-3000
; CURRENT APPLICATION NUMBER: US/09/734,583B
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
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; ORGANISM: Artificial Sequence
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; NAME/KEY: MOD RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: The Thr residue ends with CH2OH
; FEATURE:
; NAME/KEY: DISULFIDE BRIDGE
; LOCATION: (2)..(2)
; OTHER INFORMATION: A disulfide bridge is formed between Cys residues 2 and 7
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; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
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; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-734-583B-4

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Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 PCFWKTKT 8

RESULT 3
US-08-586-670A-16
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; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000

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RESULT 5
US-09-484-318-8
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; Patent No. 6180085
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,318
; CURRENT FILING DATE: 2000-01-18
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; US-09-484-318-8

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DB 1 FCFWKTC T 8

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; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,319
; CURRENT FILING DATE: 2000-01-18
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; LOCATION: (2)..(7)
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; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)

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; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-319-1

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Db      1 FCYWKTKCT 8

RESULT 7
US-09-484-319-8
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; Patent No. 6180086
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,319
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
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; LOCATION: (2)..(7)
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US-09-484-319-8

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       :|:|||||
Db      1 FCYWKTKCT 8

RESULT 8
US-09-484-320-1
; Sequence 1, Application US/09484320
; Patent No. 6180087
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastring
; CURRENT APPLICATION NUMBER: US/09/484,320
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
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US-09-484-320-1

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db      1 FCYWKTKCT 8

RESULT 9
US-09-484-320-8
; Sequence 8, Application US/09484320
; Patent No. 6180087
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastring
; CURRENT APPLICATION NUMBER: US/09/484,320
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-484-320-8

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTKCT 11
       :|:|||||
Db      1 FCYWKTKCT 8

RESULT 10
US-09-484-321-1
; Sequence 1, Application US/09484321
; Patent No. 6183726
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
; FILE REFERENCE: DNA STRING
```

;; CURRENT APPLICATION NUMBER: US/09/484,321
;; CURRENT FILING DATE: 2000-01-18
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 8
;; TYPE: PRT

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
;; NAME/KEY: SITE
;; LOCATION: (1)
;; OTHER INFORMATION: This is D-phenylalanine
;; NAME/KEY: DISULFID
;; LOCATION: (2)..(7)
;; NAME/KEY: SITE
;; LOCATION: (4)
;; OTHER INFORMATION: This is D-tryptophan
;; NAME/KEY: SITE
;; LOCATION: (8)
;; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-321-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred.No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 11
:|:|||||
Db 1 FCYWKTC 8

RESULT 11

US-09-484-321-8
;; Sequence 8, Application US/09484321
;; Patent No. 6190641

;; GENERAL INFORMATION:
;; APPLICANT: Achilefu, Samuel
;; APPLICANT: Rajagopalan, Raghavan
;; APPLICANT: Dorshow, Richard B
;; APPLICANT: Bugaj, Joseph E.
;; TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
;; FILE REFERENCE: DNA STRING
;; CURRENT APPLICATION NUMBER: US/09/484,321
;; CURRENT FILING DATE: 2000-01-18
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 8
;; LENGTH: 8
;; TYPE: PRT

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
;; NAME/KEY: SITE
;; LOCATION: (1)
;; OTHER INFORMATION: This is D-phenylalanine
;; NAME/KEY: DISULFID
;; LOCATION: (2)..(7)
;; NAME/KEY: SITE
;; LOCATION: (4)
;; OTHER INFORMATION: This is D-tryptophan
US-09-484-321-8

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred.No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 11
:|:|||||
Db 1 FCYWKTC 8

RESULT 12

US-09-484-323-1
;; Sequence 1, Application US/09484323
;; Patent No. 6190641

;; GENERAL INFORMATION:
;; APPLICANT: Achilefu, Samuel
;; APPLICANT: Rajagopalan, Raghavan
;; APPLICANT: Dorshow, Richard B
;; APPLICANT: Bugaj, Joseph E.
;; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
;; FILE REFERENCE: DNA STRING
;; CURRENT APPLICATION NUMBER: US/09/484,323
;; CURRENT FILING DATE: 2000-01-18
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 8
;; TYPE: PRT

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
;; NAME/KEY: SITE
;; LOCATION: (1)
;; OTHER INFORMATION: This is D-phenylalanine
;; NAME/KEY: DISULFID
;; LOCATION: (2)..(7)
;; NAME/KEY: SITE
;; LOCATION: (4)
;; OTHER INFORMATION: This is D-tryptophan
;; NAME/KEY: SITE
;; LOCATION: (8)
;; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-323-1

Query Match 62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred.No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 11
:|:|||||
Db 1 FCYWKTC 8

RESULT 13

US-09-484-323-8
;; Sequence 8, Application US/09484323
;; Patent No. 6190641

;; GENERAL INFORMATION:
;; APPLICANT: Achilefu, Samuel
;; APPLICANT: Rajagopalan, Raghavan
;; APPLICANT: Dorshow, Richard B
;; APPLICANT: Bugaj, Joseph E.
;; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
;; FILE REFERENCE: DNA STRING
;; CURRENT APPLICATION NUMBER: US/09/484,323
;; CURRENT FILING DATE: 2000-01-18
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 8
;; LENGTH: 8
;; TYPE: PRT

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
;; NAME/KEY: SITE
;; LOCATION: (1)
;; OTHER INFORMATION: This is D-phenylalanine
;; NAME/KEY: DISULFID
;; LOCATION: (2)..(7)
;; NAME/KEY: SITE
;; LOCATION: (4)
;; OTHER INFORMATION: This is D-tryptophan
US-09-484-323-8

```
Query Match          62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
Db      1 FCYWKTCCT 8

RESULT 14
US-09-325-769-1
; Sequence 1, Application US/09325769
; Patent No. 6217848
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Dorshow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; APPLICANT: Rajagopalan, Raghavan
; TITLE OF INVENTION: NOVEL CYANINE AND INDOCYANINE DYE BIOCONJUGATES FOR
; FILE REFERENCE: 1668-286
; CURRENT APPLICATION NUMBER: US/09/325,769
; EARLIER FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: ATTY DOCKET 1668-284
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: SITE
; LOCATION: (1)
; FEATURE:
; OTHER INFORMATION: This is D-phenylalanine.
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue has had the terminal COOH
; OTHER INFORMATION: reduced to CH2OH.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide.
; US-09-325-769-2

Query Match          62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
Db      1 FCYWKTCCT 8

RESULT 16
US-09-636-170-1
; Sequence 1, Application US/09636170
; Patent No. 6264919
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/636,170
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
; US-09-636-170-1

Query Match          62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
Db      1 FCYWKTCCT 11

RESULT 15
US-09-325-769-2
; Sequence 2, Application US/09325769
; Patent No. 6217848
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Dorshow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; APPLICANT: Rajagopalan, Raghavan
; TITLE OF INVENTION: NOVEL CYANINE AND INDOCYANINE DYE BIOCONJUGATES FOR
; FILE REFERENCE: 1668-286
; CURRENT APPLICATION NUMBER: US/09/325,769
; CURRENT FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: ATTY DOCKET 1668-284
; EARLIER FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
```

```
Db      1 FCYWKTCCT 8

RESULT 17
US-09-636-170-8
; Sequence 8, Application US/09636170
; Patent No. 6264919
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/636,170
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; US-09-636-170-8

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
       :|:|||||
Db      1 FCYWKTCCT 8

RESULT 18
US-09-637-518-1
; Sequence 1, Application US/09637518
; Patent No. 6264920
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastng
; CURRENT APPLICATION NUMBER: US/09/637,518
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; US-09-637-518-1

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
       :|:|||||
Db      1 FCYWKTCCT 8

RESULT 19
US-09-637-518-8
; Sequence 8, Application US/09637518
; Patent No. 6264920
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastng
; CURRENT APPLICATION NUMBER: US/09/637,518
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; US-09-637-518-8

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
       :|:|||||
Db      1 FCYWKTCCT 8

RESULT 20
US-09-528-200-159
; Sequence 159, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGNER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
```

```
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
; US-09-637-518-1

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
       :|:|||||
Db      1 FCYWKTCCT 8

RESULT 19
US-09-637-518-8
; Sequence 8, Application US/09637518
; Patent No. 6264920
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnastng
; CURRENT APPLICATION NUMBER: US/09/637,518
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Octreotate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; US-09-637-518-8

Query Match      62.5%; Score 50; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YCFWKTCCT 11
       :|:|||||
Db      1 FCYWKTCCT 8

RESULT 20
US-09-528-200-159
; Sequence 159, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGNER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
```

; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide

US-09-528-200-159

Query Match 62.5%; Score 50; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 4.6e+05;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11

Db 1 PCYWKTCCT 8

RESULT 21

US-09-270-767-60353

; Sequence 60353, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270.767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 60353

; LENGTH: 109

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-60353

Query Match 62.5%; Score 50; DB 2; Length 109;

Best Local Similarity 60.0%; Pred. No. 7.9;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YYCYCFWKTC 10

Db 15 YKCMCFWRAC 24

RESULT 22

US-09-528-200-156

; Sequence 156, Application US/09528200

; Patent No. 6630570

; GENERAL INFORMATION:

; APPLICANT: LICHA, KAI

; APPLICANT: BECKER, ANDREAS

; APPLICANT: SEMMLER, WOLFHARD

; APPLICANT: WEIDENMANN, BERTRAM

; APPLICANT: HESSNIUS, CARSTEN

; APPLICANT: VOLKMER-ENGERT, RUDOLF

; APPLICANT: SCHNEIDER-MERGENER, JENS

; APPLICANT: BHARGAVA, SARAH

; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA

; FILE REFERENCE: SCH-1731

; CURRENT APPLICATION NUMBER: US/09/528.200

; CURRENT FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: DE 199 17 713.9

; PRIOR FILING DATE: 1999-09-04

; NUMBER OF SEQ ID NOS: 196

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 156

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide

US-09-528-200-156

Query Match 60.0%; Score 48; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 4.6e+05;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11

Db 1 FCFWKVCT 8

RESULT 23

US-09-734-583B-2

; Sequence 2, Application US/09734583B

; Patent No. 6930088

; GENERAL INFORMATION:

; APPLICANT: Hornik, Vered

; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOG

; FILE REFERENCE: 87534-3000

; CURRENT APPLICATION NUMBER: US/09/734.583B

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; NAME/KEY: DISULFIDE BRIDGE

; LOCATION: (1)..(1)

; NAME/KEY: MOD RES

; LOCATION: (3)..(3)

; OTHER INFORMATION: The Trp residue is the D isomer

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

US-09-734-583B-2

Query Match

Best Local Similarity

Matches

Qy

Db

RESULT 24

US-09-528-200-157

; Sequence 157, Application US/09528200

; Patent No. 6630570

; GENERAL INFORMATION:

; APPLICANT: LICHA, KAI

; APPLICANT: BECKER, ANDREAS

; APPLICANT: SEMMLER, WOLFHARD

; APPLICANT: WEIDENMANN, BERTRAM

; APPLICANT: HESSNIUS, CARSTEN

; APPLICANT: VOLKMER-ENGERT, RUDOLF

; APPLICANT: SCHNEIDER-MERGENER, JENS

; APPLICANT: BHARGAVA, SARAH

; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA

; FILE REFERENCE: SCH-1731

; CURRENT APPLICATION NUMBER: US/09/528.200

; CURRENT FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: DE 199 17 713.9

; PRIOR FILING DATE: 1999-09-04

; NUMBER OF SEQ ID NOS: 196

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 156

; LENGTH: 8

;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: Patent Ver. 2.1
;; SEQ ID NO 157
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-528-200-157

Query Match 55.2%; Score 45; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKVCT 11
:|:|:|
Db 1 FCYWKVCT 8

RESULT 25
US-09-252-991A-29558
; Sequence 29558, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29558
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29558

Query Match 55.0%; Score 44; DB 2; Length 237;
Best Local Similarity 55.6%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YCYCFWKTC 10
:|:|:|
Db 17 YCWCWCC 25

RESULT 26
US-09-198-452A-642
; Sequence 642, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 642
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-642

Query Match 55.0%; Score 44; DB 2; Length 338;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYCFWK 8
:|:|:|
Db 155 FSCFCFWK 162

RESULT 27
US-09-438-185A-604
; Sequence 604, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 604
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0602
US-09-438-185A-604

Query Match 55.0%; Score 44; DB 2; Length 338;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YCYCFWK 8
:|:|:|
Db 155 FSCFCFWK 162

RESULT 28
US-08-467-472C-2
; Sequence 2, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HADIT HAPFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:

```

; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
; US-08-467-472C-2

Query Match 53.8%; Score 43; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0

QY 4 YCFWKTKT 11
Db 1 FCFWKTKT 8

RESULT 29
US-09-384-061-2
; Sequence 2, Application US/09384061
; Patent No. 6268339
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAPFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09384,061
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,472
; FILING DATE:
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHEICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby

```

```
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; TITLE: TANDEM MASS SPECTROMETRY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
; US-09-384-061-2
;
; Query Match 53.8%; Score 43; DB 2; Length 8;
; Best Local Similarity 75.0%; Pred. No. 4.6e+05;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 4 YCFWKTCCT 11
; Db 1 FCFWKTCST 8
;
; RESULT 30
; US-09-852-870A-2
; Sequence 2, Application US/09852870A
; Patent No. 6673769
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852.870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 8
;
; Query Match 53.8%; Score 43; DB 2; Length 8;
; Best Local Similarity 75.0%; Pred. No. 4.6e+05;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 4 YCFWKTCCT 11
; Db 1 FCFWKTCST 8
;
; RESULT 31
; US-09-623-548A-640
; Sequence 640, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thiбаudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 640
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-09-623-548A-640
;
; Query Match 52.5%; Score 42; DB 2; Length 7;
; Best Local Similarity 71.4%; Pred. No. 4.6e+05;
; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 5 CFWKTCCT 11
; Db 1 CYWKVCT 7
;
; RESULT 32
; US-09-657-276-640
; Sequence 640, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thiбаudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
```

```
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; TITLE: TANDEM MASS SPECTROMETRY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
; US-09-384-061-2
;
; Query Match 53.8%; Score 43; DB 2; Length 8;
; Best Local Similarity 75.0%; Pred. No. 4.6e+05;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 4 YCFWKTCCT 11
; Db 1 FCFWKTCST 8
;
; RESULT 30
; US-09-852-870A-2
; Sequence 2, Application US/09852870A
; Patent No. 6673769
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852.870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 8
;
; Query Match 53.8%; Score 43; DB 2; Length 8;
; Best Local Similarity 75.0%; Pred. No. 4.6e+05;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 4 YCFWKTCCT 11
; Db 1 FCFWKTCST 8
;
; RESULT 31
; US-09-623-548A-640
; Sequence 640, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thiбаudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
```

;; CURRENT APPLICATION NUMBER: US/09/657,276
;; CURRENT FILING DATE: 2000-09-07
;; PRIOR APPLICATION NUMBER: 60/134,406
;; PRIOR FILING DATE: 1999-05-17
;; PRIOR APPLICATION NUMBER: 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-18
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 640
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-640

Query Match 52.5%; Score 42; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 11
|:|:|
Db 1 CYWKVC 7

RESULT 33
US-08-286-748B-7
; Sequence 7, Application US/08286748B
; Patent No. 5759542
; GENERAL INFORMATION:
; APPLICANT: Victor Gurewich
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
; OF DRUGS BY PLATELETS FOR THE TREATMENT OF
; TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,748B
; FILING DATE: August 5, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: J. Peter Fasse
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04547/013001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa is D- -Naphthylalanine

US-08-286-748B-7

Query Match 52.5%; Score 42; DB 1; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 11
|:|:|
Db 2 CYWKVC 8

RESULT 34
US-08-586-670A-13
; Sequence 13, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "Xaa is D-naphthylalanine and is linked
; OTHER INFORMATION: to DTPA; Trp is in the D conformation;
US-08-586-670A-13

Query Match 52.5%; Score 42; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CFWKTC 11
|:|:|
Db 2 CYWKVC 8

RESULT 35
US-08-586-670A-14
; Sequence 14, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:

```

; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/586,670A
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "Xaa is D-naphthylalanine and is linked
; OTHER INFORMATION: to 2-ketogulonyl; Trp is in the D conformation;
; US-08-586-670A-14

```

```

Query Match          52.5%; Score 42; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      5 CFWKTC 11
       |:|:|
Db      2 CYWKVC 8

```

```

RESULT 36
US-08-586-670A-11
; Sequence 11, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Lys is linked to a BAT chelator
; OTHER INFORMATION: through the side chain nitrogen; Xaa is
; OTHER INFORMATION: D-naphthylalanine; the Cys sulfur is methylated;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5..8
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Trp residue is in the D conformation;
; OTHER INFORMATION: the Cys side chain sulfur is methylated;
; US-08-586-670A-11

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Query Match          52.5%; Score 42; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      5 CFWKTC 11
       |:|:|
Db      3 CYWKVC 9

```

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RESULT 37
US-08-586-670A-15
; Sequence 15, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD

```

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..3
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "Lys is linked to a BAT chelator
OTHER INFORMATION: through the side chain nitrogen and to DTPA
OTHER INFORMATION: at the N-terminus; Xaa is D-naphthylalanine;
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3..8
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "The Trp residue is in the D conformation;
OTHER INFORMATION: each of the Cys side chain sulfur atoms are
OTHER INFORMATION: methylated;
US-08-586-670A-15

Query Match 52.5%; Score 42; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CPWKVCT 11
|:|:|
Db 3 CYWKVCT 9

RESULT 38
US-08-752-852A-103
; Sequence 103, Application US/08752852A
; Patent No. 5994306
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Ches-Liang
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah
; APPLICANT: Lehrer, Robert
; APPLICANT: Harwig, Sylvia
; TITLE OF INVENTION: FINE-TUNED PROTEGRINS
; NUMBER OF SEQUENCES: 242
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,852A
; FILING DATE: 21-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-034-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
```

```
TELEFAX: 212-869-9741
TELEX: 66141
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-752-852A-103

Query Match 52.5%; Score 42; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CYCFWKT 10
|:|:|
Db 2 CYCFPRC 9

RESULT 39
US-09-905-243-67
; Sequence 67, Application US/09905243
; Patent No. 6936698
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; TITLE OF INVENTION: Immunogenicity
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-905-243-67

Query Match 52.5%; Score 42; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YYCYCFWKT 9
|:|:|
Db 86 YYCQCGWGT 94

RESULT 40
US-09-270-767-43249
; Sequence 43249, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43249
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43249

Query Match 52.5%; Score 42; DB 2; Length 146;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 2 YCYCFW 7
Db 30 YCYCVM 35

RESULT 41
US-08-985-526-15
; Sequence 15, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorow Jr., Robert G
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-15

Query Match 51.9%; Score 41.5; DB 2; Length 34;
Best Local Similarity 33.3%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 1; Indels 9; Gaps 1;

Qy 2 YCY-----CFWKTC 10
Db 2 FCYWKVCKGKSFYKVC 19

RESULT 42
US-08-752-852A-108
; Sequence 108, Application US/08752852A
; Patent No. 5994306
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Chee-Liang
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah
; APPLICANT: Lehrer, Robert
; APPLICANT: Harwig, Sylvia
; TITLE OF INVENTION: FINE-TUNED PROTEGRINS
; NUMBER OF SEQUENCES: 242
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-752-852A-108

Query Match 51.2%; Score 41; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CYCFWKTC 10
Db 2 CYCFRRC 9

RESULT 43
US-08-685-589A-201
; Sequence 201, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /product= "Cyclic"
US-08-685-589A-201

Query Match 51.2%; Score 41; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 22;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YCYCFWK 8
:|||||:
Db 7 FCYCLMR 13

RESULT 44
US-08-685-589A-202
; Sequence 202, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,589A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 202:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: circular
; MOLECULE TYPE: peptide

FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /product= "Cyclic"
US-08-685-589A-202

Query Match 51.2%; Score 41; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 22;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YCYCFWK 8
:|||||:
Db 7 FCYCLMR 13

RESULT 45
US-08-525-539A-18
; Sequence 18, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANT, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-18

Query Match 51.2%; Score 41; DB 2; Length 33;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YYCYCFWKT 9
:|||||:
Db 19 YYCQHPWST 27

RESULT 46
US-09-248-796A-23474
; Sequence 23474, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 23474
LENGTH: 61
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-23474

Query Match 51.2%; Score 41; DB 2; Length 61;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YYCYCFWK 8
Db 9 FYCHCTWR 16

RESULT 47
US-10-092-246-17
Sequence 17, Application US/10092246
Patent No. 6501314
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar B
APPLICANT: Nagata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc
TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/092,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patent in version 3.1
SEQ ID NO 17
LENGTH: 108
TYPE: PRT
ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-17

Query Match 51.2%; Score 41; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YYCYCFWK 9
Db 86 YYCQHFWS 94

RESULT 48
US-08-407-620A-32
Sequence 32, Application US/08407620A
Patent No. 6569430
GENERAL INFORMATION:
APPLICANT: WALDMANN, HERMAN
APPLICANT: CLARK, MICHAEL R.
APPLICANT: WINTER, GREGORY P.
APPLICANT: RIECHMANN, LUTZ
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA

COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,620A
FILING DATE: 21-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,705
FILING DATE: 29-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,480
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,601
FILING DATE: 03-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/424,233
FILING DATE: 12-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 88036228
FILING DATE: 12-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8804464
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-325
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-407-620A-32

Query Match 51.2%; Score 41; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YYCYCFWK 9
Db 86 YYCQHFWS 94

RESULT 49
US-09-726-219A-266
Sequence 266, Application US/09726219A
Patent No. 6806079
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clarkson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory

APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 266
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: light chain of D1.3
US-09-726-219A-266

Query Match 51.2%; Score 41; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YYCYCFWKT 9

Db 86 YYCQHFWS 94

RESULT 50

US-09-232-290-6
Sequence 6, Application US/09232290A
Patent No. 6815540
GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: NIEBA, LARS
APPLICANT: HONEGGER, ANNEMARIE
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
FILE REFERENCE: MORPHO/7
CURRENT APPLICATION NUMBER: US/09/232,290A
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/EP96/02230
EARLIER FILING DATE: 1996-05-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 108
TYPE: PRT
ORGANISM: Murine
US-09-232-290-6

Query Match 51.2%; Score 41; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YYCYCFWKT 9

Db 86 YYCQHFWS 94

Search completed: May 9, 2006, 12:09:08
Job time : 22.6667 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:10:26 ; Search time 99.3333 Seconds
(without alignments)
46.270 Million cell updates/sec

Title: US-10-796-158-7
Perfect score: 80
Sequence: 1 YYCVFWKTCT 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	62.5	78.1	11	5	US-10-796-158-5
3	62	77.5	11	5	US-10-796-158-6
4	57	71.2	15	5	US-10-490-326-25
5	57	71.2	15	5	US-10-490-326-27
6	57	71.2	20	5	US-10-490-326-37
7	57	71.2	20	5	US-10-490-326-38
8	57	71.2	20	5	US-10-490-326-45
9	57	71.2	22	5	US-10-490-326-22
10	57	71.2	25	5	US-10-490-326-43
11	57	71.2	25	5	US-10-490-326-46
12	57	71.2	30	5	US-10-490-326-44
13	53	66.2	8	3	US-09-781-980-5
14	53	66.2	8	5	US-10-818-246-1
15	53	66.2	8	5	US-10-473-721A-15
16	53	66.2	8	5	US-10-473-721A-16
17	53	66.2	8	5	US-10-916-522A-4
18	53	66.2	8	5	US-10-505-239-12
19	53	66.2	9	6	US-11-006-071-7
20	53	66.2	67	4	US-10-425-115-289592
21	52	65.0	53	4	US-10-424-599-264998
22	52	65.0	107	4	US-10-425-115-213258
23	51	63.7	12	5	US-10-490-326-24
24	51	63.7	14	4	US-10-258-766A-1
25	51	63.7	14	4	US-10-258-766A-6
26	51	63.7	14	4	US-10-258-766A-7
27	51	63.7	14	4	US-10-258-766A-8

28	51	63.7	14	4	US-10-258-766A-13	Sequence 13, Appl
29	51	63.7	14	4	US-10-258-766A-14	Sequence 14, Appl
30	50	62.5	7	5	US-10-490-326-34	Sequence 34, Appl
31	50	62.5	7	5	US-10-796-158-4	Sequence 4, Appl
32	50	62.5	8	3	US-09-781-980-6	Sequence 6, Appl
33	50	62.5	9	4	US-10-427-160A-22	Sequence 22, Appl
34	50	62.5	9	4	US-10-444-853A-515	Sequence 515, App
35	50	62.5	9	5	US-10-780-447-22	Sequence 22, Appl
36	50	62.5	9	5	US-10-757-803-515	Sequence 515, App
37	50	62.5	9	5	US-10-826-966-515	Sequence 515, App
38	50	62.5	12	5	US-10-490-326-30	Sequence 30, Appl
39	50	62.5	12	5	US-10-490-326-31	Sequence 31, Appl
40	50	62.5	12	5	US-10-490-326-32	Sequence 32, Appl
41	50	62.5	12	5	US-10-490-326-41	Sequence 41, Appl
42	50	62.5	15	5	US-10-490-326-21	Sequence 21, Appl
43	50	62.5	15	5	US-10-490-326-23	Sequence 23, Appl
44	50	62.5	15	5	US-10-490-326-35	Sequence 35, Appl
45	50	62.5	15	5	US-10-490-326-36	Sequence 36, Appl
46	50	62.5	15	5	US-10-490-326-42	Sequence 42, Appl
47	50	62.5	15	5	US-10-490-326-47	Sequence 47, Appl
48	50	62.5	15	5	US-10-490-326-48	Sequence 48, Appl
49	50	62.5	15	5	US-10-490-326-49	Sequence 49, Appl
50	50	62.5	15	5	US-10-490-326-51	Sequence 51, Appl
51	50	62.5	15	5	US-10-490-326-52	Sequence 52, Appl
52	50	62.5	15	5	US-10-490-326-53	Sequence 53, Appl
53	50	62.5	15	5	US-10-490-326-55	Sequence 55, Appl
54	50	62.5	16	5	US-10-490-326-50	Sequence 50, Appl
55	50	62.5	16	5	US-10-490-326-54	Sequence 54, Appl
56	50	62.5	18	5	US-10-490-326-56	Sequence 56, Appl
57	50	62.5	19	5	US-10-490-326-26	Sequence 26, Appl
58	50	62.5	19	5	US-10-490-326-58	Sequence 58, Appl
59	50	62.5	20	5	US-10-490-326-40	Sequence 40, Appl
60	50	62.5	21	5	US-10-490-326-29	Sequence 29, Appl
61	50	62.5	21	5	US-10-490-326-39	Sequence 39, Appl
62	50	62.5	22	5	US-10-490-326-57	Sequence 57, Appl
63	49	61.3	21	4	US-10-558-053A-234	Sequence 234, App
64	49	61.3	21	4	US-10-838-226-234	Sequence 234, App
65	49	61.3	40	4	US-10-558-053A-231	Sequence 231, App
66	49	61.3	40	4	US-10-838-226-231	Sequence 231, App
67	49	61.3	93	4	US-10-558-053A-116	Sequence 116, App
68	49	61.3	93	4	US-10-838-226-116	Sequence 116, App
69	48	60.0	7	5	US-10-775-180-845	Sequence 845, App
70	48	60.0	9	3	US-09-758-128-2	Sequence 2, Appl
71	48	60.0	9	3	US-09-758-426-2	Sequence 2, Appl
72	48	60.0	9	3	US-09-758-198-2	Sequence 2, Appl
73	48	60.0	9	3	US-09-861-661-2	Sequence 2, Appl
74	47.5	59.4	131	4	US-10-479-670-102	Sequence 102, App
75	47.5	59.4	260	4	US-10-479-670-186	Sequence 186, App
76	47	58.8	7	4	US-10-258-766A-5	Sequence 5, Appl
77	47	58.8	7	4	US-10-258-766A-10	Sequence 10, Appl
78	47	58.8	7	4	US-10-258-766A-12	Sequence 12, Appl
79	47	58.8	76	4	US-10-424-599-183122	Sequence 183122, Sequence 130591
80	47	58.8	163	4	US-10-437-963-130591	Sequence 3, Appl
81	46	57.5	8	3	US-09-758-128-3	Sequence 3, Appl
82	46	57.5	8	3	US-09-758-426-3	Sequence 3, Appl
83	46	57.5	8	3	US-09-758-198-3	Sequence 3, Appl
84	46	57.5	8	3	US-09-861-661-3	Sequence 3, Appl
85	46	57.5	45	4	US-10-058-053A-280	Sequence 280, App
86	46	57.5	45	4	US-10-838-226-280	Sequence 280, App
87	46	57.5	95	4	US-10-558-053A-89	Sequence 89, Appl
88	46	57.5	95	4	US-10-838-226-89	Sequence 89, Appl
89	46	57.5	267	4	US-10-425-115-297609	Sequence 297609, Sequence 45732, A
90	46	57.5	504	4	US-10-425-114-45732	Sequence 45732, A
91	46	57.5	547	4	US-10-425-114-50459	Sequence 50459, A
92	46	57.5	618	4	US-10-425-115-212199	Sequence 212199, Sequence 7541, Ap
93	46	57.5	618	5	US-10-739-930-7541	Sequence 192333, Sequence 192333, A
94	46	57.5	790	4	US-10-424-599-192333	Sequence 70109, A
95	46	57.5	795	4	US-10-425-114-70109	Sequence 192340, Sequence 9053, Ap
96	46	57.5	886	4	US-10-424-599-192340	Sequence 192334, Sequence 192334, A
97	46	57.5	886	5	US-10-739-930-9053	Sequence 192334, Sequence 192338, A
98	46	57.5	889	4	US-10-424-599-192334	Sequence 192338, A
99	46	57.5	889	4	US-10-437-963-194679	Sequence 194679, Sequence 192338, A
100	46	57.5	890	4	US-10-424-599-192338	Sequence 192338, A

101	46	57.5	904	4	US-10-425-114-53515	Sequence 53515, A	174	42	52.5	424	4	US-10-245-771-12	Sequence 12, Appl
102	46	57.5	910	4	US-10-425-115-212202	Sequence 212202, A	175	42	52.5	424	4	US-10-245-851-12	Sequence 12, Appl
103	46	57.5	955	5	US-10-450-763-33078	Sequence 33078, A	176	42	52.5	424	4	US-10-245-883-12	Sequence 12, Appl
104	45	56.2	6	5	US-10-916-522A-2	Sequence 2, Appl	177	42	52.5	424	4	US-10-237-535-12	Sequence 12, Appl
105	45	56.2	6	5	US-10-490-326-33	Sequence 3, Appl	178	42	52.5	424	4	US-10-238-183-12	Sequence 12, Appl
106	45	56.2	7	3	US-09-758-128-1	Sequence 1, Appl	179	42	52.5	424	4	US-10-238-283-12	Sequence 12, Appl
107	45	56.2	7	3	US-09-758-426-1	Sequence 1, Appl	180	42	52.5	424	4	US-10-238-370-12	Sequence 12, Appl
108	45	56.2	7	3	US-09-758-198-1	Sequence 1, Appl	181	42	52.5	424	4	US-10-245-055-12	Sequence 12, Appl
109	45	56.2	7	3	US-09-861-661-1	Sequence 1, Appl	182	42	52.5	424	4	US-10-245-147-12	Sequence 12, Appl
110	45	56.2	8	5	US-10-399-542-5	Sequence 5, Appl	183	42	52.5	424	4	US-10-245-730-12	Sequence 12, Appl
111	44.5	55.6	123	3	US-09-864-761-45509	Sequence 45509, A	184	42	52.5	424	4	US-10-245-739-12	Sequence 12, Appl
112	44	55.0	10	4	US-10-058-053A-322	Sequence 322, App	185	42	52.5	424	4	US-10-246-210-12	Sequence 12, Appl
113	44	55.0	10	4	US-10-838-226-322	Sequence 322, App	186	42	52.5	424	4	US-10-239-196-12	Sequence 12, Appl
114	44	55.0	21	4	US-10-058-053A-232	Sequence 232, App	187	42	52.5	424	4	US-10-243-024-12	Sequence 12, Appl
115	44	55.0	21	4	US-10-058-053A-233	Sequence 233, App	188	42	52.5	424	4	US-10-243-409-12	Sequence 12, Appl
116	44	55.0	21	4	US-10-838-226-232	Sequence 232, App	189	42	52.5	424	4	US-10-245-621-12	Sequence 12, Appl
117	44	55.0	21	4	US-10-838-226-233	Sequence 233, App	190	42	52.5	424	4	US-10-245-880-12	Sequence 12, Appl
118	44	55.0	40	4	US-10-058-053A-229	Sequence 229, App	191	42	52.5	424	4	US-10-245-033-12	Sequence 12, Appl
119	44	55.0	40	4	US-10-058-053A-230	Sequence 230, App	192	42	52.5	424	4	US-10-243-095-12	Sequence 12, Appl
120	44	55.0	40	4	US-10-838-226-229	Sequence 229, App	193	42	52.5	424	4	US-10-245-185-12	Sequence 12, Appl
121	44	55.0	40	4	US-10-838-226-230	Sequence 230, App	194	42	52.5	424	4	US-10-245-427-12	Sequence 12, Appl
122	44	55.0	74	4	US-10-424-599-231276	Sequence 231276, A	195	42	52.5	424	4	US-10-245-473-12	Sequence 12, Appl
123	44	55.0	93	4	US-10-058-053A-32	Sequence 32, Appl	196	42	52.5	424	4	US-10-245-770-12	Sequence 12, Appl
124	44	55.0	93	4	US-10-058-053A-41	Sequence 41, Appl	197	42	52.5	424	4	US-10-245-877-12	Sequence 12, Appl
125	44	55.0	93	4	US-10-838-226-32	Sequence 32, Appl	198	42	52.5	424	4	US-10-246-976-12	Sequence 12, Appl
126	44	55.0	93	4	US-10-838-226-41	Sequence 41, Appl	199	42	52.5	424	4	US-10-243-320-12	Sequence 12, Appl
127	44	55.0	113	3	US-09-764-891-4827	Sequence 4827, Ap	200	42	52.5	424	4	US-10-242-743-12	Sequence 12, Appl
128	44	55.0	113	4	US-10-091-572-376	Sequence 376, App	201	42	52.5	424	4	US-10-242-845-12	Sequence 12, Appl
129	44	55.0	214	4	US-10-017-161-1946	Sequence 1946, Ap	202	42	52.5	424	4	US-10-237-636-12	Sequence 12, Appl
130	44	55.0	214	4	US-10-292-798-1594	Sequence 1594, Ap	203	42	52.5	424	4	US-10-238-325-12	Sequence 12, Appl
131	44	55.0	338	4	US-10-289-762-642	Sequence 642, App	204	42	52.5	424	4	US-10-238-346-12	Sequence 12, Appl
132	44	55.0	871	4	US-10-437-963-103471	Sequence 103471, A	205	42	52.5	424	4	US-10-238-411-12	Sequence 12, Appl
133	44	55.0	2309	4	US-10-437-963-188616	Sequence 188616, A	206	42	52.5	424	4	US-10-243-124-12	Sequence 12, Appl
134	43	53.8	8	3	US-09-852-870A-2	Sequence 2, Appl	207	42	52.5	424	4	US-10-243-425-12	Sequence 12, Appl
135	43	53.8	44	4	US-10-424-599-244658	Sequence 244658, A	208	42	52.5	424	4	US-10-243-446-12	Sequence 12, Appl
136	43	53.8	52	4	US-10-243-552-985	Sequence 985, App	209	42	52.5	424	4	US-10-245-874-12	Sequence 12, Appl
137	43	53.8	52	5	US-10-450-763-47452	Sequence 47452, A	210	42	52.5	424	4	US-10-242-653-12	Sequence 12, Appl
138	43	53.8	125	4	US-10-108-260A-4824	Sequence 4824, Ap	211	42	52.5	424	4	US-10-243-167-12	Sequence 12, Appl
139	43	53.8	129	4	US-10-478-670-83	Sequence 83, Appl	212	42	52.5	424	4	US-10-243-388-12	Sequence 12, Appl
140	43	53.8	167	4	US-10-425-115-346350	Sequence 346350, A	213	42	52.5	424	4	US-10-244-947-12	Sequence 12, Appl
141	43	53.8	183	4	US-10-425-115-286012	Sequence 286012, A	214	42	52.5	424	4	US-10-244-968-12	Sequence 12, Appl
142	43	53.8	252	4	US-10-478-670-167	Sequence 167, App	215	42	52.5	424	4	US-10-244-990-12	Sequence 12, Appl
143	43	53.8	257	4	US-10-424-599-217777	Sequence 217777, A	216	42	52.5	424	4	US-10-245-079-12	Sequence 12, Appl
144	43	53.8	262	4	US-10-424-599-211637	Sequence 211637, A	217	42	52.5	424	4	US-10-245-127-12	Sequence 12, Appl
145	43	53.8	264	4	US-10-424-599-228488	Sequence 228488, A	218	42	52.5	424	4	US-10-245-207-12	Sequence 12, Appl
146	43	53.8	582	4	US-10-425-114-51697	Sequence 51697, A	219	42	52.5	424	4	US-10-245-646-12	Sequence 12, Appl
147	43	53.8	594	4	US-10-408-765A-2143	Sequence 2143, Ap	220	42	52.5	424	4	US-10-245-695-12	Sequence 12, Appl
148	43	53.8	678	4	US-10-424-599-260138	Sequence 260138, A	221	42	52.5	424	4	US-10-245-699-12	Sequence 12, Appl
149	42	52.5	7	6	US-11-066-697-640	Sequence 640, App	222	42	52.5	424	4	US-10-245-737-12	Sequence 12, Appl
150	42	52.5	8	5	US-10-399-542-9	Sequence 9, Appl	223	42	52.5	424	4	US-10-245-890-12	Sequence 12, Appl
151	42	52.5	55	4	US-10-425-115-242449	Sequence 242449, A	224	42	52.5	424	4	US-10-245-899-12	Sequence 12, Appl
152	42	52.5	72	3	US-09-864-761-41063	Sequence 41063, A	225	42	52.5	424	4	US-10-245-900-12	Sequence 12, Appl
153	42	52.5	81	4	US-10-424-599-230474	Sequence 230474, A	226	42	52.5	424	4	US-10-247-058-12	Sequence 12, Appl
154	42	52.5	91	4	US-10-425-115-307301	Sequence 307301, A	227	42	52.5	424	4	US-10-242-172-12	Sequence 12, Appl
155	42	52.5	108	4	US-10-437-963-197619	Sequence 197619, A	228	42	52.5	424	4	US-10-245-454-12	Sequence 12, Appl
156	42	52.5	109	3	US-09-905-243-67	Sequence 67, Appl	229	42	52.5	424	4	US-10-237-471-12	Sequence 12, Appl
157	42	52.5	109	6	US-11-099-331-67	Sequence 67, Appl	230	42	52.5	424	4	US-10-238-461-12	Sequence 12, Appl
158	42	52.5	144	4	US-10-425-115-270016	Sequence 270016, A	231	42	52.5	424	4	US-10-238-324-12	Sequence 12, Appl
159	42	52.5	154	4	US-10-424-599-283806	Sequence 283806, A	232	42	52.5	424	4	US-10-241-860-12	Sequence 12, Appl
160	42	52.5	162	4	US-10-425-114-41793	Sequence 41793, A	233	42	52.5	424	4	US-10-242-172-12	Sequence 12, Appl
161	42	52.5	226	4	US-10-767-701-36844	Sequence 36844, A	234	42	52.5	424	4	US-10-242-652-12	Sequence 12, Appl
162	42	52.5	281	6	US-11-097-143-21315	Sequence 21315, A	235	42	52.5	424	4	US-10-242-990-12	Sequence 12, Appl
163	42	52.5	315	5	US-10-719-993-590	Sequence 593, App	236	42	52.5	424	4	US-10-243-023-12	Sequence 12, Appl
164	42	52.5	315	5	US-10-719-993-593	Sequence 593, App	237	42	52.5	424	4	US-10-243-103-12	Sequence 12, Appl
165	42	52.5	329	4	US-10-425-115-359424	Sequence 359424, A	238	42	52.5	424	4	US-10-243-326-12	Sequence 12, Appl
166	42	52.5	387	4	US-10-425-114-37316	Sequence 37316, A	239	42	52.5	424	4	US-10-243-364-12	Sequence 12, Appl
167	42	52.5	421	5	US-10-719-993-591	Sequence 591, App	240	42	52.5	424	4	US-10-243-494-12	Sequence 12, Appl
168	42	52.5	421	5	US-10-719-993-592	Sequence 592, App	241	42	52.5	424	4	US-10-243-495-12	Sequence 12, Appl
169	42	52.5	424	4	US-10-245-752-12	Sequence 12, Appl	242	42	52.5	424	4	US-10-245-253-12	Sequence 12, Appl
170	42	52.5	424	4	US-10-245-859-12	Sequence 12, Appl	243	42	52.5	424	4	US-10-245-479-12	Sequence 12, Appl
171	42	52.5	424	4	US-10-245-103-12	Sequence 12, Appl	244	42	52.5	424	4	US-10-245-499-12	Sequence 12, Appl
172	42	52.5	424	4	US-10-245-107-12	Sequence 12, Appl	245	42	52.5	424	4		
173	42	52.5	424	4	US-10-245-143-12	Sequence 12, Appl	246	42	52.5	424	4		

247	42	52.5	424	4	US-10-245-772-12	Sequence 12, Appl	320	41	51.2	236	5	US-10-877-467A-10	Sequence 10, Appl
248	42	52.5	424	4	US-10-245-811-12	Sequence 12, Appl	321	41	51.2	236	5	US-10-877-467A-12	Sequence 12, Appl
249	42	52.5	424	4	US-10-245-812-12	Sequence 12, Appl	322	41	51.2	236	5	US-10-194-975-109	Sequence 109, App
250	42	52.5	424	4	US-10-245-852-12	Sequence 12, Appl	323	41	51.2	239	4	US-10-169-351-50	Sequence 50, Appl
251	42	52.5	424	4	US-10-245-875-12	Sequence 12, Appl	324	41	51.2	241	4	US-10-353-721-13	Sequence 13, Appl
252	42	52.5	424	4	US-10-245-881-12	Sequence 12, Appl	325	41	51.2	272	4	US-10-803-622-183	Sequence 183, App
253	42	52.5	424	4	US-10-245-911-12	Sequence 12, Appl	326	41	51.2	272	4	US-10-803-653-183	Sequence 183, App
254	42	52.5	424	4	US-10-245-913-12	Sequence 12, Appl	327	41	51.2	273	5	US-10-496-059-6	Sequence 6, Appl
255	42	52.5	424	4	US-10-246-080-12	Sequence 12, Appl	328	41	51.2	507	4	US-10-239-656-47	Sequence 47, Appl
256	42	52.5	424	4	US-10-246-121-12	Sequence 12, Appl	329	41	51.2	711	4	US-10-437-963-168408	Sequence 168408,
257	42	52.5	424	4	US-10-246-305-12	Sequence 12, Appl	330	41	51.2	916	4	US-10-437-963-200075	Sequence 200075,
258	42	52.5	424	4	US-10-246-929-12	Sequence 12, Appl	331	41	51.2	1428	4	US-10-369-493-2492	Sequence 2492, Ap
259	42	52.5	424	4	US-10-247-036-12	Sequence 12, Appl	332	40.5	50.6	56	4	US-10-029-386-30941	Sequence 30941, A
260	42	52.5	424	4	US-10-243-255-12	Sequence 12, Appl	333	40.5	50.6	507	4	US-10-425-115-227745	Sequence 227745, A
261	42	52.5	424	4	US-10-245-810-12	Sequence 12, Appl	334	40.5	50.6	521	4	US-10-425-115-64172	Sequence 64172, A
262	42	52.5	424	4	US-10-245-910-12	Sequence 12, Appl	335	40	50.0	8	6	US-11-066-697-197	Sequence 197, App
263	42	52.5	424	4	US-10-246-098-12	Sequence 12, Appl	336	40	50.0	18	6	US-11-066-697-198	Sequence 198, App
264	42	52.5	424	4	US-10-217-496-12	Sequence 12, Appl	337	40	50.0	9	4	US-10-036-869-13	Sequence 13, Appl
265	42	52.5	424	4	US-10-242-074-12	Sequence 12, Appl	338	40	50.0	10	3	US-09-852-870A-3	Sequence 3, Appl
266	42	52.5	424	4	US-10-242-505-12	Sequence 12, Appl	339	40	50.0	10	3	US-09-852-870A-4	Sequence 4, Appl
267	42	52.5	424	4	US-10-242-574-12	Sequence 12, Appl	340	40	50.0	15	5	US-10-920-244A-57	Sequence 57, Appl
268	42	52.5	424	4	US-10-243-261-12	Sequence 12, Appl	341	40	50.0	15	5	US-10-920-244A-289	Sequence 289, App
269	42	52.5	424	4	US-10-243-282-12	Sequence 12, Appl	342	40	50.0	30	4	US-10-050-704-243	Sequence 243, App
270	42	52.5	424	4	US-10-243-402-12	Sequence 12, Appl	343	40	50.0	30	4	US-10-058-053A-285	Sequence 285, App
271	42	52.5	424	4	US-10-243-431-12	Sequence 12, Appl	344	40	50.0	30	4	US-10-058-053A-286	Sequence 286, App
272	42	52.5	424	4	US-10-245-164-12	Sequence 12, Appl	345	40	50.0	30	4	US-10-798-512-243	Sequence 243, App
273	42	52.5	424	4	US-10-244-972-12	Sequence 12, Appl	346	40	50.0	30	4	US-10-838-226-285	Sequence 285, App
274	42	52.5	424	4	US-10-197-942-12	Sequence 12, Appl	347	40	50.0	30	4	US-10-838-226-286	Sequence 286, App
275	42	52.5	424	4	US-10-238-196-12	Sequence 12, Appl	348	40	50.0	30	5	US-10-456-375-28	Sequence 28, Appl
276	42	52.5	424	4	US-10-245-013-12	Sequence 12, Appl	349	40	50.0	30	5	US-10-456-375-29	Sequence 29, Appl
277	42	52.5	424	5	US-10-719-993-594	Sequence 12, Appl	350	40	50.0	33	4	US-10-300-083-3	Sequence 3, Appl
278	42	52.5	510	4	US-10-264-049-3084	Sequence 3084, App	351	40	50.0	61	4	US-10-425-115-317505	Sequence 317505,
279	42	52.5	510	4	US-10-424-599-283794	Sequence 283794, App	352	40	50.0	81	4	US-10-058-053A-92	Sequence 92, Appl
280	42	52.5	941	5	US-10-739-930-6979	Sequence 6979, App	353	40	50.0	81	4	US-10-058-053A-95	Sequence 95, Appl
281	41.5	51.9	34	4	US-10-036-869-15	Sequence 15, Appl	354	40	50.0	81	4	US-10-424-599-247026	Sequence 247026,
282	41	51.2	9	4	US-10-058-053A-316	Sequence 316, App	355	40	50.0	81	4	US-10-838-226-92	Sequence 92, Appl
283	41	51.2	9	4	US-10-838-226-316	Sequence 316, App	356	40	50.0	81	4	US-10-838-226-95	Sequence 95, Appl
284	41	51.2	11	4	US-10-058-053A-313	Sequence 313, App	357	40	50.0	88	4	US-10-425-115-353522	Sequence 353522,
285	41	51.2	11	4	US-10-838-226-313	Sequence 313, App	358	40	50.0	97	4	US-10-050-704-241	Sequence 241, App
286	41	51.2	15	4	US-10-058-053A-311	Sequence 311, App	359	40	50.0	97	4	US-10-798-512-241	Sequence 241, App
287	41	51.2	15	4	US-10-838-226-311	Sequence 311, App	360	40	50.0	103	4	US-10-437-963-189718	Sequence 193718,
288	41	51.2	33	3	US-09-986-206A-18	Sequence 18, Appl	361	40	50.0	105	4	US-10-425-115-214933	Sequence 214933,
289	41	51.2	33	5	US-10-965-616-18	Sequence 18, Appl	362	40	50.0	135	4	US-10-425-115-249974	Sequence 249974,
290	41	51.2	42	4	US-10-424-599-211279	Sequence 211279, App	363	40	50.0	239	4	US-10-437-963-192792	Sequence 192792,
291	41	51.2	55	4	US-10-424-599-269897	Sequence 269897, App	364	40	50.0	249	3	US-09-730-374-3	Sequence 3, Appl
292	41	51.2	60	4	US-10-424-599-162732	Sequence 162732, App	365	40	50.0	249	3	US-10-704-206-3	Sequence 206-3, Appl
293	41	51.2	80	4	US-10-424-599-205263	Sequence 205263, App	366	40	50.0	289	3	US-09-925-297-709	Sequence 709, App
294	41	51.2	107	4	US-10-239-656-8	Sequence 8, Appl	367	40	50.0	324	4	US-10-017-161-2414	Sequence 2414, Ap
295	41	51.2	108	4	US-10-194-975-34	Sequence 94, Appl	368	40	50.0	324	4	US-10-292-798-2054	Sequence 2054, Ap
296	41	51.2	108	4	US-10-096-246-17	Sequence 17, Appl	369	40	50.0	365	4	US-10-437-963-128809	Sequence 128809,
297	41	51.2	108	4	US-10-169-351-34	Sequence 34, Appl	370	40	50.0	430	3	US-09-734-569-174	Sequence 174, App
298	41	51.2	108	4	US-10-169-351-110	Sequence 110, App	371	40	50.0	533	5	US-10-128-558-174	Sequence 174, App
299	41	51.2	108	4	US-10-169-351-111	Sequence 111, App	372	40	50.0	790	4	US-10-437-963-180919	Sequence 180919,
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301	41	51.2	108	4	US-10-169-351-113	Sequence 113, App	374	40	50.0	859	4	US-10-148-907A-31	Sequence 31, Appl
302	41	51.2	108	4	US-10-351-748-57	Sequence 57, Appl	375	40	50.0	1456	4	US-10-437-963-180908	Sequence 180908,
303	41	51.2	108	4	US-10-803-653-266	Sequence 266, App	376	40	50.0	1546	4	US-10-437-963-180921	Sequence 180921,
304	41	51.2	108	4	US-10-803-653-266	Sequence 266, App	377	40	50.0	1546	4	US-10-437-963-180921	Sequence 180921,
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307	41	51.2	126	4	US-10-428-662-17	Sequence 17, Appl	380	39.5	49.4	182	5	US-10-450-763-50118	Sequence 50118, A
308	41	51.2	127	4	US-10-452-646-8	Sequence 8, Appl	381	39.5	49.4	383	5	US-10-719-993-730	Sequence 730, App
309	41	51.2	127	4	US-10-351-748-59	Sequence 59, Appl	382	39.5	49.4	489	5	US-10-719-993-732	Sequence 732, App
310	41	51.2	127	4	US-10-351-748-59	Sequence 59, Appl	383	39	48.8	8	3	US-09-852-870A-5	Sequence 5, Appl
311	41	51.2	129	4	US-10-767-701-37591	Sequence 37591, A	384	39	48.8	39	5	US-10-808-187-784	Sequence 784, App
312	41	51.2	140	4	US-10-437-963-139398	Sequence 139398, A	385	39	48.8	39	5	US-10-807-807-784	Sequence 784, App
313	41	51.2	187	4	US-10-425-115-226174	Sequence 226174, A	386	39	48.8	40	3	US-09-864-761-43830	Sequence 43830, A
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315	41	51.2	234	3	US-09-770-916-4	Sequence 4, Appl	388	39	48.8	55	4	US-10-425-115-312893	Sequence 312893,
316	41	51.2	234	5	US-10-496-059-4	Sequence 4, Appl	389	39	48.8	62	4	US-10-029-386-34270	Sequence 34270, A
317	41	51.2	236	4	US-10-803-622-188	Sequence 188, App	390	39	48.8	69	5	US-10-380-437-60	Sequence 60, Appl
318	41	51.2	236	4	US-10-803-653-188	Sequence 188, App	391	39	48.8	82	4	US-10-424-599-144166	Sequence 144166,
319	41	51.2	236	5	US-10-877-467A-8	Sequence 8, Appl	392	39	48.8	89	4	US-10-424-599-279499	Sequence 279499,

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394	39	48.8	99	4	US-10-425-115-301477	Sequence 301477,	467	38	47.5	20	4	US-10-344-381A-26	Sequence 26, Appl
395	39	48.8	101	4	US-10-425-115-314289	Sequence 314289,	468	38	47.5	20	4	US-10-344-381A-28	Sequence 28, Appl
396	39	48.8	110	4	US-10-096-246-14	Sequence 14, Appl	469	38	47.5	22	4	US-10-058-053A-266	Sequence 266, App
397	39	48.8	111	4	US-10-425-115-311820	Sequence 311820,	470	38	47.5	22	4	US-10-838-226-266	Sequence 266, App
398	39	48.8	118	4	US-10-437-963-186191	Sequence 186191,	471	38	47.5	23	3	US-09-864-761-40321	Sequence 40321, A
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401	39	48.8	136	4	US-10-767-701-61437	Sequence 61437, A	474	38	47.5	24	4	US-10-344-381A-29	Sequence 29, Appl
402	39	48.8	137	4	US-10-425-115-296054	Sequence 296054,	475	38	47.5	27	4	US-10-121-282-33	Sequence 33, Appl
403	39	48.8	145	4	US-10-424-599-173251	Sequence 173251,	476	38	47.5	28	4	US-10-121-282-31	Sequence 31, Appl
404	39	48.8	150	5	US-10-450-763-40365	Sequence 40365, A	477	38	47.5	29	4	US-10-121-282-18	Sequence 18, Appl
405	39	48.8	160	5	US-10-485-555-42	Sequence 42, Appl	478	38	47.5	29	4	US-10-121-282-21	Sequence 21, Appl
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409	39	48.8	271	3	US-09-226-157-4	Sequence 4, Appl	482	38	47.5	29	4	US-10-121-282-26	Sequence 26, Appl
410	39	48.8	315	4	US-10-767-701-462236	Sequence 462236, A	483	38	47.5	29	4	US-10-121-282-27	Sequence 27, Appl
411	39	48.8	315	4	US-10-425-115-377876	Sequence 277876, A	484	38	47.5	29	4	US-10-121-282-30	Sequence 30, Appl
412	39	48.8	316	4	US-10-425-114-48225	Sequence 48225, A	485	38	47.5	29	4	US-10-121-282-32	Sequence 32, Appl
413	39	48.8	318	4	US-10-437-963-181822	Sequence 181822,	486	38	47.5	29	4	US-10-121-282-37	Sequence 37, Appl
414	39	48.8	331	4	US-10-335-977-6603	Sequence 6603, Ap	487	38	47.5	32	4	US-10-121-282-40	Sequence 40, Appl
415	39	48.8	352	5	US-10-732-923-15092	Sequence 15092, A	488	38	47.5	39	4	US-10-424-599-232517	Sequence 232517,
416	39	48.8	383	4	US-10-425-114-63893	Sequence 63893, A	489	38	47.5	46	4	US-10-012-600B-157	Sequence 157, App
417	39	48.8	411	3	US-08-815-242-5746	Sequence 5746, Ap	490	38	47.5	47	4	US-10-424-599-144824	Sequence 144824,
418	39	48.8	464	4	US-10-282-122A-64999	Sequence 64999, A	491	38	47.5	58	3	US-09-739-254-98	Sequence 98, Appl
419	39	48.8	464	4	US-10-282-122A-65664	Sequence 65664, A	492	38	47.5	58	3	US-09-904-615-98	Sequence 98, Appl
420	39	48.8	476	4	US-10-369-433-9638	Sequence 9638, Ap	493	38	47.5	58	4	US-10-054-988-98	Sequence 98, Appl
421	39	48.8	485	5	US-10-380-437-12	Sequence 12, Appl	494	38	47.5	63	4	US-10-425-115-283642	Sequence 283642,
422	39	48.8	485	6	US-11-041-553-6	Sequence 6, Appl	495	38	47.5	65	4	US-10-767-701-62741	Sequence 62741, A
423	39	48.8	490	4	US-10-282-122A-47109	Sequence 47109, A	496	38	47.5	69	4	US-10-424-599-238855	Sequence 238855,
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425	39	48.8	604	6	US-11-097-143-36975	Sequence 36975, A	498	38	47.5	72	4	US-10-058-053A-137	Sequence 137, App
426	39	48.8	613	5	US-10-485-555-5201	Sequence 5201, Ap	499	38	47.5	72	4	US-10-838-226-137	Sequence 137, App
427	39	48.8	671	5	US-10-732-923-15091	Sequence 15091, A	500	38	47.5	78	4	US-10-425-115-302250	Sequence 302250,
428	39	48.8	671	5	US-10-732-923-15093	Sequence 15093, A	501	38	47.5	81	4	US-10-424-599-167419	Sequence 167419,
429	39	48.8	702	6	US-11-035-599-52	Sequence 52, Appl	502	38	47.5	85	4	US-10-344-381A-8	Sequence 8, Appl
430	39	48.8	702	6	US-11-035-599-53	Sequence 53, Appl	503	38	47.5	85	4	US-10-425-115-186311	Sequence 186311,
431	39	48.8	728	5	US-10-213-974-11	Sequence 11, Appl	504	38	47.5	87	4	US-10-424-599-269255	Sequence 269255,
432	39	48.8	731	6	US-11-035-599-31	Sequence 31, Appl	505	38	47.5	88	4	US-10-425-114-60907	Sequence 60907, A
433	39	48.8	733	6	US-10-732-923-14218	Sequence 14218, A	506	38	47.5	93	4	US-10-425-115-255267	Sequence 255267,
434	39	48.8	734	6	US-11-035-599-50	Sequence 50, Appl	507	38	47.5	93	4	US-10-425-115-323077	Sequence 323077,
435	39	48.8	936	4	US-10-243-552-850	Sequence 850, App	508	38	47.5	95	3	US-09-943-002-10	Sequence 10, Appl
436	39	48.8	936	5	US-10-450-763-47998	Sequence 47998, A	509	38	47.5	97	4	US-10-437-963-195940	Sequence 195940,
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440	39	48.8	1047	5	US-10-450-763-40377	Sequence 40377, A	513	38	47.5	108	4	US-10-108-260A-4714	Sequence 4714, Ap
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442	38.5	48.1	30	4	US-10-203-969A-29	Sequence 29, Appl	515	38	47.5	119	4	US-10-104-047-2041	Sequence 2041, Ap
443	38.5	48.1	58	4	US-10-424-599-222430	Sequence 222430,	516	38	47.5	121	4	US-10-344-381A-7	Sequence 7, Appl
444	38.5	48.1	85	4	US-10-437-963-165235	Sequence 165235,	517	38	47.5	122	4	US-10-344-381A-14	Sequence 14, Appl
445	38.5	48.1	85	4	US-10-425-115-322704	Sequence 322704,	518	38	47.5	123	4	US-10-344-381A-17	Sequence 17, Appl
446	38.5	48.1	125	4	US-10-083-357-715	Sequence 715, App	519	38	47.5	123	4	US-10-344-381A-23	Sequence 23, Appl
447	38	47.5	6	5	US-10-399-542-1	Sequence 1, Appl	520	38	47.5	124	3	US-09-989-722-266	Sequence 266, App
448	38	47.5	8	3	US-09-853-870A-9	Sequence 9, Appl	521	38	47.5	124	3	US-09-989-722-266	Sequence 266, App
449	38	47.5	8	5	US-10-399-542-3	Sequence 3, Appl	522	38	47.5	124	3	US-09-989-279-266	Sequence 266, App
450	38	47.5	8	5	US-10-399-542-11	Sequence 11, Appl	523	38	47.5	124	3	US-09-989-727-266	Sequence 266, App
451	38	47.5	10	4	US-10-058-053A-320	Sequence 320, App	524	38	47.5	124	3	US-09-989-731-266	Sequence 266, App
452	38	47.5	10	4	US-10-838-226-320	Sequence 320, App	525	38	47.5	124	3	US-09-989-732-266	Sequence 266, App
453	38	47.5	11	4	US-10-344-381A-10	Sequence 10, Appl	526	38	47.5	124	3	US-09-991-073-266	Sequence 266, App
454	38	47.5	12	4	US-10-360-101-98	Sequence 98, Appl	527	38	47.5	124	3	US-09-990-442-266	Sequence 266, App
455	38	47.5	12	4	US-10-344-381A-1	Sequence 1, Appl	528	38	47.5	124	3	US-09-991-163-266	Sequence 266, App
456	38	47.5	12	4	US-10-344-381A-2	Sequence 2, Appl	529	38	47.5	124	3	US-09-993-604-266	Sequence 266, App
457	38	47.5	12	4	US-10-344-381A-9	Sequence 9, Appl	530	38	47.5	124	3	US-09-990-456-266	Sequence 266, App
458	38	47.5	12	5	US-10-714-078-7	Sequence 7, Appl	531	38	47.5	124	3	US-09-989-721-266	Sequence 266, App
459	38	47.5	12	5	US-10-603-891-3	Sequence 3, Appl	532	38	47.5	124	3	US-09-992-598-266	Sequence 266, App
460	38	47.5	12	5	US-10-718-071-35	Sequence 35, Appl	533	38	47.5	124	3	US-09-989-293A-266	Sequence 266, App
461	38	47.5	12	5	US-10-952-275-3	Sequence 3, Appl	534	38	47.5	124	3	US-09-989-735-266	Sequence 266, App
462	38	47.5	12	6	US-11-066-697-99	Sequence 99, Appl	535	38	47.5	124	3	US-09-990-444-266	Sequence 266, App
463	38	47.5	13	6	US-11-066-697-100	Sequence 100, App	536	38	47.5	124	3	US-09-991-181-266	Sequence 266, App
464	38	47.5	14	4	US-10-344-381A-19	Sequence 19, Appl	537	38	47.5	124	3	US-09-989-730-266	Sequence 266, App
465	38	47.5	17	4	US-10-344-381A-18	Sequence 18, Appl	538	38	47.5	124	3	US-09-990-436-266	Sequence 266, App

539	38	47.5	124	3	US-09-993-687-266	Sequence 266, App	612	38	47.5	124	4	US-10-245-880-26	Sequence 26, App
540	38	47.5	124	3	US-09-989-734-266	Sequence 266, App	613	38	47.5	124	4	US-10-245-033-26	Sequence 26, App
541	38	47.5	124	3	US-09-997-653-266	Sequence 266, App	614	38	47.5	124	4	US-10-243-095-26	Sequence 26, App
542	38	47.5	124	3	US-09-989-724-266	Sequence 266, App	615	38	47.5	124	4	US-10-245-185-26	Sequence 26, App
543	38	47.5	124	3	US-09-989-728-266	Sequence 266, App	616	38	47.5	124	4	US-10-245-437-26	Sequence 26, App
544	38	47.5	124	3	US-09-990-441-266	Sequence 266, App	617	38	47.5	124	4	US-10-245-473-26	Sequence 26, App
545	38	47.5	124	3	US-09-993-667-266	Sequence 266, App	618	38	47.5	124	4	US-10-245-770-26	Sequence 26, App
546	38	47.5	124	3	US-09-997-428-266	Sequence 266, App	619	38	47.5	124	4	US-10-245-877-26	Sequence 26, App
547	38	47.5	124	3	US-09-997-666-266	Sequence 266, App	620	38	47.5	124	4	US-10-246-976-26	Sequence 26, App
548	38	47.5	124	3	US-09-990-438-266	Sequence 266, App	621	38	47.5	124	4	US-10-243-320-26	Sequence 26, App
549	38	47.5	124	3	US-09-990-562-266	Sequence 266, App	622	38	47.5	124	4	US-10-242-743-26	Sequence 26, App
550	38	47.5	124	3	US-09-990-711-266	Sequence 266, App	623	38	47.5	124	4	US-10-242-845-26	Sequence 26, App
551	38	47.5	124	3	US-09-989-726-266	Sequence 266, App	624	38	47.5	124	4	US-10-237-636-26	Sequence 26, App
552	38	47.5	124	3	US-09-998-156-266	Sequence 266, App	625	38	47.5	124	4	US-10-238-325-26	Sequence 26, App
553	38	47.5	124	3	US-09-990-437-266	Sequence 266, App	626	38	47.5	124	4	US-10-238-346-26	Sequence 26, App
554	38	47.5	124	3	US-09-991-157-266	Sequence 266, App	627	38	47.5	124	4	US-10-238-411-26	Sequence 26, App
555	38	47.5	124	3	US-09-997-514-266	Sequence 266, App	628	38	47.5	124	4	US-10-243-124-26	Sequence 26, App
556	38	47.5	124	3	US-09-997-573-266	Sequence 266, App	629	38	47.5	124	4	US-10-243-425-26	Sequence 26, App
557	38	47.5	124	3	US-09-991-172-266	Sequence 266, App	630	38	47.5	124	4	US-10-243-446-26	Sequence 26, App
558	38	47.5	124	3	US-09-990-726-266	Sequence 266, App	631	38	47.5	124	4	US-10-245-874-26	Sequence 26, App
559	38	47.5	124	3	US-09-997-559-266	Sequence 266, App	632	38	47.5	124	4	US-10-242-653-26	Sequence 26, App
560	38	47.5	124	3	US-09-997-601-266	Sequence 266, App	633	38	47.5	124	4	US-10-243-167-26	Sequence 26, App
561	38	47.5	124	3	US-09-990-443-266	Sequence 266, App	634	38	47.5	124	4	US-10-243-388-26	Sequence 26, App
562	38	47.5	124	3	US-09-991-854-266	Sequence 266, App	635	38	47.5	124	4	US-10-244-947-26	Sequence 26, App
563	38	47.5	124	3	US-09-997-628-266	Sequence 266, App	636	38	47.5	124	4	US-10-244-968-26	Sequence 26, App
564	38	47.5	124	3	US-09-997-683-266	Sequence 266, App	637	38	47.5	124	4	US-10-244-990-26	Sequence 26, App
565	38	47.5	124	3	US-09-989-729A-266	Sequence 266, App	638	38	47.5	124	4	US-10-245-079-26	Sequence 26, App
566	38	47.5	124	3	US-09-997-349-266	Sequence 266, App	639	38	47.5	124	4	US-10-245-137-26	Sequence 26, App
567	38	47.5	124	3	US-09-997-440-266	Sequence 266, App	640	38	47.5	124	4	US-10-245-207-26	Sequence 26, App
568	38	47.5	124	3	US-09-990-440-266	Sequence 266, App	641	38	47.5	124	4	US-10-245-646-26	Sequence 26, App
569	38	47.5	124	3	US-09-997-857-266	Sequence 266, App	642	38	47.5	124	4	US-10-245-695-26	Sequence 26, App
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571	38	47.5	124	3	US-09-997-542-266	Sequence 266, App	644	38	47.5	124	4	US-10-245-737-26	Sequence 26, App
572	38	47.5	124	3	US-09-993-748-266	Sequence 266, App	645	38	47.5	124	4	US-10-245-878-26	Sequence 26, App
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576	38	47.5	124	3	US-09-993-583-266	Sequence 266, App	649	38	47.5	124	4	US-10-247-058-26	Sequence 26, App
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578	38	47.5	124	3	US-09-992-521-266	Sequence 266, App	651	38	47.5	124	4	US-10-237-471-26	Sequence 26, App
579	38	47.5	124	3	US-09-997-333-266	Sequence 266, App	652	38	47.5	124	4	US-10-238-261-26	Sequence 26, App
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581	38	47.5	124	3	US-09-998-041-266	Sequence 266, App	654	38	47.5	124	4	US-10-241-860-26	Sequence 26, App
582	38	47.5	124	3	US-09-997-585-266	Sequence 266, App	655	38	47.5	124	4	US-10-242-172-26	Sequence 26, App
583	38	47.5	124	3	US-09-997-614-266	Sequence 266, App	656	38	47.5	124	4	US-10-242-652-26	Sequence 26, App
584	38	47.5	124	3	US-09-989-733-266	Sequence 266, App	657	38	47.5	124	4	US-10-242-990-26	Sequence 26, App
585	38	47.5	124	3	US-09-989-862-266	Sequence 266, App	658	38	47.5	124	4	US-10-243-023-26	Sequence 26, App
586	38	47.5	124	3	US-09-997-529-266	Sequence 266, App	659	38	47.5	124	4	US-10-243-103-26	Sequence 26, App
587	38	47.5	124	3	US-09-989-725-266	Sequence 266, App	660	38	47.5	124	4	US-10-243-276-26	Sequence 26, App
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589	38	47.5	124	3	US-09-997-641-266	Sequence 266, App	662	38	47.5	124	4	US-10-243-326-26	Sequence 26, App
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591	38	47.5	124	3	US-09-992-643-266	Sequence 266, App	664	38	47.5	124	4	US-10-243-494-26	Sequence 26, App
592	38	47.5	124	3	US-10-245-752-26	Sequence 26, App	665	38	47.5	124	4	US-10-244-985-26	Sequence 26, App
593	38	47.5	124	3	US-10-245-859-26	Sequence 26, App	666	38	47.5	124	4	US-10-245-230-26	Sequence 26, App
594	38	47.5	124	3	US-10-245-103-26	Sequence 26, App	667	38	47.5	124	4	US-10-245-479-26	Sequence 26, App
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597	38	47.5	124	3	US-10-245-771-26	Sequence 26, App	670	38	47.5	124	4	US-10-245-811-26	Sequence 26, App
598	38	47.5	124	3	US-10-245-851-26	Sequence 26, App	671	38	47.5	124	4	US-10-245-812-26	Sequence 26, App
599	38	47.5	124	3	US-10-245-883-26	Sequence 26, App	672	38	47.5	124	4	US-10-245-852-26	Sequence 26, App
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603	38	47.5	124	3	US-10-238-370-26	Sequence 26, App	676	38	47.5	124	4	US-10-245-911-26	Sequence 26, App
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605	38	47.5	124	3	US-10-245-147-26	Sequence 26, App	678	38	47.5	124	4	US-10-246-080-26	Sequence 26, App
606	38	47.5	124	3	US-10-245-730-26	Sequence 26, App	679	38	47.5	124	4	US-10-246-121-26	Sequence 26, App
607	38	47.5	124	3	US-10-245-739-26	Sequence 26, App	680	38	47.5	124	4	US-10-246-305-26	Sequence 26, App
608	38	47.5	124	3	US-10-246-210-26	Sequence 26, App	681	38	47.5	124	4	US-10-246-929-26	Sequence 26, App
609	38	47.5	124	3	US-10-239-196-26	Sequence 26, App	682	38	47.5	124	4	US-10-247-036-26	Sequence 26, App
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611	38	47.5	124	3	US-10-243-409-26	Sequence 26, App	684	38	47.5	124	4	US-10-243-810-26	Sequence 26, App
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833	37	46.2	67	3	US-09-796-692-1512	Sequence 1512, App	906	37	46.2	155	3	US-09-981-876-164	Sequence 164, App
834	37	46.2	67	4	US-10-040-862-686	Sequence 686, App	907	37	46.2	155	3	US-09-981-876-225	Sequence 225, App
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841	37	46.2	67	4	US-10-764-324-1512	Sequence 1512, App	914	37	46.2	163	3	US-09-764-875-720	Sequence 720, App
842	37	46.2	68	5	US-10-721-793-132	Sequence 132, App	915	37	46.2	181	4	US-10-108-260A-4852	Sequence 4852, App
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846	37	46.2	76	4	US-10-425-115-329495	Sequence 329495,	919	37	46.2	200	4	US-10-264-049-2243	Sequence 2243, App
847	37	46.2	76	4	US-09-764-891-4062	Sequence 4062, App	920	37	46.2	200	4	US-10-264-049-2243	Sequence 2243, App
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849	37	46.2	78	4	US-10-058-053A-212	Sequence 212, App	922	37	46.2	209	4	US-10-469-626-34	Sequence 34, App
850	37	46.2	78	4	US-10-838-226-38	Sequence 226, App	923	37	46.2	212	3	US-09-801-944B-203	Sequence 203, App
851	37	46.2	78	4	US-10-838-226-38	Sequence 38, App	924	37	46.2	215	4	US-10-424-599-162583	Sequence 162583,
852	37	46.2	78	5	US-10-450-763-36130	Sequence 212, App	925	37	46.2	240	3	US-09-833-245-1157	Sequence 1157, App
853	37	46.2	80	4	US-10-058-053A-98	Sequence 36130, A	926	37	46.2	240	3	US-09-833-245-1157	Sequence 1157, App
854	37	46.2	80	4	US-10-838-226-38	Sequence 98, App	927	37	46.2	240	5	US-10-469-626-26	Sequence 26, App
855	37	46.2	82	4	US-10-838-226-38	Sequence 98, App	928	37	46.2	240	5	US-10-974-148-28	Sequence 28, App
856	37	46.2	86	4	US-10-424-599-255690	Sequence 255690,	929	37	46.2	248	2	US-08-996-140-23	Sequence 23, App
857	37	46.2	86	4	US-10-425-115-365404	Sequence 265404,	930	37	46.2	273	4	US-10-424-599-244875	Sequence 244875,
858	37	46.2	87	4	US-10-002-631C-201	Sequence 201, App	931	37	46.2	306	5	US-10-739-930-5816	Sequence 5816, App
859	37	46.2	90	4	US-10-721-793-130	Sequence 130, App	932	37	46.2	342	3	US-09-886-055-207	Sequence 207, App
860	37	46.2	92	4	US-10-425-115-334852	Sequence 200577,	933	37	46.2	342	3	US-09-804-291-207	Sequence 207, App
861	37	46.2	95	4	US-10-058-053A-35	Sequence 334852,	934	37	46.2	342	5	US-10-819-316-207	Sequence 207, App
862	37	46.2	95	4	US-10-838-226-35	Sequence 35, App	935	37	46.2	342	4	US-10-289-762-933	Sequence 933, App
863	37	46.2	99	4	US-10-198-070-5	Sequence 35, App	936	37	46.2	442	4	US-10-108-260A-3049	Sequence 3049, App
864	37	46.2	106	4	US-10-138-516-4	Sequence 183064,	937	37	46.2	512	4	US-10-437-963-158406	Sequence 158406,
865	37	46.2	106	4	US-10-146-130-5	Sequence 4, Appli	938	37	46.2	515	4	US-10-139-092-1	Sequence 1, Appli
866	37	46.2	106	4	US-10-092-934-5	Sequence 6, Appli	939	37	46.2	525	4	US-10-139-092-3	Sequence 3, Appli
867	37	46.2	106	4	US-10-153-334-5	Sequence 5, Appli	940	37	46.2	540	4	US-10-139-092-9	Sequence 9, Appli
868	37	46.2	106	4	US-10-198-069-5	Sequence 5, Appli	941	37	46.2	559	4	US-10-369-493-5652	Sequence 5652, App
869	37	46.2	106	4	US-10-198-070-5	Sequence 5, Appli	942	37	46.2	593	5	US-10-450-763-34527	Sequence 34527, A
870	37	46.2	106	4	US-10-437-963-163458	Sequence 5, Appli	943	37	46.2	723	5	US-10-732-923-22819	Sequence 22819, A
871	37	46.2	106	4	US-10-437-963-163458	Sequence 163458,	944	37	46.2	760	4	US-10-139-092-8	Sequence 8, Appli
872	37	46.2	108	2	US-08-996-140-12	Sequence 237914,	945	37	46.2	809	4	US-10-437-963-137541	Sequence 137541,
873	37	46.2	114	4	US-10-424-599-234479	Sequence 12, Appli	946	37	46.2	1040	5	US-10-450-763-51071	Sequence 51071, A
874	37	46.2	114	5	US-10-915-490-19	Sequence 234479,	947	37	46.2	1076	5	US-10-450-763-51073	Sequence 51073, A
875	37	46.2	116	4	US-10-425-115-303310	Sequence 13, Appli	948	37	46.2	1100	4	US-10-139-092-7	Sequence 7, Appli
876	37	46.2	117	4	US-10-300-675-38	Sequence 303310,	949	37	46.2	1253	4	US-10-139-092-2	Sequence 2, Appli
877	37	46.2	118	3	US-09-987-655-5	Sequence 38, Appli	950	36.5	45.6	9	3	US-09-252-150-80	Sequence 80, Appli
878	37	46.2	118	3	US-09-987-655-5	Sequence 5, Appli	951	36.5	45.6	9	5	US-10-646-381-80	Sequence 80, Appli
879	37	46.2	118	4	US-10-024-298A-31	Sequence 5, Appli	952	36.5	45.6	21	4	US-10-381-112-436	Sequence 436, App
880	37	46.2	118	4	US-10-042-211A-31	Sequence 31, Appli	953	36.5	45.6	58	3	US-09-925-299-952	Sequence 952, App
881	37	46.2	118	4	US-10-617-217A-31	Sequence 31, Appli	954	36.5	45.6	58	3	US-10-106-698-5690	Sequence 5690, App
882	37	46.2	118	4	US-10-024-298A-31	Sequence 31, Appli	955	36.5	45.6	76	4	US-10-425-115-366674	Sequence 366674,
883	37	46.2	118	6	US-11-119-831-5	Sequence 5, Appli	956	36.5	45.6	91	4	US-10-425-115-224175	Sequence 224175,
884	37	46.2	121	4	US-10-425-114-69144	Sequence 69144, A	957	36.5	45.6	102	4	US-10-424-599-262798	Sequence 262798,
885	37	46.2	128	4	US-10-425-115-271287	Sequence 271287,	958	36.5	45.6	149	5	US-10-910-901-22	Sequence 22, Appli
886	37	46.2	129	4	US-10-437-963-166541	Sequence 166541,	959	36.5	45.6	214	4	US-10-425-115-291496	Sequence 291496,
887	37	46.2	131	4	US-10-425-115-189171	Sequence 189171,	960	36.5	45.6	269	5	US-10-756-149-5495	Sequence 5495, App
888	37	46.2	134	4	US-10-136-728-64	Sequence 64, Appli	961	36.5	45.6	328	3	US-09-738-626-4590	Sequence 4590, App
889	37	46.2	135	5	US-10-935-490-33	Sequence 33, Appli	962	36.5	45.6	331	4	US-10-425-115-267414	Sequence 267414,
890	37	46.2	137	3	US-09-993-999-9	Sequence 9, Appli	963	36.5	45.6	622	4	US-10-425-114-51351	Sequence 51351, A
891	37	46.2	137	3	US-09-903-190-109	Sequence 109, App	964	36.5	45.6	900	5	US-10-450-763-57406	Sequence 57406, A
892	37	46.2	137	3	US-09-978-360A-765	Sequence 765, App	965	36.5	45.6	917	4	US-10-601-807-6	Sequence 6, Appli
893	37	46.2	137	4	US-10-024-298A-29	Sequence 29, App	966	36	45.0	10	3	US-09-852-870A-6	Sequence 15, Appli
894	37	46.2	137	4	US-10-042-211A-29	Sequence 29, App	967	36	45.0	14	4	US-10-162-134A-15	Sequence 333, App
895	37	46.2	137	4	US-10-617-217A-29	Sequence 29, App	968	36	45.0	22	4	US-10-058-053A-333	Sequence 333, App
896	37	46.2	137	4	US-10-469-626-37	Sequence 37, Appli	969	36	45.0	22	4	US-10-838-226-333	Sequence 333, App
897	37	46.2	137	4	US-10-024-298A-29	Sequence 29, App	970	36	45.0	23	3	US-09-864-761-38459	Sequence 38459, A
898	37	46.2	137	5	US-10-930-331-109	Sequence 109, App	971	36	45.0	37	5	US-10-472-928-2314	Sequence 2314, App
899	37	46.2	138	3	US-09-975-456B-9	Sequence 9, Appli	972	36	45.0	40	4	US-10-058-053A-117	Sequence 117, App
900	37	46.2	138	3	US-09-917-805-2	Sequence 2, Appli	973	36	45.0	40	4	US-10-280-066-174	Sequence 174, App
901	37	46.2	138	3	US-09-917-805-7	Sequence 7, Appli	974	36	45.0	40	4	US-10-838-226-117	Sequence 117, App
902	37	46.2	139	4	US-10-425-115-337979	Sequence 337979,	975	36	45.0	44	4	US-10-264-049-3647	Sequence 3647, App
903	37	46.2	149	3	US-09-791-279-158	Sequence 158, App	976	36	45.0	48	4	US-10-424-599-164020	Sequence 164020,

977 36 45.0 51 4 US-10-424-599-169219 Sequence 169219, A
978 36 45.0 52 4 US-10-767-701-53710 Sequence 53710, A
979 36 45.0 53 4 US-10-424-599-218633 Sequence 218633,
980 36 45.0 54 3 US-09-796-692-1735 Sequence 1735, Ap
981 36 45.0 54 4 US-10-040-862-1735 Sequence 1735, Ap
982 36 45.0 54 4 US-10-057-475B-1735 Sequence 1735, Ap
983 36 45.0 54 4 US-10-154-884B-1735 Sequence 1735, Ap
984 36 45.0 54 4 US-10-764-324-1735 Sequence 1735, Ap
985 36 45.0 55 4 US-10-029-386-30169 Sequence 30169, A
986 36 45.0 57 4 US-10-425-115-327363 Sequence 327363,
987 36 45.0 57 4 US-10-425-115-346973 Sequence 346973,
988 36 45.0 57 4 US-10-425-115-346979 Sequence 346979,
989 36 45.0 58 4 US-10-424-599-255055 Sequence 255055,
990 36 45.0 58 4 US-10-425-115-373241 Sequence 273241,
991 36 45.0 61 4 US-10-424-599-176714 Sequence 176714,
992 36 45.0 62 4 US-10-424-599-212336 Sequence 212336,
993 36 45.0 62 4 US-10-767-701-57724 Sequence 57724, A
994 36 45.0 64 4 US-10-424-599-221328 Sequence 221328,
995 36 45.0 64 4 US-10-425-114-52751 Sequence 52751, A
996 36 45.0 64 5 US-10-721-793-96 Sequence 96, Appl
997 36 45.0 66 4 US-10-264-480-19 Sequence 19, Appl
998 36 45.0 66 4 US-10-264-480-20 Sequence 20, Appl
999 36 45.0 66 4 US-10-264-480-21 Sequence 21, Appl
1000 36 45.0 66 4 US-10-425-115-323394 Sequence 323394,

ALIGNMENTS

RESULT 1
US-10-796-158-7
; Sequence 7, Application US/10796158
; Publication No. US20050118099A1
; GENERAL INFORMATION:
; APPLICANT: IDEC Pharmaceuticals
; APPLICANT: Braslawsky, Gary
; APPLICANT: Chinn, Paul
; APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: THIOL-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
; FILE REFERENCE: 037003-0308678
; CURRENT APPLICATION NUMBER: US/10/796.158
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic SST analog
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: D stereoisomer
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDATION OR ALCOHOL
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDE OR ALCOHOL
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: D stereoisomer
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: D stereoisomer
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (5)..(10)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDE OR ALCOHOL

US-10-796-158-7
Query Match 100.0%; Score 80; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YYCYCFWKTC 11

Db 1 YYCYCFWKTC 11
RESULT 2
US-10-796-158-5
; Sequence 5, Application US/10796158
; Publication No. US20050118099A1
; GENERAL INFORMATION:
; APPLICANT: IDEC Pharmaceuticals
; APPLICANT: Braslawsky, Gary
; APPLICANT: Chinn, Paul
; APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: THIOL-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
; FILE REFERENCE: 037003-0308678
; CURRENT APPLICATION NUMBER: US/10/796.158
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic SST analog
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: D stereoisomer
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDATION OR ALCOHOL
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDE OR ALCOHOL
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: D stereoisomer
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: D stereoisomer
; US-10-796-158-5

Query Match 78.1%; Score 62.5; DB 5; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 YC-YCFWKTC 11
Db 1 YYCYCFWKTC 11

RESULT 3
US-10-796-158-6
; Sequence 6, Application US/10796158
; Publication No. US20050118099A1
; GENERAL INFORMATION:
; APPLICANT: IDEC Pharmaceuticals
; APPLICANT: Braslawsky, Gary
; APPLICANT: Chinn, Paul
; APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: THIOL-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
; FILE REFERENCE: 037003-0308678
; CURRENT APPLICATION NUMBER: US/10/796.158
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 11

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; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic SST analog
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: D stereoisomer
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: D stereoisomer
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (5)..(10)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDE OR ALCOHOL
US-10-796-158-6

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```

Query Match          77.5%; Score 62; DB 5; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

```

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Qy      2 YCYCFWKTCCT 11
      |||||
Db      2 YYCFWKTCCT 11

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RESULT 4
US-10-490-326-25
; Sequence 25, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-25

```

```

Query Match          71.2%; Score 57; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      4 YCFWKTCCT 11
      |||||
Db      8 YCFWKTCCT 15

```

```

RESULT 5
US-10-490-326-27
; Sequence 27, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:

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; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
US-10-490-326-27

```

```

Query Match          71.2%; Score 57; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 YCFWKTCCT 11
      |||||
Db      8 YCFWKTCCT 15

```

```

RESULT 6
US-10-490-326-37
; Sequence 37, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-37

```

```

Query Match          71.2%; Score 57; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      4 YCFWKTCCT 11
      |||||
Db      13 YCFWKTCCT 20

```

RESULT 7
 US-10-490-326-38
 ; Sequence 38, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; Bombesin Analog Conjugates and Uses Thereof
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: 14..19
 ; OTHER INFORMATION: Cys at positions 14 and 19 are circularized
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-490-326-38

Query Match 71.2%; Score 57; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
 |||||
 Db 13 YCFWKTCCT 20

RESULT 8
 US-10-490-326-45
 ; Sequence 45, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; Bombesin Analog Conjugates and Uses Thereof
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 45
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: 14..19
 ; OTHER INFORMATION: Cys at positions 14 and 19 are circularized
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-490-326-45

Query Match 71.2%; Score 57; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YCFWKTCCT 11
 |||||
 Db 13 YCFWKTCCT 20
 RESULT 9
 US-10-490-326-22
 ; Sequence 22, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; Bombesin Analog Conjugates and Uses Thereof
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 22
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: 16..21
 ; OTHER INFORMATION: Cys at positions 16 and 21 are circularized
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-490-326-22

Query Match 71.2%; Score 57; DB 5; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
 |||||
 Db 15 YCFWKTCCT 22

RESULT 10
 US-10-490-326-43
 ; Sequence 43, Application US/10490326
 ; Publication No. US20050070470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Murphy, William A.
 ; APPLICANT: Sun, Lichun
 ; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
 ; Bombesin Analog Conjugates and Uses Thereof
 ; FILE REFERENCE: 07005/005002
 ; CURRENT APPLICATION NUMBER: US/10/490,326
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US02/30143
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/323,851
 ; PRIOR FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 43
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: 14..19
 ; OTHER INFORMATION: Cys at positions 14 and 19 are circularized
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-490-326-43

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 19-24
; OTHER INFORMATION: Cys at positions 19 and 24 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-43

Query Match 71.2%; Score 57; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Qy 4 YCFWKTKT 11
Db 18 YCFWKTKT 25

RESULT 11
US-10-490-326-46
; Sequence 46, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; TITLE OF INVENTION: Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490.326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 19-24
; OTHER INFORMATION: Cys at positions 19 and 24 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-46

Query Match 71.2%; Score 57; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Qy 4 YCFWKTKT 11
Db 18 YCFWKTKT 25

RESULT 12
US-10-490-326-44
; Sequence 44, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; TITLE OF INVENTION: Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490.326
; CURRENT FILING DATE: 2004-03-19

; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 24, 29
; OTHER INFORMATION: Cys at positions 24 and 29 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-44

Query Match 71.2%; Score 57; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
Db 23 YCFWKTKT 30

RESULT 13
US-09-781-980-5
; Sequence 5, Application US/09781980
; Publication No. US20010029035A1
; GENERAL INFORMATION:
; APPLICANT: EISENHUT, MICHAEL
; APPLICANT: MIER, WALTER
; APPLICANT: ERITJA, RAMON
; APPLICANT: HABERKORN, UWE
; TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
; FILE REFERENCE: 2502498.991110
; CURRENT APPLICATION NUMBER: US/09/781,980
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: DE 100 06 572
; PRIOR FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-781-980-5

Query Match 66.2%; Score 53; DB 3; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
Db 1 FCFWKTKT 8

RESULT 14
US-10-818-246-1
; Sequence 1, Application US/10818246
; Publication No. US20040249121A1
; GENERAL INFORMATION:
; APPLICANT: Novetide, Ltd.
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF CYCLIC PEPTIDES
; FILE REFERENCE: 12647/46002
; CURRENT APPLICATION NUMBER: US/10/818,246
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: 60/461,222

; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-818-246-1

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||||
Db 1 PCFWKTCCT 8

RESULT 15
US-10-473-721A-15
; Sequence 15, Application US/10473721A
; Publication No. US2005004000A1
; GENERAL INFORMATION:
; APPLICANT: SHECHTER, Yoram
; APPLICANT: GOLDWASER, Itzhak
; APPLICANT: LAVON, Iris
; APPLICANT: BRODIE, David
; APPLICANT: EYAL, Nurit
; APPLICANT: FASS, Stanley
; APPLICANT: FRIDKIN, Matityahu
; TITLE OF INVENTION: ORAL ABSORBED DRUGS
; FILE REFERENCE: SHECTERS
; CURRENT APPLICATION NUMBER: US/10/473,721A
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/IL02/00252
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: IL 142353
; PRIOR FILING DATE: 2001-04-01
; PRIOR APPLICATION NUMBER: IL 146383
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(8)
; OTHER INFORMATION: Cyclic eight-amino acid peptide. Phe (residue 1) is D-Phe. Trp (residue 4) is D-Trp. Thr (residue 8) is Thr-O-acetate.
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; OTHER INFORMATION: Disulfide bond between the two Cys amino acid residues.
US-10-473-721A-15

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||||
Db 1 PCFWKTCCT 8

RESULT 16
US-10-473-721A-16
; Sequence 16, Application US/10473721A

; Publication No. US2005004000A1
; GENERAL INFORMATION:
; APPLICANT: SHECHTER, Yoram
; APPLICANT: GOLDWASER, Itzhak
; APPLICANT: LAVON, Iris
; APPLICANT: BRODIE, David
; APPLICANT: EYAL, Nurit
; APPLICANT: FASS, Stanley
; APPLICANT: FRIDKIN, Matityahu
; TITLE OF INVENTION: ORAL ABSORBED DRUGS
; FILE REFERENCE: SHECTERS
; CURRENT APPLICATION NUMBER: US/10/473,721A
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/IL02/00252
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: IL 142353
; PRIOR FILING DATE: 2001-04-01
; PRIOR APPLICATION NUMBER: IL 146383
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(8)
; OTHER INFORMATION: Cyclic eight-amino acid peptide. Phe (residue 1) is D-Phe. Trp (residue 4) is D-Trp. Lys (residue 5) is N-Fmoc-Lys or N-Fms-Lys.
; OTHER INFORMATION: Thr (residue 8) is Thr-O-acetate.
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; OTHER INFORMATION: Disulfide bond between the two Cys amino acid groups.
US-10-473-721A-16

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||||
Db 1 PCFWKTCCT 8

RESULT 17
US-10-916-522A-4
; Sequence 4, Application US/10916522A
; Publication No. US2005004326A1
; GENERAL INFORMATION:
; APPLICANT: HORNIK, Vared
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOG
; FILE REFERENCE: 87534-3099
; CURRENT APPLICATION NUMBER: US/10/916,522A
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 09/734,583
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Phe residue is a D isomer
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)

OTHER INFORMATION: The Thr residue ends with CH2OH
FEATURE: NAME/KEY: DISULFIDE BRIDGE
LOCATION: (2)..(2)
OTHER INFORMATION: A disulfide bridge is formed between Cys residues 2 and 7
FEATURE: NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: The Trp residue is a D isomer
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-916-522A-4

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||
Db 1 FCFWKTCCT 8

RESULT 18

US-10-505-239-12
Sequence 12, Application US/10505239
Publication No. US20050171014A1
GENERAL INFORMATION:
APPLICANT: TARASOVA, Nadva I
APPLICANT: MICHEJDA, Christopher J
APPLICANT: DYBA, Marcin
APPLICANT: COHRAN, Carolyn
TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
FILE REFERENCE: 229694
CURRENT APPLICATION NUMBER: US/10/505,239
CURRENT FILING DATE: 2004-08-19
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: 60/360,543
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 60/370,189
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
NAME/KEY: misc feature
LOCATION: (1)..(8)
OTHER INFORMATION: wherein the peptide is carboxylated at either the N-or C-terminus
US-10-505-239-12

Query Match 66.2%; Score 53; DB 5; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||
Db 1 FCFWKTCCT 8

RESULT 19

US-11-006-071-7
Sequence 7, Application US/11006071
Publication No. US20050229275A1
GENERAL INFORMATION:
APPLICANT: Koprowski, Hilary
APPLICANT: Yusibov, Vidadi

TITLE OF INVENTION: Production Of Biomedical Peptides And Proteins In
FILE REFERENCE: JEFF-KOP01.P0001
CURRENT FILING DATE: 2004-12-07
PRIOR APPLICATION NUMBER: US/09/673,174
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/118,867
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: PCT/US99/25566
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: A peptide to
OTHER INFORMATION: suppress the synthesis of human growth hormone
US-11-006-071-7

Query Match 66.2%; Score 53; DB 6; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
:|||||
Db 2 FCFWKTCCT 9

RESULT 20

US-10-425-115-289592
Sequence 289592, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 289592
LENGTH: 67
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_27197C.1.pep
US-10-425-115-289592

Query Match 66.2%; Score 53; DB 4; Length 67;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YYCYCFWKTC 10
:|||||
Db 45 YYCFCFMKIC 54

RESULT 21

US-10-424-599-264998
Sequence 264998, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 26498
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_81312C.1.pcp
US-10-424-599-26498

Query Match 65.0%; Score 52; DB 4; Length 53;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 16 YPCYCFW 22

RESULT 22

US-10-425-115-213258
; Sequence 213258, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 213258
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_12608C.1.pcp
US-10-425-115-213258

Query Match 65.0%; Score 52; DB 4; Length 107;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYCYCFW 7
Db 40 YPCYCFW 46

RESULT 23

US-10-490-326-24
; Sequence 24, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; TITLE OF INVENTION: Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-24

Query Match 63.7%; Score 51; DB 5; Length 12;
Best Local Similarity 72.7%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YYCYCFWKCT 11
Db 2 YKYCFWKCT 12

RESULT 24

US-10-258-766A-1
; Sequence 1, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosyntherma, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816.17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Arg (Pmc)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: Asp (OtBu)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: D Tyr (OtBu)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Asp (beta-Oall)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: Lys (Mtt)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: DPhe
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Cys (Acm)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: Tyr (OtBu)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: D Trp (tBoc)
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)..(11)

; OTHER INFORMATION: Lys (cBoc)
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (12)..(12)
 ; OTHER INFORMATION: Thr (OtBu)
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (13)..(13)
 ; OTHER INFORMATION: Cys (Acm)
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (14)..(14)
 ; OTHER INFORMATION: Thr (OtBu)-O-RESIN
 ; US-10-258-766A-1

Query Match 63.7%; Score 51; DB 4; Length 14;
 Best Local Similarity 63.6%; Pred. No. 6.9;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YYCYCFWKTKT 11
 | :|:||||
 Db 4 YDKFCYWKTKT 14

RESULT 25

US-10-258-766A-6
 ; Sequence 6, Application US/10258766A
 ; Publication No. US20040136907A1
 ; GENERAL INFORMATION:

; APPLICANT: Biosynthesma, Inc.
 ; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
 ; FILE REFERENCE: 717816.17
 ; CURRENT APPLICATION NUMBER: US/10/258,766A
 ; CURRENT FILING DATE: 2002-10-25
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6

LENGTH: 14

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: DISULFID

LOCATION: (8)..(13)

OTHER INFORMATION:

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (1)..(5)

OTHER INFORMATION: Amide bond between residues 1 and 5

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (4)..(4)

OTHER INFORMATION: Dtyr

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (7)..(7)

OTHER INFORMATION: DPhe

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (10)..(10)

OTHER INFORMATION: DTrp

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (14)..(14)

OTHER INFORMATION: Thr-OH

US-10-258-766A-6

Query Match 63.7%; Score 51; DB 4; Length 14;
 Best Local Similarity 63.6%; Pred. No. 6.9;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YYCYCFWKTKT 11
 | :|:||||
 Db 4 YDKFCYWKTKT 14

RESULT 26

US-10-258-766A-7

; Sequence 7, Application US/10258766A

; Publication No. US20040136907A1

; GENERAL INFORMATION:

; APPLICANT: Biosynthesma, Inc.

; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES

; FILE REFERENCE: 717816.17

; CURRENT APPLICATION NUMBER: US/10/258,766A

; CURRENT FILING DATE: 2002-10-25

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

LENGTH: 14

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: DISULFID

LOCATION: (8)..(13)

OTHER INFORMATION:

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (1)..(5)

OTHER INFORMATION: Amide bond between residues 1 and 5

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (4)..(4)

OTHER INFORMATION: Dtyr

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (6)..(6)

OTHER INFORMATION: NH-DTPA

OTHER INFORMATION:

OTHER INFORMATION: Lys

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (7)..(7)

OTHER INFORMATION: DPhe

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (10)..(10)

OTHER INFORMATION: DTrp

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (14)..(14)

OTHER INFORMATION: Thr-OH

US-10-258-766A-7

Query Match 63.7%; Score 51; DB 4; Length 14;

Best Local Similarity 63.6%; Pred. No. 6.9;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YYCYCFWKTKT 11

| :|:||||

Db 4 YDKFCYWKTKT 14

RESULT 27

US-10-258-766A-8

; Sequence 8, Application US/10258766A

; Publication No. US20040136907A1

; GENERAL INFORMATION:

; APPLICANT: Biosynthesma, Inc.

; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES

; FILE REFERENCE: 717816.17

; CURRENT APPLICATION NUMBER: US/10/258,766A

; CURRENT FILING DATE: 2002-10-25

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

LENGTH: 14

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Arg(Pmc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: DTyr(OtBu)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Asp(beta-Oall)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: Lys(Mtt)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: DPhe
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Cys(Acm)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: Tyr(OtBu)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: DTrp(tBoc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: Lys(tBoc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)..(12)
; OTHER INFORMATION: Thr(OtBu)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: Cys(Acm)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Thr(ol)(OtBu)-O-RESIN
; US-10-258-766A-8
```

```
Query Match 63.7%; Score 51; DB 4; Length 14;
Best Local Similarity 63.6%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 YYCYCFWKTC 11
| : |||||
Db 4 YDKFCYWKTC 14
```

```
RESULT 28
US-10-258-766A-13
; Sequence 13, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosynthea, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816.17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 13
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: DTyr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: DPhe
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: DTrp
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Thr(ol)-OH
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)..(13)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Amide bond between residues 1 and 5
; US-10-258-766A-13
```

```
Query Match 63.7%; Score 51; DB 4; Length 14;
Best Local Similarity 63.6%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 YYCYCFWKTC 11
| : |||||
Db 4 YDKFCYWKTC 14
```

```
RESULT 29
US-10-258-766A-14
; Sequence 14, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosynthea, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816.17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
```

```
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: DTyr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: NH-DTPA
; OTHER INFORMATION:
; OTHER INFORMATION: Lys
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: DPhe
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: DTrp
```

```
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Thr(ol)-OH
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)..(13)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Amide bond between residues 1 and 5
US-10-258-766A-14

Query Match      63.7%; Score 51; DB 4; Length 14;
Best Local Similarity 63.6%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YYCYCFWKTC 11
Db 4 YDRFCYWKTC 14

RESULT 30
US-10-490-326-34
; Sequence 34, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fueslier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR FILING DATE: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1, 6
; OTHER INFORMATION: Cys at positions 1 and 6 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-34

Query Match      62.5%; Score 50; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTC 11
Db 1 CFWKTC 7

RESULT 31
US-10-796-158-4
; Sequence 4, Application US/10796158
; Publication No. US20050118099A1
; GENERAL INFORMATION:
; APPLICANT: IDEC Pharmaceuticals
; APPLICANT: Braslowsky, Gary
; APPLICANT: Chinn, Paul
; APPLICANT: Hanna, Nabil
```

```
; TITLE OF INVENTION: THIOL-SPECIFIC DRUG ATTACHMENT TO TARGETING PEPTIDES
; FILE REFERENCE: 037003-0308678
; CURRENT APPLICATION NUMBER: US/10/796,158
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic SSSTR binding domain
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (1)..(6)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: AMIDE OR ALCOHOL
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (2)..(2)
; OTHER INFORMATION: D stereoisomer
US-10-796-158-4

Query Match      62.5%; Score 50; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTC 11
Db 1 CFWKTC 7

RESULT 32
US-09-781-980-6
; Sequence 6, Application US/09781980
; Publication No. US20010029035A1
; GENERAL INFORMATION:
; APPLICANT: EISENHUT, MICHAEL
; APPLICANT: MIER, WALTER
; APPLICANT: ERITJA, RAMON
; APPLICANT: HABERKORN, UWE
; TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
; FILE REFERENCE: 2502498.991110
; CURRENT APPLICATION NUMBER: US/09/781,980
; CURRENT FILING DATE: 2001-02-14
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: DE 100 06 572
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-781-980-6

Query Match      62.5%; Score 50; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 11
Db 1 FCYWKTC 8

RESULT 33
US-10-427-160A-22
; Sequence 22, Application US/10427160A
```

Publication No. US20040110296A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Vargeese, Chandra
APPLICANT: Haerberli, Peter
APPLICANT: Wang, Weimin
APPLICANT: Chen, Tongqian
TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery
FILE REFERENCE: 600/032 (MBH02-312-A)
CURRENT APPLICATION NUMBER: US/10/427,160A
CURRENT FILING DATE: 2003-04-30
PRIORITY APPLICATION NUMBER: PCT/US 02/15876
PRIORITY FILING DATE: 2002-05-17
PRIORITY APPLICATION NUMBER: US 60/292,217
PRIORITY FILING DATE: 2001-05-18
PRIORITY APPLICATION NUMBER: US 60/362,016
PRIORITY FILING DATE: 2002-03-06
PRIORITY APPLICATION NUMBER: US 60/306,883
PRIORITY FILING DATE: 2001-07-20
PRIORITY APPLICATION NUMBER: US 60/311,865
PRIORITY FILING DATE: 2001-08-13
PRIORITY APPLICATION NUMBER: PCT/US 03/05346
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: PCT/US 03/05028
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: US 60/358,580
PRIORITY FILING DATE: 2002-02-20
PRIORITY APPLICATION NUMBER: US 60/363,124
PRIORITY FILING DATE: 2002-03-11
PRIORITY APPLICATION NUMBER: US 60/386,782
PRIORITY FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: Ser stands for optional Serine for coupling
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(2)
OTHER INFORMATION: Phe stands for optional D isomer for stability
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5)..(5)
OTHER INFORMATION: Trp stands for optional D isomer for stability
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic peptide
US-10-427-160A-22

Query Match 62.5%; Score 50; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YCFWKTCCT 11
:|||||
Db 2 FCYWKTCCT 9

RESULT 34
US-10-444-853A-515
Sequence 515, Application US/10444853A
Publication No. US20040192626A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Haerberli, Peter
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid

APPLICANT: Macejak, Dennis
APPLICANT: Zinnen, Shawn
APPLICANT: Pavco, Pamela
APPLICANT: Morrissey, David
APPLICANT: Poenaugh, Kathy
APPLICANT: Mokler, Victor
APPLICANT: Jamison, Sharon
APPLICANT: Vaish, Narendra
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/114 (MBH03-465)
CURRENT APPLICATION NUMBER: US/10/444,853A
CURRENT FILING DATE: 2003-05-23
PRIORITY APPLICATION NUMBER: US 10/417,012
PRIORITY FILING DATE: 2003-04-16
PRIORITY APPLICATION NUMBER: PCT/US03/05346
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: PCT/US03/05028
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: US 60/358,580
PRIORITY FILING DATE: 2002-02-20
PRIORITY APPLICATION NUMBER: US 60/363,124
PRIORITY FILING DATE: 2002-03-11
PRIORITY APPLICATION NUMBER: US 60/386,782
PRIORITY FILING DATE: 2002-06-06
PRIORITY APPLICATION NUMBER: US 60/406,784
PRIORITY FILING DATE: 2002-08-29
PRIORITY APPLICATION NUMBER: US 60/408,378
PRIORITY FILING DATE: 2002-09-05
PRIORITY APPLICATION NUMBER: US 60/409,293
PRIORITY FILING DATE: 2002-09-09
PRIORITY APPLICATION NUMBER: US 60/440,129
PRIORITY FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 515
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Somatostatin (tyr-3-octreotate)
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: Ser at position 1 is optionally present for coupling.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (2)..(2)
OTHER INFORMATION: Phe at position 2 is optionally the D-isomer.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (5)..(5)
OTHER INFORMATION: Trp at position 5 is optionally the D-isomer.
US-10-444-853A-515

Query Match 62.5%; Score 50; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YCFWKTCCT 11
:|||||
Db 2 FCYWKTCCT 9

RESULT 35
US-10-780-447-22
Sequence 22, Application US/10780447
Publication No. US20040249178A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Vargeese, Chandra
APPLICANT: Haerberli, Peter

APPLICANT: Wang, Weimin
APPLICANT: Chen, Tongqian
TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery
FILE REFERENCE: 600/032 (MBH02-312-A)
CURRENT APPLICATION NUMBER: US/10/780,447
CURRENT FILING DATE: 2004-02-13
PRIORITY APPLICATION NUMBER: PCT/US 02/15876
PRIORITY FILING DATE: 2002-05-17
PRIORITY APPLICATION NUMBER: US 60/292,217
PRIORITY FILING DATE: 2001-05-18
PRIORITY APPLICATION NUMBER: US 60/362,016
PRIORITY FILING DATE: 2002-03-06
PRIORITY APPLICATION NUMBER: US 60/306,883
PRIORITY FILING DATE: 2001-07-20
PRIORITY APPLICATION NUMBER: US 60/311,865
PRIORITY FILING DATE: 2001-08-13
PRIORITY APPLICATION NUMBER: PCT/US 03/05346
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: PCT/US 03/05028
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: US 60/358,580
PRIORITY FILING DATE: 2002-02-20
PRIORITY APPLICATION NUMBER: US 60/363,124
PRIORITY FILING DATE: 2002-03-11
PRIORITY APPLICATION NUMBER: US 60/386,782
PRIORITY FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1)
FEATURE:
OTHER INFORMATION: Ser stands for optional Serine for coupling

NAME/KEY: misc feature
LOCATION: (2)..(2)
FEATURE:
NAME/KEY: misc feature
LOCATION: (5)..(5)
OTHER INFORMATION: Trp stands for optional D isomer for stability
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthetic peptide
US-10-780-447-22

Query Match 62.5%; Score 50; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
:|:|:|:|
Db 2 FCYWKTKT 9

RESULT 36
US-10-757-803-515
Sequence 515, Application US/10757803
Publication No. US20050020525A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Haeblerli, Peter
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Macejak, Dennis
APPLICANT: Zinnen, Shawn
APPLICANT: Pavco, Pamela
APPLICANT: Morrissey, David
APPLICANT: Fosnaugh, Kathy

APPLICANT: Jamison, Sharon
APPLICANT: Vaish, Narendra
APPLICANT: Chowira, Bharat
APPLICANT: Usman, Nassim
APPLICANT: James, Thompson
APPLICANT: Vargeese, Chandra
APPLICANT: Wang, Weimin
APPLICANT: Tongqian, Chen
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
FILE REFERENCE: 400/142 (03-465-C)
CURRENT APPLICATION NUMBER: US/10/757,803
CURRENT FILING DATE: 2004-01-14
PRIORITY APPLICATION NUMBER: US 10/720,448
PRIORITY FILING DATE: 2003-11-24
PRIORITY APPLICATION NUMBER: US 10/693,059
PRIORITY FILING DATE: 2003-10-23
PRIORITY APPLICATION NUMBER: US 10/444,853
PRIORITY FILING DATE: 2003-05-23
PRIORITY APPLICATION NUMBER: US 10/652,791
PRIORITY FILING DATE: 2003-08-29
PRIORITY APPLICATION NUMBER: US 10/422,704
PRIORITY FILING DATE: 2003-04-24
PRIORITY APPLICATION NUMBER: US 10/417,012
PRIORITY FILING DATE: 2003-04-16
PRIORITY APPLICATION NUMBER: US 10/427,160
PRIORITY FILING DATE: 2003-04-30
PRIORITY APPLICATION NUMBER: PCT/US03/05346
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: PCT/US03/05028
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: US 60/358,580
PRIORITY FILING DATE: 2002-02-20
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 669
SOFTWARE: PatentIn version 3.3
SEQ ID NO 515
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Conjugating peptide derived
OTHER INFORMATION: from Somatostatin (tyr-3-octreotate)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: Serine is optionally present for coupling
FEATURE:
NAME/KEY: misc feature
LOCATION: (2)..(2)
OTHER INFORMATION: Optional D-isomer
FEATURE:
NAME/KEY: misc feature
LOCATION: (5)..(5)
OTHER INFORMATION: Optional D-isomer
US-10-757-803-515

Query Match 62.5%; Score 50; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTKT 11
:|:|:|:|
Db 2 FCYWKTKT 9

RESULT 37
US-10-826-966-515
Sequence 515, Application US/10826966
Publication No. US2005003273A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James

APPLICANT: Macejak, Dennis
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/151 (03-465-D)
CURRENT APPLICATION NUMBER: US/10/826,966
PRIORITY FILING DATE: 2004-04-16
PRIORITY FILING DATE: 2004-01-14
PRIORITY FILING DATE: 2003-11-24
PRIORITY FILING DATE: 2003-10-23
PRIORITY FILING DATE: 2003-05-23
PRIORITY APPLICATION NUMBER: US 10/444,853
PRIORITY FILING DATE: 2003-08-29
PRIORITY APPLICATION NUMBER: US 10/652,791
PRIORITY FILING DATE: 2003-04-24
PRIORITY APPLICATION NUMBER: US 10/422,704
PRIORITY FILING DATE: 2003-04-16
PRIORITY APPLICATION NUMBER: US 10/417,012
PRIORITY FILING DATE: 2003-04-30
PRIORITY APPLICATION NUMBER: US 10/427,160
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: PCT/US03/05346
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: PCT/US03/05028
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 669
SOFTWARE: PatentIn version 3.3
SEQ ID NO 515
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Conjugating peptide derived
OTHER INFORMATION: from Somatostatin (tyr-3-octreotate)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
FEATURE:
OTHER INFORMATION: Serine is optionally present for coupling
NAME/KEY: misc_feature
LOCATION: (2)..(2)
OTHER INFORMATION: Optional D-isomer
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5)..(5)
OTHER INFORMATION: Optional D-isomer
US-10-826-966-515

Query Match 62.5%; Score 50; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCFWKTCCT 11
:|:|||||
Db 2 FCYWKTCCT 9

RESULT 38
US-10-490-326-30
Sequence 30, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
Bombesin Analog Conjugates and Uses Thereof
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326

CURRENT FILING DATE: 2004-03-19
PRIORITY APPLICATION NUMBER: PCT/US02/30143
PRIORITY FILING DATE: 2002-09-20
PRIORITY APPLICATION NUMBER: 60/323,851
PRIORITY FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: 1
OTHER INFORMATION: Xaa = Sar
FEATURE:
NAME/KEY: VARIANT
LOCATION: 3
OTHER INFORMATION: Xaa = Nle
NAME/KEY: MOD RES
LOCATION: 6, 11
OTHER INFORMATION: Cys at positions 6 and 11 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-30

Query Match 62.5%; Score 50; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CFWKTCCT 11
|||||||
Db 6 CFWKTCCT 12

RESULT 39
US-10-490-326-31
Sequence 31, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
Bombesin Analog Conjugates and Uses Thereof
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIORITY APPLICATION NUMBER: PCT/US02/30143
PRIORITY FILING DATE: 2002-09-20
PRIORITY APPLICATION NUMBER: 60/323,851
PRIORITY FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: 3
OTHER INFORMATION: Xaa = Nle
NAME/KEY: MOD RES
LOCATION: 6, 11
OTHER INFORMATION: Cys at positions 6 and 11 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-31

Query Match 62.5%; Score 50; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 5 CPWKTCCT 11
    |||||
Db 6 CPWKTCCT 12

RESULT 40
US-10-490-326-32
; Sequence 32, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fusellier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa = OH-Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 6, 11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-32

Query Match 62.5%; Score 50; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CPWKTCCT 11
    |||||
Db 6 CPWKTCCT 12

RESULT 41
US-10-490-326-41
; Sequence 41, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fusellier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-41

Query Match 62.5%; Score 50; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CPWKTCCT 11
    |||||
Db 6 CPWKTCCT 12

RESULT 42
US-10-490-326-21
; Sequence 21, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fusellier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa = Nle
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-21

Query Match 62.5%; Score 50; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CPWKTCCT 11
    |||||
Db 9 CPWKTCCT 15

RESULT 43
US-10-490-326-23
; Sequence 23, Application US/10490326
; Publication No. US20050070470A1
```

GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
Bomdesin Analog Conjugates and Uses Thereof
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: 9, 14
OTHER INFORMATION: Cys at positions 9 and 14 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-23

Query Match 62.5%; Score 50; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTCCT 11
| | | | |
Db 9 CFWKTCCT 15

RESULT 44
US-10-490-326-35
Sequence 35, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
Bomdesin Analog Conjugates and Uses Thereof
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: 6
OTHER INFORMATION: Xaa = Nle
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-35

Query Match 62.5%; Score 50; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTCCT 11
| | | | |
Db 9 CFWKTCCT 15

RESULT 45
US-10-490-326-36
Sequence 36, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
Bomdesin Analog Conjugates and Uses Thereof
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: 6
OTHER INFORMATION: Xaa = Nle
NAME/KEY: MOD_RES
LOCATION: 9, 14
OTHER INFORMATION: Cys at positions 9 and 14 are circularized
FEATURE:
OTHER INFORMATION: Synthetic
US-10-490-326-36

Query Match 62.5%; Score 50; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTCCT 11
| | | | |
Db 9 CFWKTCCT 15

RESULT 46
US-10-490-326-42
Sequence 42, Application US/10490326
Publication No. US20050070470A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Fuselier, Joseph A.
APPLICANT: Murphy, William A.
APPLICANT: Sun, Lichun
TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
Bomdesin Analog Conjugates and Uses Thereof
FILE REFERENCE: 07005/005002
CURRENT APPLICATION NUMBER: US/10/490,326
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/US02/30143
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/323,851
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence


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; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-42

Query Match          62.5%; Score 50; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTKT 11
Db 9 CFWKTKT 15

RESULT 47
US-10-490-326-47
; Sequence 47, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa = 4Pal
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-47

Query Match          62.5%; Score 50; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTKT 11
Db 9 CFWKTKT 15

RESULT 48
US-10-490-326-48
; Sequence 48, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
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; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-48

Query Match          62.5%; Score 50; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTKT 11
Db 9 CFWKTKT 15

RESULT 49
US-10-490-326-49
; Sequence 49, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Murphy, William A.
; APPLICANT: Sun, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: MOD RES
; LOCATION: 9, 14
; OTHER INFORMATION: Cys at positions 9 and 14 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-49

Query Match          62.5%; Score 50; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTKT 11
Db 9 CFWKTKT 15

RESULT 50
US-10-490-326-51
; Sequence 51, Application US/10490326
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/ Publication No. US20050070470A1
/ GENERAL INFORMATION:
/ APPLICANT: Coy, David H.
/ APPLICANT: Fuseller, Joseph A.
/ APPLICANT: Murphy, William A.
/ APPLICANT: Sun, Lichun
/ TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
/ Bombesin Analog Conjugates and Uses Thereof
/ FILE REFERENCE: 07005/005002
/ CURRENT APPLICATION NUMBER: US/10/490,326
/ CURRENT FILING DATE: 2004-03-19
/ PRIOR APPLICATION NUMBER: PCT/US02/30143
/ PRIOR FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/323,851
/ PRIOR FILING DATE: 2001-09-21
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 51
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: 9, 14
/ OTHER INFORMATION: Cys at positions 9 and 14 are circularized
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-490-326-51
```

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Query Match      62.5%; Score 50; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      5 CPWKTKT 11
Db      9 CPWKTKT 15
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Search completed: May 9, 2006, 12:15:43
Job time : 112.333 secs
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 12:10:45 ; Search time 10 Seconds
(without alignments)
50.913 Million cell updates/sec

Title: US-10-796-158-7

Perfect score: 80

Sequence: 1 YYCWFVKTCT 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*
1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
7: /SIDSS/ptodata/1/pubpaa/US03_NEW_PUB.pep.*
8: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
10: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
11: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
12: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	53	66.2	8	US-10-626-719-158
2	50	62.5	8	US-10-626-719-159
3	50	62.5	12	US-10-506-223-16
4	50	62.5	12	US-10-506-223-17
5	50	62.5	12	US-10-506-223-39
6	50	62.5	12	US-10-506-223-40
7	50	62.5	13	US-10-506-223-21
8	50	62.5	13	US-10-506-223-22
9	50	62.5	14	US-10-506-223-23
10	50	62.5	15	US-10-506-223-24
11	50	62.5	16	US-10-506-223-25
12	50	62.5	17	US-10-506-223-26
13	50	62.5	18	US-10-506-223-27
14	50	62.5	19	US-10-506-223-28
15	50	62.5	20	US-10-506-223-29
16	50	62.5	21	US-10-506-223-30
17	50	62.5	22	US-10-506-223-31
18	50	62.5	23	US-10-506-223-32
19	50	62.5	24	US-10-506-223-33
20	50	62.5	25	US-10-506-223-34
21	50	62.5	26	US-10-506-223-35
22	53	66.2	8	Sequence 158, App
23	50	62.5	8	Sequence 159, App
24	50	62.5	12	Sequence 16, Appl
25	50	62.5	12	Sequence 17, Appl
26	50	62.5	12	Sequence 39, Appl
27	50	62.5	12	Sequence 40, Appl
28	50	62.5	13	Sequence 21, Appl
29	50	62.5	13	Sequence 22, Appl
30	50	62.5	14	Sequence 23, Appl
31	50	62.5	15	Sequence 24, Appl
32	50	62.5	16	Sequence 25, Appl
33	50	62.5	17	Sequence 26, Appl
34	50	62.5	18	Sequence 27, Appl
35	50	62.5	19	Sequence 28, Appl
36	50	62.5	20	Sequence 29, Appl
37	50	62.5	21	Sequence 30, Appl
38	50	62.5	22	Sequence 31, Appl
39	50	62.5	23	Sequence 32, Appl
40	50	62.5	24	Sequence 33, Appl
41	50	62.5	25	Sequence 34, Appl
42	50	62.5	26	Sequence 35, Appl

22	50	62.5	27	9	US-10-506-223-36	Sequence 36, Appl
23	49	61.3	21	11	US-11-198-847-234	Sequence 234, App
24	49	61.3	40	11	US-11-198-847-231	Sequence 231, App
25	49	61.3	93	11	US-11-198-847-116	Sequence 116, App
26	48	60.0	8	9	US-10-626-719-156	Sequence 156, App
27	46	57.5	45	11	US-11-198-847-280	Sequence 280, App
28	46	57.5	95	11	US-11-198-847-89	Sequence 89, Appl
29	45	56.2	6	9	US-10-506-223-37	Sequence 37, Appl
30	45	56.2	6	9	US-10-506-223-38	Sequence 38, Appl
31	45	56.2	8	9	US-10-626-719-157	Sequence 157, App
32	44	55.0	10	11	US-11-198-847-332	Sequence 332, App
33	44	55.0	21	11	US-11-198-847-232	Sequence 232, App
34	44	55.0	21	11	US-11-198-847-233	Sequence 233, App
35	44	55.0	40	11	US-11-198-847-229	Sequence 229, App
36	44	55.0	40	11	US-11-198-847-230	Sequence 230, App
37	44	55.0	93	11	US-11-198-847-32	Sequence 32, Appl
38	44	55.0	93	11	US-11-198-847-41	Sequence 41, Appl
39	43	53.8	285	11	US-11-045-004-1161	Sequence 1161, Ap
40	43	53.8	566	11	US-11-096-568A-25706	Sequence 25706, A
41	43	53.8	593	11	US-11-096-568A-25705	Sequence 25705, A
42	43	53.8	648	11	US-11-096-568A-25704	Sequence 25704, A
43	42	52.5	131	11	US-11-188-298-15828	Sequence 15828, A
44	42	52.5	424	9	US-10-242-586-12	Sequence 12, Appl
45	42	52.5	424	9	US-10-242-902-12	Sequence 12, Appl
46	42	52.5	424	9	US-10-243-116-12	Sequence 12, Appl
47	42	52.5	424	9	US-10-243-136-12	Sequence 12, Appl
48	42	52.5	424	9	US-10-243-189-12	Sequence 12, Appl
49	42	52.5	424	9	US-10-243-215-12	Sequence 12, Appl
50	42	52.5	424	9	US-10-243-236-12	Sequence 12, Appl
51	42	52.5	424	9	US-10-243-298-12	Sequence 12, Appl
52	42	52.5	424	9	US-10-243-304-12	Sequence 12, Appl
53	42	52.5	424	9	US-10-243-338-12	Sequence 12, Appl
54	42	52.5	424	9	US-10-243-345-12	Sequence 12, Appl
55	42	52.5	424	9	US-10-243-357-12	Sequence 12, Appl
56	42	52.5	424	9	US-10-245-083-12	Sequence 12, Appl
57	42	52.5	424	9	US-10-247-015-12	Sequence 12, Appl
58	42	52.5	433	11	US-11-096-568A-5633	Sequence 5633, Ap
59	42	52.5	838	11	US-11-096-568A-32096	Sequence 32096, A
60	42	52.5	917	11	US-11-096-568A-32095	Sequence 32095, A
61	42	52.5	949	11	US-11-096-568A-32094	Sequence 32094, A
62	41	51.2	9	11	US-11-198-847-316	Sequence 316, App
63	41	51.2	11	11	US-11-198-847-313	Sequence 313, App
64	41	51.2	15	11	US-11-198-847-311	Sequence 311, App
65	41	51.2	107	11	US-11-040-159-17	Sequence 17, Appl
66	41	51.2	108	11	US-11-040-159-15	Sequence 15, Appl
67	41	51.2	108	11	US-11-054-669-94	Sequence 94, Appl
68	41	51.2	108	11	US-11-054-669-111	Sequence 111, App
69	41	51.2	109	11	US-11-040-159-7	Sequence 7, Appl
70	41	51.2	109	11	US-11-040-159-9	Sequence 9, Appl
71	41	51.2	109	11	US-11-040-159-11	Sequence 11, Appl
72	41	51.2	109	11	US-11-040-159-13	Sequence 13, Appl
73	41	51.2	237	11	US-11-054-669-109	Sequence 109, App
74	40	50.0	7	9	US-10-626-719-160	Sequence 160, App
75	40	50.0	30	11	US-11-198-847-285	Sequence 285, App
76	40	50.0	30	11	US-11-198-847-286	Sequence 286, App
77	40	50.0	81	11	US-11-198-847-92	Sequence 92, Appl
78	40	50.0	81	11	US-11-198-847-95	Sequence 95, Appl
79	40	50.0	308	11	US-11-098-686-10572	Sequence 10572, A
80	39	48.8	39	11	US-11-004-399-1477	Sequence 1477, Ap
81	39	48.8	296	11	US-11-096-568A-15576	Sequence 15576, A
82	39	48.8	313	11	US-11-096-568A-15575	Sequence 15575, A
83	39	48.8	315	11	US-11-096-568A-15574	Sequence 15574, A
84	39	48.8	484	9	US-10-467-657-8518	Sequence 8518, Ap
85	38	47.5	6	9	US-10-532-452-9	Sequence 9, Appl
86	38	47.5	8	9	US-10-532-452-7	Sequence 7, Appl
87	38	47.5	10	11	US-11-198-847-320	Sequence 320, App
88	38	47.5	11	9	US-10-532-452-1	Sequence 1, Appl
89	38	47.5	12	9	US-10-875-800-7	Sequence 7, Appl
90	38	47.5	12	9	US-10-532-452-2	Sequence 2, Appl
91	38	47.5	12	9	US-10-532-452-3	Sequence 3, Appl
92	38	47.5	12	9	US-10-532-452-4	Sequence 4, Appl
93	38	47.5	12	9	US-10-532-452-6	Sequence 6, Appl
94	38	47.5	14	9	US-10-532-452-5	Sequence 5, Appl

95	38	47.5	14	9	US-10-532-452-8	Sequence 8, Appli	168	35	43.8	26	11	US-11-009-769A-131	Sequence 131, App
96	38	47.5	22	11	US-11-198-847-266	Sequence 266, App	169	35	43.8	95	11	US-11-096-568A-15646	Sequence 15646, A
97	38	47.5	24	11	US-11-120-501-36	Sequence 36, Appl	170	35	43.8	109	11	US-11-096-568A-15645	Sequence 15645, A
98	38	47.5	27	11	US-11-120-501-33	Sequence 33, Appl	171	35	43.8	115	11	US-11-096-568A-8517	Sequence 8517, Ap
99	38	47.5	28	11	US-11-120-501-31	Sequence 31, Appl	172	35	43.8	144	9	US-10-467-657-4916	Sequence 4916, Ap
100	38	47.5	29	11	US-11-120-501-18	Sequence 18, Appl	173	35	43.8	149	11	US-11-096-568A-15644	Sequence 15644, A
101	38	47.5	29	11	US-11-120-501-21	Sequence 21, Appl	174	35	43.8	173	11	US-11-096-568A-20604	Sequence 20604, A
102	38	47.5	29	11	US-11-120-501-22	Sequence 22, Appl	175	35	43.8	191	11	US-11-096-568A-20603	Sequence 20603, A
103	38	47.5	29	11	US-11-120-501-24	Sequence 24, Appl	176	35	43.8	211	9	US-10-467-657-8552	Sequence 8552, Ap
104	38	47.5	29	11	US-11-120-501-25	Sequence 25, Appl	177	35	43.8	219	11	US-11-096-568A-20602	Sequence 20602, A
105	38	47.5	29	11	US-11-120-501-26	Sequence 26, Appl	178	35	43.8	229	11	US-11-096-568A-31617	Sequence 31617, A
106	38	47.5	29	11	US-11-120-501-27	Sequence 27, Appl	179	35	43.8	241	11	US-11-054-515-2060	Sequence 2060, Ap
107	38	47.5	29	11	US-11-120-501-30	Sequence 30, Appl	180	35	43.8	241	11	US-11-266-444-2060	Sequence 2060, Ap
108	38	47.5	29	11	US-11-120-501-32	Sequence 32, Appl	181	35	43.8	261	11	US-11-227-543-4	Sequence 4, Appli
109	38	47.5	29	11	US-11-120-501-37	Sequence 37, Appl	182	35	43.8	291	11	US-11-096-568A-31616	Sequence 31616, A
110	38	47.5	32	11	US-11-120-501-40	Sequence 40, Appl	183	35	43.8	357	11	US-11-096-568A-5833	Sequence 5833, Ap
111	38	47.5	66	11	US-11-079-463-9692	Sequence 9692, Ap	184	35	43.8	360	9	US-10-851-667A-26	Sequence 26, Appl
112	38	47.5	72	11	US-11-198-847-137	Sequence 137, App	185	35	43.8	360	9	US-10-330-773-933	Sequence 933, App
113	38	47.5	107	9	US-10-982-357-8	Sequence 8, Appli	186	35	43.8	361	11	US-11-096-568A-5832	Sequence 5832, Ap
114	38	47.5	119	11	US-11-072-512-2041	Sequence 2041, Ap	187	35	43.8	428	11	US-11-096-568A-31615	Sequence 31615, A
115	38	47.5	124	9	US-10-242-586-26	Sequence 26, Appl	188	35	43.8	444	11	US-11-096-568A-5831	Sequence 5831, Ap
116	38	47.5	124	9	US-10-242-586-26	Sequence 26, Appl	189	35	43.8	461	9	US-10-330-773-327	Sequence 327, App
117	38	47.5	124	9	US-10-243-116-26	Sequence 26, Appl	190	35	43.8	544	11	US-11-188-298-4372	Sequence 4372, Ap
118	38	47.5	124	9	US-10-243-136-26	Sequence 26, Appl	191	35	43.8	1684	11	US-11-188-298-13722	Sequence 13722, A
119	38	47.5	124	9	US-10-243-189-26	Sequence 26, Appl	192	35	43.8	1971	9	US-10-961-231-1	Sequence 1, Appli
120	38	47.5	124	9	US-10-243-215-26	Sequence 26, Appl	193	35	43.8	1971	11	US-11-179-624-1	Sequence 9, Appli
121	38	47.5	124	9	US-10-243-236-26	Sequence 26, Appl	194	35	43.8	2244	11	US-11-131-263-9	Sequence 9, Appli
122	38	47.5	124	9	US-10-243-238-26	Sequence 26, Appl	195	35	43.8	2244	11	US-11-131-263-18	Sequence 18, Appl
123	38	47.5	124	9	US-10-243-304-26	Sequence 26, Appl	196	35	43.8	2244	11	US-11-131-263-30	Sequence 30, Appl
124	38	47.5	124	9	US-10-243-338-26	Sequence 26, Appl	197	35	43.8	2244	11	US-11-131-263-41	Sequence 41, Appl
125	38	47.5	124	9	US-10-243-345-26	Sequence 26, Appl	198	35	43.8	3712	11	US-11-019-711-48	Sequence 48, Appl
126	38	47.5	124	9	US-10-243-357-26	Sequence 26, Appl	199	35	43.8	3712	11	US-11-019-711-51	Sequence 51, Appl
127	38	47.5	124	9	US-10-245-083-26	Sequence 26, Appl	200	35	43.8	5179	11	US-11-108-172-1068	Sequence 1068, Ap
128	38	47.5	124	9	US-10-245-083-26	Sequence 26, Appl	201	34.5	43.1	57	9	US-10-613-744-38	Sequence 38, Appl
129	38	47.5	4913	9	US-10-453-372-1142	Sequence 1142, Ap	202	34.5	43.1	219	11	US-11-098-686-11237	Sequence 11237, A
130	38	47.5	4961	9	US-10-453-372-1132	Sequence 1132, Ap	203	34.5	43.1	261	9	US-10-613-744-18	Sequence 18, Appl
131	37	46.2	6	9	US-10-626-719-195	Sequence 195, App	204	34.5	43.1	663	9	US-10-486-316-2	Sequence 2, Appli
132	37	46.2	27	11	US-11-198-847-263	Sequence 263, App	205	34.5	43.1	663	9	US-10-486-316-6	Sequence 4, Appli
133	37	46.2	29	11	US-11-120-501-19	Sequence 19, Appl	206	34.5	43.1	663	9	US-10-486-316-6	Sequence 6, Appli
134	37	46.2	30	11	US-11-198-847-284	Sequence 284, App	207	34	42.5	21	11	US-11-198-847-290	Sequence 290, App
135	37	46.2	45	11	US-11-198-847-279	Sequence 279, App	208	34	42.5	21	11	US-11-198-847-292	Sequence 292, App
136	37	46.2	78	11	US-11-198-847-38	Sequence 38, Appl	209	34	42.5	21	11	US-11-198-847-340	Sequence 340, App
137	37	46.2	78	11	US-11-198-847-212	Sequence 212, App	210	34	42.5	22	11	US-11-198-847-258	Sequence 258, App
138	37	46.2	80	11	US-11-198-847-98	Sequence 98, Appl	211	34	42.5	22	11	US-11-198-847-299	Sequence 299, App
139	37	46.2	95	11	US-11-198-847-35	Sequence 35, Appl	212	34	42.5	23	11	US-11-198-847-244	Sequence 244, App
140	37	46.2	106	11	US-11-045-004-210	Sequence 210, App	213	34	42.5	25	9	US-10-644-807-394	Sequence 394, App
141	37	46.2	137	7	US-09-978-360A-765	Sequence 765, App	214	34	42.5	25	11	US-11-198-847-245	Sequence 245, App
142	37	46.2	240	11	US-11-264-096-1157	Sequence 1157, Ap	215	34	42.5	25	11	US-11-198-847-252	Sequence 252, App
143	37	46.2	240	11	US-11-264-096-1158	Sequence 1158, Ap	216	34	42.5	25	11	US-11-198-847-259	Sequence 259, App
144	37	46.2	990	11	US-11-188-298-2875	Sequence 2875, Ap	217	34	42.5	25	11	US-11-198-847-260	Sequence 260, App
145	37	46.2	1075	9	US-10-821-234-1202	Sequence 1202, Ap	218	34	42.5	25	11	US-11-198-847-261	Sequence 261, App
146	36.5	45.6	9	11	US-11-128-440-80	Sequence 80, Appl	219	34	42.5	25	11	US-11-198-847-262	Sequence 262, App
147	36.5	45.6	104	11	US-11-079-463-7249	Sequence 7249, Ap	220	34	42.5	26	11	US-11-198-847-247	Sequence 247, App
148	36	45.0	11	11	US-11-004-399-213	Sequence 213, App	221	34	42.5	26	11	US-11-198-847-249	Sequence 249, App
149	36	45.0	11	11	US-11-004-399-544	Sequence 544, App	222	34	42.5	26	11	US-11-198-847-295	Sequence 295, App
150	36	45.0	11	11	US-11-004-399-3838	Sequence 3838, Ap	223	34	42.5	26	11	US-11-198-847-296	Sequence 296, App
151	36	45.0	11	11	US-11-004-399-3962	Sequence 3962, Ap	224	34	42.5	26	11	US-11-198-847-303	Sequence 303, App
152	36	45.0	22	11	US-11-198-847-333	Sequence 333, App	225	34	42.5	27	11	US-11-198-847-297	Sequence 297, App
153	36	45.0	34	11	US-11-233-798-25	Sequence 25, Appl	226	34	42.5	28	11	US-11-198-847-246	Sequence 246, App
154	36	45.0	40	11	US-11-198-847-117	Sequence 117, App	227	34	42.5	28	11	US-11-198-847-255	Sequence 255, App
155	36	45.0	62	11	US-11-096-568A-8776	Sequence 8776, Ap	228	34	42.5	28	11	US-11-198-847-257	Sequence 257, App
156	36	45.0	326	9	US-11-233-798-6	Sequence 6, Appli	229	34	42.5	29	11	US-11-198-847-304	Sequence 304, App
157	36	45.0	363	9	US-10-838-616-10	Sequence 10, Appl	230	34	42.5	32	11	US-11-198-847-256	Sequence 256, App
158	36	45.0	439	10	US-11-181-115-33	Sequence 33, Appl	231	34	42.5	33	11	US-11-198-847-238	Sequence 238, App
159	36	45.0	439	10	US-11-181-115-45	Sequence 45, Appl	232	34	42.5	33	11	US-11-198-847-239	Sequence 239, App
160	36	45.0	504	11	US-11-098-686-11172	Sequence 11172, A	233	34	42.5	34	11	US-11-198-847-253	Sequence 253, App
161	36	45.0	519	11	US-11-079-463-5948	Sequence 5948, Ap	234	34	42.5	37	11	US-11-198-847-254	Sequence 254, App
162	36	45.0	553	11	US-11-090-439-18	Sequence 18, Appl	235	34	42.5	37	11	US-11-198-847-289	Sequence 289, App
163	36	45.0	1014	11	US-11-204-187-20	Sequence 20, Appl	236	34	42.5	38	11	US-11-198-847-250	Sequence 250, App
164	35.5	44.4	57	11	US-11-284-096-2064	Sequence 2064, Ap	237	34	42.5	38	11	US-11-198-847-251	Sequence 251, App
165	35.5	44.4	456	11	US-11-096-568A-12536	Sequence 12536, A	238	34	42.5	43	11	US-11-004-399-1653	Sequence 1653, Ap
166	35	43.8	26	11	US-11-009-840A-131	Sequence 131, App	239	34	42.5	54	11	US-11-033-105A-14	Sequence 14, App
167	35	43.8	26	11	US-11-009-873A-131	Sequence 131, App	240	34	42.5	67	11	US-11-004-399-1065	Sequence 1065, Ap

241	34	42.5	71	11	US-11-198-847-29	Sequence 29, Appl	314	34	42.5	361	11	US-11-188-298-2272	Sequence 2272, Ap
242	34	42.5	71	11	US-11-198-847-71	Sequence 71, Appl	315	34	42.5	369	11	US-11-096-568A-28936	Sequence 28936, A
243	34	42.5	71	11	US-11-198-847-74	Sequence 74, Appl	316	34	42.5	373	11	US-11-188-298-990	Sequence 990, App
244	34	42.5	72	11	US-11-198-847-20	Sequence 20, Appl	317	34	42.5	375	11	US-11-096-568A-6079	Sequence 6079, Ap
245	34	42.5	72	11	US-11-198-847-77	Sequence 77, Appl	318	34	42.5	378	11	US-11-096-568A-28935	Sequence 28935, A
246	34	42.5	72	11	US-11-198-847-113	Sequence 113, App	319	34	42.5	379	11	US-11-096-568A-27519	Sequence 27519, A
247	34	42.5	74	11	US-11-198-847-26	Sequence 26, Appl	320	34	42.5	407	11	US-11-188-298-15343	Sequence 15343, A
248	34	42.5	74	11	US-11-198-847-59	Sequence 59, Appl	321	34	42.5	419	11	US-11-096-568A-28934	Sequence 28934, A
249	34	42.5	74	11	US-11-198-847-104	Sequence 104, App	322	34	42.5	422	11	US-11-087-099-1471	Sequence 1471, Ap
250	34	42.5	74	11	US-11-198-847-107	Sequence 107, App	323	34	42.5	458	11	US-11-087-099-9012	Sequence 9012, Ap
251	34	42.5	74	11	US-11-198-847-140	Sequence 140, App	324	34	42.5	500	10	US-11-254-195-6	Sequence 6, Appl
252	34	42.5	74	11	US-11-198-847-170	Sequence 170, App	325	34	42.5	508	11	US-11-079-463-6229	Sequence 6229, Ap
253	34	42.5	80	11	US-11-198-847-23	Sequence 23, Appl	326	34	42.5	537	11	US-11-096-568A-12380	Sequence 12380, A
254	34	42.5	80	11	US-11-198-847-47	Sequence 47, Appl	327	34	42.5	550	11	US-11-096-568A-12379	Sequence 12379, A
255	34	42.5	80	11	US-11-198-847-65	Sequence 65, Appl	328	34	42.5	551	11	US-11-188-298-11009	Sequence 11009, A
256	34	42.5	80	11	US-11-198-847-86	Sequence 86, Appl	329	34	42.5	566	11	US-11-188-298-17049	Sequence 17049, A
257	34	42.5	80	11	US-11-198-847-110	Sequence 110, App	330	34	42.5	584	11	US-11-096-568A-12378	Sequence 12378, A
258	34	42.5	80	11	US-11-198-847-200	Sequence 200, App	331	34	42.5	642	9	US-10-995-561-631	Sequence 631, App
259	34	42.5	80	11	US-11-198-847-203	Sequence 203, App	332	34	42.5	657	9	US-10-995-561-622	Sequence 622, App
260	34	42.5	81	11	US-11-198-847-101	Sequence 101, App	333	34	42.5	657	11	US-11-193-561-27	Sequence 27, Appl
261	34	42.5	82	11	US-11-198-847-185	Sequence 185, App	334	34	42.5	657	11	US-11-193-771-27	Sequence 27, Appl
262	34	42.5	82	11	US-11-198-847-188	Sequence 188, App	335	34	42.5	657	11	US-11-193-789-27	Sequence 27, Appl
263	34	42.5	82	11	US-11-198-847-191	Sequence 191, App	336	34	42.5	657	11	US-11-193-806-27	Sequence 27, Appl
264	34	42.5	83	11	US-11-198-847-191	Sequence 191, App	337	34	42.5	657	11	US-11-193-857-27	Sequence 27, Appl
265	34	42.5	83	11	US-11-198-847-44	Sequence 44, Appl	338	34	42.5	706	11	US-11-188-298-11676	Sequence 11676, A
266	34	42.5	83	11	US-11-198-847-53	Sequence 53, Appl	339	34	42.5	708	11	US-11-188-298-15235	Sequence 15235, A
267	34	42.5	83	11	US-11-198-847-56	Sequence 56, Appl	340	34	42.5	816	11	US-11-087-099-10395	Sequence 10395, A
268	34	42.5	89	11	US-11-198-847-62	Sequence 62, Appl	341	34	42.5	818	11	US-11-144-985-13	Sequence 13, Appl
269	34	42.5	89	11	US-11-198-847-197	Sequence 197, App	342	34	42.5	847	11	US-11-087-099-3302	Sequence 3302, Ap
270	34	42.5	93	11	US-11-079-463-5874	Sequence 5874, Ap	343	34	42.5	967	11	US-11-124-367A-312	Sequence 312, App
271	34	42.5	105	9	US-10-821-234-1149	Sequence 1149, Ap	344	34	42.5	984	9	US-10-995-561-629	Sequence 629, App
272	34	42.5	109	11	US-11-198-847-143	Sequence 143, App	345	34	42.5	1020	11	US-11-144-985-3	Sequence 3, Appl
273	34	42.5	116	11	US-11-264-096-1934	Sequence 1934, A	346	34	42.5	1238	11	US-11-078-735-21	Sequence 21, Appl
274	34	42.5	118	11	US-11-072-512-3738	Sequence 3738, Ap	347	34	42.5	1238	11	US-11-050-346-66	Sequence 66, Appl
275	34	42.5	160	9	US-10-995-561-819	Sequence 819, App	348	34	42.5	1238	11	US-11-103-077-21	Sequence 21, Appl
276	34	42.5	177	11	US-11-087-099-4172	Sequence 4172, App	349	34	42.5	1238	11	US-11-058-066-21	Sequence 21, Appl
277	34	42.5	181	11	US-11-000-463-890	Sequence 890, App	350	34	42.5	1257	11	US-11-022-478-6	Sequence 6, Appl
278	34	42.5	182	11	US-11-000-463-418	Sequence 418, App	351	34	42.5	1369	11	US-11-124-367A-311	Sequence 311, App
279	34	42.5	194	11	US-11-079-463-7502	Sequence 7502, Ap	352	34	42.5	1276	11	US-11-193-561-25	Sequence 25, Appl
280	34	42.5	222	9	US-10-330-773-330	Sequence 330, App	353	34	42.5	2176	11	US-11-193-771-25	Sequence 25, Appl
281	34	42.5	224	11	US-11-096-568A-29718	Sequence 29718, A	354	34	42.5	2176	11	US-11-193-789-25	Sequence 25, Appl
282	34	42.5	227	11	US-11-087-099-2505	Sequence 2505, Ap	355	34	42.5	2176	11	US-11-193-806-25	Sequence 25, Appl
283	34	42.5	228	11	US-11-096-568A-29717	Sequence 29717, A	356	34	42.5	2176	11	US-11-193-857-25	Sequence 25, Appl
284	34	42.5	229	11	US-11-045-004-1407	Sequence 1407, Ap	357	34	42.5	2217	11	US-11-193-561-38	Sequence 38, Appl
285	34	42.5	233	11	US-11-087-099-1775	Sequence 1775, Ap	358	34	42.5	2217	11	US-11-193-771-38	Sequence 38, Appl
286	34	42.5	233	11	US-11-087-099-3052	Sequence 3052, Ap	359	34	42.5	2217	11	US-11-193-789-38	Sequence 38, Appl
287	34	42.5	233	11	US-11-087-099-6395	Sequence 6395, Ap	360	34	42.5	2217	11	US-11-193-806-38	Sequence 38, Appl
288	34	42.5	233	11	US-11-087-099-6579	Sequence 6579, Ap	361	34	42.5	2217	11	US-11-193-857-38	Sequence 38, Appl
289	34	42.5	233	11	US-11-087-099-7318	Sequence 7318, Ap	362	34	42.5	2223	11	US-11-193-561-2	Sequence 2, Appl
290	34	42.5	234	11	US-11-087-099-3077	Sequence 3077, Ap	363	34	42.5	2223	11	US-11-193-789-2	Sequence 2, Appl
291	34	42.5	235	11	US-11-087-099-3482	Sequence 3482, Ap	364	34	42.5	2223	11	US-11-193-806-2	Sequence 2, Appl
292	34	42.5	235	11	US-11-087-099-4175	Sequence 4175, Ap	365	34	42.5	2223	11	US-11-193-857-2	Sequence 2, Appl
293	34	42.5	235	11	US-11-087-099-4588	Sequence 4588, Ap	366	34	42.5	2236	9	US-10-995-561-633	Sequence 633, App
294	34	42.5	235	11	US-11-087-099-5684	Sequence 5684, Ap	367	34	42.5	2236	11	US-11-193-561-23	Sequence 23, Appl
295	34	42.5	235	11	US-11-087-099-8574	Sequence 8574, Ap	368	34	42.5	2236	11	US-11-193-771-23	Sequence 23, Appl
296	34	42.5	236	11	US-11-087-099-7684	Sequence 7684, Ap	369	34	42.5	2236	11	US-11-193-789-23	Sequence 23, Appl
297	34	42.5	236	11	US-11-087-099-8761	Sequence 8761, Ap	370	34	42.5	2236	11	US-11-193-806-23	Sequence 23, Appl
298	34	42.5	236	11	US-11-054-515-1299	Sequence 1299, Ap	371	34	42.5	2236	11	US-11-193-857-23	Sequence 23, Appl
299	34	42.5	249	11	US-11-266-444-1299	Sequence 1299, Ap	372	34	42.5	2330	11	US-11-193-561-21	Sequence 21, Appl
300	34	42.5	252	11	US-11-087-099-10413	Sequence 10413, A	373	34	42.5	2330	11	US-11-193-771-21	Sequence 21, Appl
301	34	42.5	252	11	US-11-087-099-11103	Sequence 11103, A	374	34	42.5	2330	11	US-11-193-806-21	Sequence 21, Appl
302	34	42.5	262	11	US-11-087-099-8793	Sequence 8793, Ap	375	34	42.5	2330	11	US-11-193-857-21	Sequence 21, Appl
303	34	42.5	324	11	US-11-087-099-8410	Sequence 8410, Ap	376	34	42.5	2330	11	US-11-193-806-21	Sequence 21, Appl
304	34	42.5	329	11	US-11-096-568A-27521	Sequence 27521, A	377	34	42.5	2330	11	US-11-193-857-21	Sequence 21, Appl
305	34	42.5	338	11	US-11-096-568A-27520	Sequence 27520, A	378	34	42.5	2335	9	US-10-995-561-623	Sequence 623, App
306	34	42.5	353	10	US-11-254-195-4	Sequence 4, Appl	379	34	42.5	2355	9	US-10-995-561-627	Sequence 627, App
307	34	42.5	354	9	US-10-131-826A-400	Sequence 400, App	380	34	42.5	2355	11	US-11-193-561-19	Sequence 19, Appl
308	34	42.5	354	9	US-10-973-115B-400	Sequence 400, App	381	34	42.5	2355	11	US-11-193-771-19	Sequence 19, Appl
309	34	42.5	354	9	US-10-216-161A-178	Sequence 178, App	382	34	42.5	2355	11	US-11-193-789-19	Sequence 19, Appl
310	34	42.5	354	9	US-10-137-873A-400	Sequence 400, App	383	34	42.5	2355	11	US-11-193-806-19	Sequence 19, Appl
311	34	42.5	354	9	US-10-152-370-400	Sequence 400, App	384	34	42.5	2355	11	US-11-193-857-19	Sequence 19, Appl
312	34	42.5	354	9	US-11-290-153-400	Sequence 400, App	385	34	42.5	2384	9	US-10-821-234-1545	Sequence 1545, Ap
313	34	42.5	354	11			386	34	42.5	2386	9	US-10-995-561-626	Sequence 626, App

387	34	42.5	2421	11	US-11-193-561-17	Sequence 17, Appl	460	33	41.2	79	11	US-11-198-847-149	Sequence 149, App
388	34	42.5	2421	11	US-11-193-771-17	Sequence 17, Appl	461	33	41.2	79	11	US-11-198-847-224	Sequence 224, App
389	34	42.5	2421	11	US-11-193-789-17	Sequence 17, Appl	462	33	41.2	82	11	US-11-198-847-119	Sequence 119, App
390	34	42.5	2421	11	US-11-193-806-17	Sequence 17, Appl	463	33	41.2	82	11	US-11-198-847-122	Sequence 122, App
391	34	42.5	2421	11	US-11-193-857-17	Sequence 17, Appl	464	33	41.2	86	11	US-11-123-896-227	Sequence 227, App
392	34	42.5	2477	11	US-11-193-561-15	Sequence 15, Appl	465	33	41.2	86	11	US-11-123-896-230	Sequence 230, App
393	34	42.5	2477	11	US-11-193-771-15	Sequence 15, Appl	466	33	41.2	86	11	US-11-123-896-233	Sequence 233, App
394	34	42.5	2477	11	US-11-193-789-15	Sequence 15, Appl	467	33	41.2	87	9	US-10-745-586-21	Sequence 21, Appl
395	34	42.5	2477	11	US-11-193-806-15	Sequence 15, Appl	468	33	41.2	93	11	US-11-198-847-131	Sequence 131, App
396	34	42.5	2477	11	US-11-193-857-15	Sequence 15, Appl	469	33	41.2	100	11	US-11-072-512-2364	Sequence 2364, App
397	33.5	41.9	16	11	US-11-198-847-309	Sequence 309, App	470	33	41.2	108	11	US-11-102-512-11	Sequence 11, Appl
398	33.5	41.9	276	11	US-11-054-281-85	Sequence 85, Appl	471	33	41.2	108	11	US-11-102-512-82	Sequence 82, Appl
399	33.5	41.9	277	11	US-11-054-281-84	Sequence 84, Appl	472	33	41.2	109	11	US-11-072-512-3088	Sequence 3088, App
400	33.5	41.9	367	9	US-10-455-772-500	Sequence 500, App	473	33	41.2	110	11	US-11-198-847-167	Sequence 167, App
401	33.5	41.9	479	11	US-11-087-099-6677	Sequence 6677, App	474	33	41.2	110	11	US-11-198-847-173	Sequence 173, App
402	33.5	41.9	479	11	US-11-198-298-17131	Sequence 17131, App	475	33	41.2	133	9	US-10-644-807-297	Sequence 297, App
403	33.5	41.9	2613	9	US-10-455-772-530	Sequence 530, App	476	33	41.2	143	9	US-10-475-075-822	Sequence 822, App
404	33.5	41.9	2628	9	US-10-455-772-502	Sequence 502, App	477	33	41.2	145	9	US-10-194-487-580	Sequence 580, App
405	33.5	41.9	2715	11	US-11-096-051-2	Sequence 2, Appli	478	33	41.2	145	9	US-10-195-883-580	Sequence 580, App
406	33.5	41.9	2721	9	US-10-455-772-522	Sequence 522, App	479	33	41.2	145	9	US-10-195-888-580	Sequence 580, App
407	33.5	41.9	2721	11	US-11-096-051-10	Sequence 10, Appl	480	33	41.2	145	9	US-10-195-889-580	Sequence 580, App
408	33.5	41.9	2725	9	US-10-455-772-486	Sequence 486, App	481	33	41.2	131	11	US-11-079-463-9380	Sequence 9380, App
409	33.5	41.9	2725	9	US-10-455-772-526	Sequence 526, App	482	33	41.2	215	11	US-11-096-568A-25682	Sequence 25682, App
410	33.5	41.9	2725	9	US-10-455-772-544	Sequence 544, App	483	33	41.2	222	9	US-10-517-939-168	Sequence 168, App
411	33.5	41.9	2725	9	US-10-455-772-546	Sequence 546, App	484	33	41.2	222	11	US-11-087-099-7292	Sequence 7292, App
412	33.5	41.9	2725	9	US-10-455-772-548	Sequence 548, App	485	33	41.2	234	11	US-11-098-686-10787	Sequence 10787, App
413	33.5	41.9	2725	9	US-10-455-772-550	Sequence 550, App	486	33	41.2	239	11	US-11-000-463-875	Sequence 875, App
414	33.5	41.9	2725	9	US-10-455-772-552	Sequence 552, App	487	33	41.2	239	11	US-11-000-463-876	Sequence 876, App
415	33.5	41.9	2725	11	US-11-096-051-8	Sequence 8, Appli	488	33	41.2	250	11	US-11-079-463-5894	Sequence 5894, App
416	33	41.2	5	11	US-11-249-847-104	Sequence 104, Appl	489	33	41.2	254	7	US-09-810-501-69	Sequence 69, Appl
417	33	41.2	7	11	US-11-129-741-3979	Sequence 3979, App	490	33	41.2	254	11	US-11-167-831-16	Sequence 16, Appl
418	33	41.2	10	11	US-11-104-923A-9	Sequence 9, Appli	491	33	41.2	254	11	US-11-167-831-17	Sequence 17, Appl
419	33	41.2	11	9	US-10-895-064-182	Sequence 182, App	492	33	41.2	254	11	US-11-167-831-18	Sequence 18, Appl
420	33	41.2	11	11	US-11-129-741-182	Sequence 182, App	493	33	41.2	254	11	US-11-167-831-19	Sequence 19, Appl
421	33	41.2	11	11	US-11-129-741-3115	Sequence 3115, App	494	33	41.2	254	11	US-11-167-831-22	Sequence 22, Appl
422	33	41.2	13	11	US-11-198-847-306	Sequence 306, App	495	33	41.2	261	11	US-11-000-463-404	Sequence 404, App
423	33	41.2	18	9	US-10-895-064-235	Sequence 235, App	496	33	41.2	327	11	US-11-233-798-2	Sequence 2, Appli
424	33	41.2	18	11	US-11-129-741-235	Sequence 235, App	497	33	41.2	335	11	US-11-188-298-18806	Sequence 18806, App
425	33	41.2	18	11	US-11-129-741-3167	Sequence 3167, App	498	33	41.2	350	9	US-10-517-939-176	Sequence 176, App
426	33	41.2	21	11	US-11-198-847-291	Sequence 291, App	499	33	41.2	354	9	US-10-517-939-216	Sequence 216, App
427	33	41.2	28	11	US-11-198-847-240	Sequence 240, App	500	33	41.2	354	9	US-10-838-616-16	Sequence 16, Appl
428	33	41.2	28	11	US-11-198-847-241	Sequence 241, App	501	33	41.2	358	9	US-10-517-939-182	Sequence 182, App
429	33	41.2	28	11	US-11-198-847-242	Sequence 242, App	502	33	41.2	361	11	US-11-096-568A-5295	Sequence 5295, App
430	33	41.2	28	11	US-11-198-847-243	Sequence 243, App	503	33	41.2	362	11	US-11-079-463-7253	Sequence 7253, App
431	33	41.2	29	11	US-11-198-847-283	Sequence 283, App	504	33	41.2	370	11	US-11-229-371-15	Sequence 15, Appl
432	33	41.2	30	11	US-11-198-847-298	Sequence 298, App	505	33	41.2	370	11	US-11-228-923-15	Sequence 15, Appl
433	33	41.2	32	11	US-11-198-847-298	Sequence 298, App	506	33	41.2	370	11	US-11-228-923-15	Sequence 15, Appl
434	33	41.2	32	11	US-11-198-847-268	Sequence 268, App	507	33	41.2	374	11	US-11-228-875-15	Sequence 15, Appl
435	33	41.2	34	11	US-11-233-798-26	Sequence 26, Appl	508	33	41.2	376	11	US-11-096-568A-5294	Sequence 5294, App
436	33	41.2	37	11	US-11-198-847-287	Sequence 287, App	509	33	41.2	378	11	US-11-229-371-42	Sequence 42, App
437	33	41.2	37	11	US-11-198-847-288	Sequence 288, App	510	33	41.2	378	11	US-11-229-371-88	Sequence 88, Appl
438	33	41.2	38	11	US-11-198-847-293	Sequence 293, App	511	33	41.2	378	11	US-11-228-923-42	Sequence 42, Appl
439	33	41.2	38	11	US-11-198-847-294	Sequence 294, App	512	33	41.2	378	11	US-11-228-923-88	Sequence 88, Appl
440	33	41.2	45	11	US-11-198-847-90	Sequence 90, Appl	513	33	41.2	378	11	US-11-228-875-42	Sequence 42, Appl
441	33	41.2	46	11	US-11-123-896-297	Sequence 297, App	514	33	41.2	378	11	US-11-228-875-88	Sequence 88, Appl
442	33	41.2	50	11	US-11-198-847-302	Sequence 302, App	515	33	41.2	394	11	US-11-229-371-94	Sequence 94, Appl
443	33	41.2	51	11	US-11-123-896-296	Sequence 296, App	516	33	41.2	394	11	US-11-228-923-94	Sequence 94, Appl
444	33	41.2	52	11	US-11-000-463-339	Sequence 339, App	517	33	41.2	394	11	US-11-228-875-94	Sequence 94, Appl
445	33	41.2	52	11	US-11-000-463-811	Sequence 811, App	518	33	41.2	400	11	US-11-229-371-2	Sequence 2, Appli
446	33	41.2	58	11	US-11-123-896-228	Sequence 228, App	519	33	41.2	400	11	US-11-228-923-2	Sequence 2, Appli
447	33	41.2	58	11	US-11-123-896-231	Sequence 231, App	520	33	41.2	400	11	US-11-228-875-2	Sequence 2, Appli
448	33	41.2	58	11	US-11-123-896-234	Sequence 234, App	521	33	41.2	414	11	US-11-229-371-45	Sequence 45, Appl
449	33	41.2	64	11	US-11-096-568A-8330	Sequence 8330, App	522	33	41.2	414	11	US-11-229-371-89	Sequence 89, Appl
450	33	41.2	66	9	US-10-948-571-104	Sequence 104, App	523	33	41.2	414	11	US-11-228-923-45	Sequence 45, Appl
451	33	41.2	68	9	US-11-096-568A-8329	Sequence 8329, App	524	33	41.2	414	11	US-11-228-923-89	Sequence 89, Appl
452	33	41.2	70	7	US-09-978-360A-502	Sequence 502, App	525	33	41.2	414	11	US-11-228-875-45	Sequence 45, Appl
453	33	41.2	70	11	US-11-198-847-17	Sequence 17, Appl	526	33	41.2	414	11	US-11-228-875-89	Sequence 89, Appl
454	33	41.2	75	11	US-11-198-847-68	Sequence 68, Appl	527	33	41.2	420	11	US-11-228-875-90	Sequence 90, Appl
455	33	41.2	75	11	US-11-198-847-164	Sequence 164, App	528	33	41.2	420	11	US-11-228-923-90	Sequence 90, Appl
456	33	41.2	78	11	US-11-198-847-125	Sequence 125, App	529	33	41.2	425	11	US-11-228-875-90	Sequence 90, Appl
457	33	41.2	78	11	US-11-198-847-128	Sequence 128, App	530	33	41.2	425	11	US-11-037-243-92	Sequence 92, Appl
458	33	41.2	78	11	US-11-198-847-215	Sequence 215, App	531	33	41.2	432	9	US-10-517-939-178	Sequence 178, App
459	33	41.2	78	11	US-11-198-847-218	Sequence 218, App	532	33	41.2	436	9	US-10-131-826A-404	Sequence 404, App

533	33	41.2	436	9	US-10-973-115B-404	Sequence 404, App	606	32	40.0	29	11	US-11-198-847-305	Sequence 305, App
534	33	41.2	436	9	US-10-216-161A-442	Sequence 442, App	607	32	40.0	31	11	US-11-096-568A-2691	Sequence 2691, App
535	33	41.2	436	9	US-10-137-873A-404	Sequence 404, App	608	32	40.0	36	11	US-11-198-847-301	Sequence 301, App
536	33	41.2	436	9	US-10-152-370-404	Sequence 404, App	609	32	40.0	40	11	US-11-198-847-264	Sequence 264, App
537	33	41.2	436	11	US-11-290-153-404	Sequence 404, App	610	32	40.0	49	11	US-11-198-847-270	Sequence 270, App
538	33	41.2	439	11	US-11-096-568A-10315	Sequence 10315, A	611	32	40.0	49	11	US-11-198-847-271	Sequence 271, App
539	33	41.2	446	11	US-11-229-371-92	Sequence 92, Appl	612	32	40.0	49	11	US-11-198-847-272	Sequence 272, App
540	33	41.2	446	11	US-11-228-923-92	Sequence 92, Appl	613	32	40.0	56	11	US-11-207-078-127	Sequence 127, App
541	33	41.2	446	11	US-11-228-875-92	Sequence 1201, Ap	614	32	40.0	69	7	US-09-378-360A-704	Sequence 704, App
542	33	41.2	447	11	US-11-264-096-1201	Sequence 1201, Ap	615	32	40.0	80	11	US-11-198-847-83	Sequence 83, Appl
543	33	41.2	470	11	US-11-229-371-91	Sequence 91, Appl	616	32	40.0	80	11	US-11-198-847-152	Sequence 152, App
544	33	41.2	470	11	US-11-228-923-91	Sequence 91, Appl	617	32	40.0	80	11	US-11-198-847-161	Sequence 161, App
545	33	41.2	470	11	US-11-228-875-91	Sequence 91, Appl	618	32	40.0	81	9	US-10-821-234-1613	Sequence 1613, Ap
546	33	41.2	482	11	US-11-229-371-87	Sequence 87, Appl	619	32	40.0	81	11	US-11-198-847-158	Sequence 158, App
547	33	41.2	482	11	US-11-229-371-177	Sequence 177, App	620	32	40.0	85	11	US-11-198-847-134	Sequence 134, App
548	33	41.2	482	11	US-11-228-923-87	Sequence 87, Appl	621	32	40.0	90	11	US-11-198-847-80	Sequence 80, Appl
549	33	41.2	482	11	US-11-228-923-177	Sequence 177, App	622	32	40.0	90	11	US-11-096-568A-8059	Sequence 8059, Ap
550	33	41.2	482	11	US-11-228-875-87	Sequence 87, Appl	623	32	40.0	96	7	US-09-978-360A-654	Sequence 654, App
551	33	41.2	482	11	US-11-228-875-177	Sequence 177, App	624	32	40.0	102	11	US-11-264-096-1133	Sequence 1133, Ap
552	33	41.2	504	11	US-11-096-568A-10314	Sequence 10314, A	625	32	40.0	102	11	US-11-264-096-1185	Sequence 1185, Ap
553	33	41.2	509	11	US-11-055-309A-12	Sequence 12, Appl	626	32	40.0	108	9	US-10-925-366A-203	Sequence 203, App
554	33	41.2	509	11	US-11-072-175-219	Sequence 219, App	627	32	40.0	108	11	US-11-098-758-203	Sequence 203, App
555	33	41.2	518	11	US-11-135-603-7	Sequence 7, Appli	628	32	40.0	112	9	US-10-392-234A-44	Sequence 44, Appl
556	33	41.2	528	11	US-11-096-568A-10313	Sequence 10313, A	629	32	40.0	121	9	US-10-789-273-9	Sequence 9, Appli
557	33	41.2	532	9	US-10-821-234-918	Sequence 918, App	630	32	40.0	123	9	US-10-982-440-17	Sequence 17, Appl
558	33	41.2	542	9	US-10-517-939-362	Sequence 262, App	631	32	40.0	126	9	US-10-771-257-45	Sequence 45, Appl
559	33	41.2	614	11	US-11-110-748-2	Sequence 2, Appli	632	32	40.0	126	11	US-11-127-677-43	Sequence 43, Appl
560	33	41.2	620	11	US-11-096-568A-27709	Sequence 27709, A	633	32	40.0	128	9	US-10-771-257-55	Sequence 55, Appl
561	33	41.2	649	11	US-11-096-568A-27708	Sequence 27708, A	634	32	40.0	128	11	US-11-127-677-53	Sequence 53, Appl
562	33	41.2	664	11	US-11-045-004-224	Sequence 224, App	635	32	40.0	129	11	US-11-056-186-2	Sequence 2, Appli
563	33	41.2	666	11	US-11-188-298-3594	Sequence 3594, App	636	32	40.0	134	11	US-11-079-463-6842	Sequence 6842, Ap
564	33	41.2	666	11	US-11-188-298-7174	Sequence 7174, Ap	637	32	40.0	153	11	US-11-079-463-5585	Sequence 5585, Ap
565	33	41.2	678	11	US-11-096-568A-27775	Sequence 27775, A	638	32	40.0	159	11	US-11-000-463-333	Sequence 333, App
566	33	41.2	689	11	US-11-096-568A-27707	Sequence 27707, A	639	32	40.0	168	11	US-11-200-389-3	Sequence 3, Appli
567	33	41.2	702	11	US-11-188-298-2417	Sequence 2417, Ap	640	32	40.0	169	11	US-11-200-389-9	Sequence 9, Appli
568	33	41.2	707	11	US-11-096-568A-27774	Sequence 27774, A	641	32	40.0	169	11	US-11-200-389-11	Sequence 11, Appl
569	33	41.2	747	11	US-11-096-568A-27773	Sequence 27773, A	642	32	40.0	175	11	US-11-096-568A-2290	Sequence 2290, Ap
570	33	41.2	794	11	US-11-264-096-1292	Sequence 1292, Ap	643	32	40.0	178	11	US-11-188-298-15956	Sequence 15956, A
571	33	41.2	798	11	US-11-079-463-10034	Sequence 10034, A	644	32	40.0	191	11	US-11-200-389-2	Sequence 2, Appli
572	33	41.2	829	9	US-10-644-807-209	Sequence 209, App	645	32	40.0	192	11	US-11-072-512-3462	Sequence 3462, Ap
573	33	41.2	849	11	US-11-188-298-3853	Sequence 3853, Ap	646	32	40.0	193	9	US-10-204-639-8	Sequence 8, Appli
574	33	41.2	852	11	US-11-104-923A-5	Sequence 5, Appli	647	32	40.0	196	9	US-10-131-826A-168	Sequence 168, App
575	33	41.2	915	9	US-10-131-826A-294	Sequence 294, App	648	32	40.0	196	9	US-10-973-115B-168	Sequence 168, App
576	33	41.2	915	9	US-10-973-115B-294	Sequence 294, App	649	32	40.0	196	9	US-10-137-873A-168	Sequence 168, App
577	33	41.2	915	9	US-10-137-873A-294	Sequence 294, App	650	32	40.0	196	9	US-10-152-370-168	Sequence 168, App
578	33	41.2	915	9	US-10-152-370-294	Sequence 294, App	651	32	40.0	196	11	US-11-290-153-168	Sequence 168, App
579	33	41.2	915	11	US-11-290-153-294	Sequence 294, App	652	32	40.0	200	11	US-11-264-096-2040	Sequence 2040, Ap
580	33	41.2	934	11	US-11-264-096-1291	Sequence 1291, Ap	653	32	40.0	220	11	US-11-188-298-1762	Sequence 1762, Ap
581	33	41.2	956	11	US-11-113-424-39	Sequence 39, Appl	654	32	40.0	241	11	US-11-096-568A-6296	Sequence 6296, Ap
582	33	41.2	1188	11	US-11-188-298-20484	Sequence 20484, A	655	32	40.0	247	11	US-11-188-298-16159	Sequence 16159, A
583	33	41.2	2107	9	US-10-995-561-827	Sequence 827, App	656	32	40.0	251	11	US-11-054-515-945	Sequence 945, App
584	33	41.2	2480	9	US-10-995-561-825	Sequence 825, App	657	32	40.0	251	11	US-11-266-444-945	Sequence 945, App
585	33	41.2	3116	9	US-10-995-561-826	Sequence 826, App	658	32	40.0	258	9	US-10-537-002-13	Sequence 13, Appl
586	32.5	40.6	9	11	US-11-041-676A-5	Sequence 5, Appli	659	32	40.0	266	9	US-10-467-657-5258	Sequence 5258, Ap
587	32.5	40.6	9	11	US-11-041-676A-8	Sequence 8, Appli	660	32	40.0	267	11	US-11-096-568A-17567	Sequence 17567, A
588	32.5	40.6	35	11	US-11-004-399-1121	Sequence 1121, Ap	661	32	40.0	270	11	US-11-096-568A-13455	Sequence 13455, A
589	32.5	40.6	115	11	US-11-108-135-37	Sequence 37, Appl	662	32	40.0	271	9	US-10-821-234-922	Sequence 922, App
590	32.5	40.6	115	11	US-11-126-978-37	Sequence 37, Appl	663	32	40.0	281	9	US-10-055-877-125	Sequence 125, App
591	32.5	40.6	124	9	US-10-982-440-25	Sequence 25, Appl	664	32	40.0	281	9	US-10-055-877-262	Sequence 262, App
592	32.5	40.6	130	9	US-10-993-543-144	Sequence 144, App	665	32	40.0	281	11	US-11-087-177-15	Sequence 15, Appl
593	32.5	40.6	178	11	US-11-079-463-6828	Sequence 6828, Ap	666	32	40.0	281	11	US-11-087-177-17	Sequence 17, Appl
594	32.5	40.6	289	11	US-11-096-568A-24861	Sequence 24861, A	667	32	40.0	289	11	US-11-096-568A-13454	Sequence 13454, A
595	32.5	40.6	290	11	US-11-096-568A-24860	Sequence 24860, A	668	32	40.0	291	11	US-11-096-568A-13453	Sequence 13453, A
596	32.5	40.6	309	11	US-11-096-568A-24859	Sequence 24859, A	669	32	40.0	289	11	US-11-045-004-2757	Sequence 2757, App
597	32.5	40.6	473	9	US-10-509-464-5	Sequence 5, Appli	670	32	40.0	305	11	US-11-087-099-534	Sequence 534, App
598	32.5	40.6	473	9	US-10-509-464-6	Sequence 6, Appli	671	32	40.0	313	11	US-11-096-568A-6295	Sequence 6295, Ap
599	32.5	40.6	515	11	US-11-135-603-9	Sequence 9, Appli	672	32	40.0	318	9	US-10-986-405-307	Sequence 307, App
600	32.5	40.6	816	11	US-11-090-439-48	Sequence 48, Appl	673	32	40.0	330	11	US-11-087-099-5512	Sequence 5512, Ap
601	32.5	40.6	850	11	US-11-037-243-108	Sequence 108, App	674	32	40.0	334	11	US-11-096-568A-6294	Sequence 6294, Ap
602	32.5	40.6	1115	9	US-10-922-232B-60	Sequence 60, Appl	675	32	40.0	361	11	US-11-188-298-10934	Sequence 10934, A
603	32.5	40.6	6738	9	US-10-922-232B-56	Sequence 56, Appl	676	32	40.0	371	11	US-11-205-904-4	Sequence 4, Appli
604	32	40.0	8	11	US-11-007-772A-35	Sequence 35, Appl	677	32	40.0	377	11	US-11-188-298-5869	Sequence 5869, Ap
605	32	40.0	23	11	US-11-264-096-823	Sequence 823, App	678	32	40.0	404	11	US-11-045-004-2830	Sequence 2830, Ap

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680	32	40.0	419	11	US-11-230-321-2	Sequence 2, Appl	753	31	38.8	9	11	US-11-198-847-319	Sequence 317, App
681	32	40.0	422	11	US-11-169-041-224	Sequence 224, Appl	754	31	38.8	10	11	US-11-198-847-319	Sequence 319, App
682	32	40.0	427	11	US-11-079-463-5237	Sequence 5237, Ap	755	31	38.8	11	11	US-11-198-847-314	Sequence 314, App
683	32	40.0	429	9	US-10-523-038-48	Sequence 48, Appl	756	31	38.8	13	9	US-10-895-064-61	Sequence 61, Appl
684	32	40.0	429	11	US-11-129-442-40	Sequence 40, Appl	757	31	38.8	13	11	US-11-129-741-61	Sequence 61, Appl
685	32	40.0	488	11	US-11-024-959-474	Sequence 474, Appl	758	31	38.8	13	11	US-11-129-741-2998	Sequence 2998, Ap
686	32	40.0	490	11	US-11-198-886-25	Sequence 25, Appl	759	31	38.8	14	11	US-11-232-439-52	Sequence 52, Appl
687	32	40.0	504	11	US-11-188-298-3106	Sequence 3106, Ap	760	31	38.8	16	11	US-11-198-847-310	Sequence 310, App
688	32	40.0	508	11	US-11-024-959-467	Sequence 467, App	761	31	38.8	19	11	US-11-198-847-265	Sequence 265, App
689	32	40.0	513	11	US-11-096-568A-28076	Sequence 28076, A	762	31	38.8	22	9	US-10-939-890-397	Sequence 397, App
690	32	40.0	523	9	US-10-453-372-1006	Sequence 1006, Ap	763	31	38.8	22	9	US-10-939-890-412	Sequence 412, App
691	32	40.0	523	9	US-10-453-372-1008	Sequence 1008, Ap	764	31	38.8	22	9	US-10-895-064-671	Sequence 671, App
692	32	40.0	531	11	US-11-096-568A-28075	Sequence 28075, A	765	31	38.8	22	11	US-11-129-741-671	Sequence 671, App
693	32	40.0	555	11	US-11-096-568A-28074	Sequence 28074, A	766	31	38.8	26	11	US-11-198-847-248	Sequence 248, App
694	32	40.0	575	11	US-11-072-512-3176	Sequence 3176, Ap	767	31	38.8	28	11	US-11-120-501-34	Sequence 34, Appl
695	32	40.0	595	9	US-10-745-586-61	Sequence 61, Appl	768	31	38.8	32	11	US-11-264-096-130	Sequence 130, App
696	32	40.0	620	11	US-11-072-512-2045	Sequence 2045, Ap	769	31	38.8	37	11	US-11-129-741-3675	Sequence 3675, Ap
697	32	40.0	626	11	US-11-188-298-298	Sequence 298, App	770	31	38.8	40	11	US-11-198-847-33	Sequence 33, Appl
698	32	40.0	645	11	US-11-072-512-3418	Sequence 3418, Ap	771	31	38.8	40	11	US-11-198-847-42	Sequence 42, Appl
699	32	40.0	675	11	US-11-072-512-3810	Sequence 3810, Ap	772	31	38.8	41	11	US-11-198-847-269	Sequence 269, App
700	32	40.0	690	11	US-11-079-463-6770	Sequence 6770, Ap	773	31	38.8	51	11	US-11-172-571-29	Sequence 29, Appl
701	32	40.0	693	9	US-10-714-995-24	Sequence 24, Appl	774	31	38.8	52	9	US-10-475-075-801	Sequence 801, App
702	32	40.0	790	9	US-10-763-712A-75	Sequence 75, Appl	775	31	38.8	52	11	US-11-000-463-358	Sequence 358, App
703	32	40.0	1070	9	US-10-537-002-14	Sequence 14, Appl	776	31	38.8	52	11	US-11-000-463-830	Sequence 830, App
704	32	40.0	1073	9	US-10-537-002-11	Sequence 11, Appl	777	31	38.8	58	11	US-11-096-568A-3534	Sequence 3534, Ap
705	32	40.0	1327	11	US-11-019-711-70	Sequence 70, Appl	778	31	38.8	59	9	US-10-914-391A-3	Sequence 3, Appl
706	32	40.0	1493	9	US-10-330-773-502	Sequence 502, App	779	31	38.8	63	11	US-11-096-568A-3533	Sequence 3533, Ap
707	32	40.0	1826	9	US-10-330-773-499	Sequence 499, App	780	31	38.8	65	11	US-11-096-568A-1604	Sequence 1604, Ap
708	31.5	39.4	38	11	US-11-068-783-81	Sequence 81, Appl	781	31	38.8	66	11	US-11-172-536-1	Sequence 1, Appl
709	31.5	39.4	83	11	US-11-123-896-466	Sequence 466, App	782	31	38.8	66	11	US-11-172-536-4	Sequence 4, Appl
710	31.5	39.4	91	11	US-11-096-568A-28552	Sequence 28552, A	783	31	38.8	66	11	US-11-172-536-10	Sequence 10, Appl
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712	31.5	39.4	95	11	US-11-079-463-8009	Sequence 8009, Ap	785	31	38.8	69	11	US-11-198-847-50	Sequence 50, Appl
713	31.5	39.4	100	11	US-11-096-568A-11154	Sequence 11154, A	786	31	38.8	72	11	US-11-198-847-155	Sequence 155, App
714	31.5	39.4	107	11	US-11-096-568A-11152	Sequence 11152, A	787	31	38.8	75	11	US-11-229-769-171	Sequence 171, App
715	31.5	39.4	107	11	US-11-188-298-20880	Sequence 20880, A	788	31	38.8	76	11	US-11-172-571-28	Sequence 28, Appl
716	31.5	39.4	125	11	US-11-049-536-242	Sequence 242, App	789	31	38.8	79	11	US-11-198-847-206	Sequence 206, App
717	31.5	39.4	125	11	US-11-199-739-242	Sequence 242, App	790	31	38.8	79	11	US-11-264-096-1737	Sequence 1737, Ap
718	31.5	39.4	128	11	US-11-049-536-234	Sequence 234, App	791	31	38.8	80	11	US-11-096-568A-8560	Sequence 8560, Ap
719	31.5	39.4	128	11	US-11-199-739-234	Sequence 234, App	792	31	38.8	83	11	US-11-087-099-900	Sequence 900, App
720	31.5	39.4	129	11	US-11-049-536-554	Sequence 554, App	793	31	38.8	86	11	US-11-096-568A-5887	Sequence 5887, App
721	31.5	39.4	129	11	US-11-199-739-554	Sequence 554, App	794	31	38.8	89	11	US-11-004-399-2701	Sequence 2701, Ap
722	31.5	39.4	137	9	US-10-993-543-76	Sequence 76, Appl	795	31	38.8	90	11	US-11-087-099-8565	Sequence 8565, Ap
723	31.5	39.4	171	11	US-11-128-900-83	Sequence 83, Appl	796	31	38.8	93	11	US-11-096-568A-1429	Sequence 1429, Ap
724	31.5	39.4	174	11	US-11-128-900-12	Sequence 12, Appl	797	31	38.8	93	11	US-11-096-568A-8559	Sequence 8559, Ap
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726	31.5	39.4	249	11	US-11-054-515-413	Sequence 413, App	799	31	38.8	94	11	US-11-087-099-7557	Sequence 7557, Ap
727	31.5	39.4	249	11	US-11-054-515-633	Sequence 633, App	800	31	38.8	96	11	US-11-188-298-11586	Sequence 11586, A
728	31.5	39.4	249	11	US-11-266-444-413	Sequence 413, App	801	31	38.8	97	11	US-11-172-536-2	Sequence 2, Appl
729	31.5	39.4	249	11	US-11-266-444-633	Sequence 633, App	802	31	38.8	97	11	US-11-079-463-7540	Sequence 7540, Ap
730	31.5	39.4	275	11	US-11-264-096-1910	Sequence 1910, Ap	803	31	38.8	100	11	US-11-087-099-3327	Sequence 3327, Ap
731	31.5	39.4	275	11	US-11-264-096-1911	Sequence 1911, Ap	804	31	38.8	100	11	US-11-087-099-10374	Sequence 10374, A
732	31.5	39.4	364	11	US-11-140-284-38	Sequence 38, Appl	805	31	38.8	101	11	US-11-087-099-266	Sequence 266, App
733	31.5	39.4	370	11	US-11-140-284-36	Sequence 36, Appl	806	31	38.8	104	11	US-11-087-099-3565	Sequence 3565, Ap
734	31.5	39.4	445	9	US-10-063-703-32	Sequence 32, Appl	807	31	38.8	104	11	US-11-188-298-14340	Sequence 14340, A
735	31.5	39.4	445	9	US-10-194-487-148	Sequence 148, App	808	31	38.8	105	11	US-11-172-536-11	Sequence 11, Appl
736	31.5	39.4	445	9	US-10-195-883-148	Sequence 148, App	809	31	38.8	105	11	US-11-072-512-2746	Sequence 2746, Ap
737	31.5	39.4	445	9	US-10-195-888-148	Sequence 148, App	810	31	38.8	105	11	US-11-188-298-16587	Sequence 16587, A
738	31.5	39.4	445	9	US-10-195-889-148	Sequence 148, App	811	31	38.8	107	8	US-10-546-594-82	Sequence 82, Appl
739	31.5	39.4	445	11	US-11-102-240-32	Sequence 32, Appl	812	31	38.8	107	11	US-11-105-268-22	Sequence 22, Appl
740	31.5	39.4	445	11	US-11-103-195-32	Sequence 32, Appl	813	31	38.8	107	11	US-11-105-268-24	Sequence 24, Appl
741	31.5	39.4	481	11	US-11-227-177-1	Sequence 1, Appl	814	31	38.8	109	11	US-11-096-568A-8558	Sequence 8558, Ap
742	31.5	39.4	517	9	US-10-055-877-304	Sequence 304, App	815	31	38.8	110	9	US-10-332-234A-38	Sequence 38, Appl
743	31.5	39.4	648	9	US-10-330-773-825	Sequence 825, App	816	31	38.8	110	9	US-10-644-807-423	Sequence 423, App
744	31.5	39.4	737	11	US-11-087-099-665	Sequence 665, App	817	31	38.8	110	11	US-11-049-536-336	Sequence 336, App
745	31.5	39.4	845	9	US-11-221-470-54	Sequence 54, Appl	818	31	38.8	110	11	US-11-172-536-5	Sequence 5, Appl
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748	31.5	39.4	2723	11	US-11-129-741-388	Sequence 388, App	821	31	38.8	112	11	US-11-188-298-3404	Sequence 3404, Ap
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827	31	38.8	114	11	US-11-087-099-10263	Sequence 10263, A	900	31	38.8	328	11	US-11-096-568A-1749	Sequence 1749, Ap
828	31	38.8	115	9	US-10-546-594-115	Sequence 115, App	901	31	38.8	329	11	US-11-096-568A-34102	Sequence 34102, A
829	31	38.8	117	8	US-10-546-595-252	Sequence 252, App	902	31	38.8	329	11	US-11-096-568A-1748	Sequence 1748, Ap
830	31	38.8	122	10	US-11-254-182-74	Sequence 74, App	903	31	38.8	329	11	US-11-096-568A-34101	Sequence 34101, A
831	31	38.8	122	11	US-11-120-338-24	Sequence 24, App	904	31	38.8	332	11	US-11-096-568A-31701	Sequence 31701, A
832	31	38.8	122	11	US-11-143-077-24	Sequence 24, App	905	31	38.8	333	11	US-11-188-298-3343	Sequence 3343, Ap
833	31	38.8	122	11	US-11-143-386-24	Sequence 24, App	906	31	38.8	337	11	US-11-096-568A-7705	Sequence 7705, Ap
834	31	38.8	122	11	US-11-187-364-36	Sequence 36, App	907	31	38.8	340	11	US-11-096-568A-7704	Sequence 7704, Ap
835	31	38.8	122	11	US-11-208-422-45	Sequence 45, App	908	31	38.8	343	11	US-11-000-463-936	Sequence 936, App
836	31	38.8	123	8	US-10-546-594-65	Sequence 64, App	909	31	38.8	350	9	US-10-515-604-2	Sequence 2, Appli
837	31	38.8	123	8	US-10-546-594-66	Sequence 66, App	910	31	38.8	350	11	US-11-153-880-4	Sequence 4, Appli
838	31	38.8	123	8	US-10-546-594-68	Sequence 68, App	911	31	38.8	350	11	US-11-233-113-4	Sequence 4, Appli
839	31	38.8	123	8	US-10-546-594-70	Sequence 70, App	912	31	38.8	350	11	US-11-249-422-4	Sequence 4, Appli
840	31	38.8	123	11	US-11-012-353-73	Sequence 73, App	913	31	38.8	353	11	US-11-096-568A-28198	Sequence 28198, A
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842	31	38.8	126	8	US-10-546-594-119	Sequence 119, App	915	31	38.8	376	11	US-11-096-568A-7703	Sequence 7703, Ap
843	31	38.8	126	11	US-11-087-099-11619	Sequence 11619, A	916	31	38.8	376	11	US-11-096-568A-16238	Sequence 16238, A
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845	31	38.8	129	10	US-11-096-568A-5886	Sequence 5886, Ap	918	31	38.8	384	11	US-11-096-568A-21965	Sequence 21965, A
846	31	38.8	129	10	US-11-183-218-14	Sequence 14, App	919	31	38.8	386	11	US-11-096-568A-28197	Sequence 28197, A
847	31	38.8	129	11	US-11-183-205-14	Sequence 14, App	920	31	38.8	390	11	US-11-096-568A-25267	Sequence 25267, A
848	31	38.8	136	11	US-11-087-099-2791	Sequence 2791, Ap	921	31	38.8	397	11	US-11-096-568A-1747	Sequence 1747, Ap
849	31	38.8	143	9	US-10-821-234-1216	Sequence 1216, Ap	922	31	38.8	397	11	US-11-096-568A-34100	Sequence 34100, A
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851	31	38.8	146	11	US-11-087-099-4208	Sequence 4208, Ap	924	31	38.8	401	11	US-11-096-568A-31700	Sequence 31700, A
852	31	38.8	148	11	US-11-087-099-3712	Sequence 3712, Ap	925	31	38.8	403	11	US-11-072-512-2454	Sequence 2454, Ap
853	31	38.8	148	11	US-11-087-099-7556	Sequence 7556, Ap	926	31	38.8	405	11	US-11-096-568A-25266	Sequence 25266, A
854	31	38.8	148	11	US-11-153-071-24	Sequence 24, App	927	31	38.8	406	11	US-11-188-298-436	Sequence 436, App
855	31	38.8	150	9	US-10-496-284-57	Sequence 57, App	928	31	38.8	419	8	US-10-505-928-436	Sequence 436, App
856	31	38.8	152	11	US-11-079-463-6202	Sequence 6202, Ap	929	31	38.8	419	8	US-10-505-928-864	Sequence 864, App
857	31	38.8	152	11	US-11-144-947-558	Sequence 558, App	930	31	38.8	419	9	US-10-921-793-68	Sequence 68, Appl
858	31	38.8	157	11	US-11-087-099-11010	Sequence 11010, A	931	31	38.8	419	9	US-10-931-198-68	Sequence 68, Appl
859	31	38.8	164	9	US-10-131-826A-314	Sequence 314, App	932	31	38.8	419	9	US-10-942-042-68	Sequence 68, Appl
860	31	38.8	164	9	US-10-973-115B-314	Sequence 314, App	933	31	38.8	419	11	US-11-064-769-2	Sequence 2, Appli
861	31	38.8	164	9	US-10-137-873A-314	Sequence 314, App	934	31	38.8	419	11	US-11-153-880-2	Sequence 2, Appli
862	31	38.8	164	9	US-10-152-370-314	Sequence 314, App	935	31	38.8	419	11	US-11-064-740A-22	Sequence 22, Appli
863	31	38.8	164	11	US-11-290-153-314	Sequence 314, App	936	31	38.8	419	11	US-11-075-400-8	Sequence 8, Appli
864	31	38.8	173	9	US-10-644-807-339	Sequence 339, App	937	31	38.8	419	11	US-11-211-724-2	Sequence 2, Appli
865	31	38.8	173	11	US-11-096-568A-5885	Sequence 5885, Ap	938	31	38.8	419	11	US-11-226-005-2	Sequence 2, Appli
866	31	38.8	178	9	US-10-784-004-729	Sequence 729, App	939	31	38.8	419	11	US-11-129-076-11	Sequence 11, Appl
867	31	38.8	185	11	US-11-144-947-404	Sequence 404, App	940	31	38.8	419	11	US-11-074-373-2	Sequence 2, Appli
868	31	38.8	186	9	US-10-644-807-245	Sequence 245, App	941	31	38.8	419	11	US-11-076-427A-6	Sequence 6, Appli
869	31	38.8	189	11	US-11-096-568A-22034	Sequence 22034, A	942	31	38.8	419	11	US-11-233-119-2	Sequence 2, Appli
870	31	38.8	194	9	US-10-873-528-136	Sequence 136, App	943	31	38.8	419	11	US-11-233-119-18	Sequence 18, Appl
871	31	38.8	194	11	US-11-045-004-374	Sequence 374, App	944	31	38.8	419	11	US-11-075-047A-83	Sequence 83, Appl
872	31	38.8	209	11	US-11-096-568A-3423	Sequence 3423, Ap	945	31	38.8	419	11	US-11-249-422-2	Sequence 2, Appli
873	31	38.8	227	11	US-11-087-099-9875	Sequence 9875, Ap	946	31	38.8	424	11	US-11-096-568A-25265	Sequence 25265, A
874	31	38.8	229	11	US-11-096-568A-31702	Sequence 31702, A	947	31	38.8	431	11	US-11-092-140-6	Sequence 6, Appli
875	31	38.8	231	11	US-11-096-568A-23503	Sequence 23503, A	948	31	38.8	434	11	US-11-096-568A-28196	Sequence 28196, A
876	31	38.8	234	11	US-11-076-164-11	Sequence 11, Appl	949	31	38.8	436	9	US-10-455-772-914	Sequence 914, App
877	31	38.8	234	11	US-11-096-568A-7573	Sequence 7573, Ap	950	31	38.8	436	11	US-11-079-463-6661	Sequence 6661, App
878	31	38.8	236	9	US-10-926-406A-9	Sequence 9, Appli	951	31	38.8	437	11	US-11-194-246-324	Sequence 324, App
879	31	38.8	236	11	US-11-087-099-11734	Sequence 11734, A	952	31	38.8	446	11	US-11-096-568A-12783	Sequence 12783, A
880	31	38.8	239	9	US-10-496-284-11	Sequence 11, Appl	953	31	38.8	446	11	US-11-096-568A-21964	Sequence 21964, A
881	31	38.8	242	9	US-10-926-406A-10	Sequence 10, Appl	954	31	38.8	449	11	US-11-096-568A-8176	Sequence 8176, Ap
882	31	38.8	242	11	US-11-087-099-11398	Sequence 11398, A	955	31	38.8	451	10	US-11-254-182-72	Sequence 72, Appl
883	31	38.8	249	9	US-10-926-406A-7	Sequence 7, Appli	956	31	38.8	451	11	US-11-120-338-25	Sequence 25, Appl
884	31	38.8	256	11	US-11-087-099-5474	Sequence 5474, Ap	957	31	38.8	451	11	US-11-143-077-22	Sequence 22, Appl
885	31	38.8	263	11	US-11-087-099-5632	Sequence 5632, Ap	958	31	38.8	451	11	US-11-143-386-25	Sequence 25, Appl
886	31	38.8	263	11	US-11-087-099-10938	Sequence 10938, A	959	31	38.8	451	11	US-11-187-364-29	Sequence 29, Appl
887	31	38.8	266	11	US-11-000-463-464	Sequence 464, App	960	31	38.8	451	11	US-11-187-364-34	Sequence 34, Appl
888	31	38.8	266	11	US-11-188-298-13105	Sequence 13105, A	961	31	38.8	452	10	US-11-254-182-66	Sequence 66, Appl
889	31	38.8	267	11	US-11-096-568A-7572	Sequence 7572, Ap	962	31	38.8	452	11	US-11-120-338-17	Sequence 17, Appl
890	31	38.8	268	11	US-11-045-004-2466	Sequence 2466, Ap	963	31	38.8	452	11	US-11-107-028-47	Sequence 47, Appl
891	31	38.8	269	11	US-11-000-463-403	Sequence 403, App	964	31	38.8	452	11	US-11-106-820-45	Sequence 45, Appl
892	31	38.8	280	11	US-11-264-096-1818	Sequence 1818, Ap	965	31	38.8	452	11	US-11-143-386-17	Sequence 17, Appl
893	31	38.8	282	11	US-11-079-463-6874	Sequence 6874, Ap	966	31	38.8	452	11	US-11-143-386-17	Sequence 17, Appl
894	31	38.8	289	11	US-11-096-568A-16240	Sequence 16240, A	967	31	38.8	452	11	US-11-208-423-46	Sequence 46, Appl
895	31	38.8	293	11	US-11-087-099-5836	Sequence 5836, Ap	968	31	38.8	455	9	US-10-063-703-4	Sequence 4, Appli
896	31	38.8	295	11	US-11-096-568A-16239	Sequence 16239, A	969	31	38.8	455	9	US-10-194-487-14	Sequence 14, Appl
897	31	38.8	301	11	US-11-079-463-6653	Sequence 6653, Ap	970	31	38.8	455	9	US-10-195-883-14	Sequence 14, Appl

771 31 38.8 455 9 US-10-195-888-14 Sequence 14, Appl
772 31 38.8 455 9 US-10-195-889-14 Sequence 14, Appl
773 31 38.8 455 9 US-10-216-161A-430 Sequence 430, App
774 31 38.8 455 11 US-11-102-240-4 Sequence 4, Appl
775 31 38.8 455 11 US-11-103-195-4 Sequence 4, Appl
776 31 38.8 456 9 US-10-641-678-51 Sequence 51, Appl
777 31 38.8 458 11 US-11-079-463-8126 Sequence 8126, Ap
778 31 38.8 467 11 US-11-037-243-63 Sequence 63, Appl
779 31 38.8 472 8 US-10-546-594-130 Sequence 130, App
780 31 38.8 480 11 US-11-096-568A-12782 Sequence 12782, A
781 31 38.8 484 11 US-11-264-096-706 Sequence 706, App
782 31 38.8 489 11 US-11-087-099-8528 Sequence 8528, Ap
783 31 38.8 490 11 US-11-079-463-5351 Sequence 5351, Ap
784 31 38.8 491 11 US-11-087-099-6452 Sequence 6452, Ap
785 31 38.8 497 11 US-11-087-099-6452 Sequence 6452, Ap
786 31 38.8 505 11 US-11-087-099-362 Sequence 362, App
787 31 38.8 516 11 US-11-087-099-10758 Sequence 10758, A
788 31 38.8 519 11 US-11-188-298-408 Sequence 408, App
789 31 38.8 527 8 US-10-505-928-266 Sequence 266, App
790 31 38.8 527 9 US-10-821-234-1574 Sequence 1574, Ap
791 31 38.8 535 9 US-10-641-678-61 Sequence 61, Appl
792 31 38.8 537 11 US-11-087-099-3945 Sequence 3945, Ap
793 31 38.8 537 11 US-11-087-099-10695 Sequence 10695, A
794 31 38.8 544 11 US-11-165-226-126 Sequence 126, App
795 31 38.8 548 9 US-10-055-877-320 Sequence 320, App
796 31 38.8 549 11 US-11-188-298-3355 Sequence 3355, Ap
797 31 38.8 559 11 US-11-087-099-11163 Sequence 11163, A
798 31 38.8 565 11 US-11-087-099-3971 Sequence 3971, Ap
799 31 38.8 566 11 US-11-065-695-2 Sequence 2, Appl
1000 31 38.8 569 11 US-11-188-298-3937 Sequence 3937, Ap

ALIGNMENTS

RESULT 1
US-10-626-719-158
; Sequence 158, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 158
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-626-719-158
Query Match 66.2%; Score 53; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11

Db 1 FCFWKTCCT 8

RESULT 2
US-10-626-719-159
; Sequence 159, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 159
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-626-719-159

Query Match 62.5%; Score 50; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTCCT 11
Db 1 FCFWKTCCT 8

RESULT 3
US-10-506-223-16
; Sequence 16, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: FUSELIER, JOSEPH A.
; APPLICANT: COY, DAVID H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 3

```
; OTHER INFORMATION: Xaa at position 3 is Nle
US-10-506-223-16

Query Match      62.5%; Score 50; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTCCT 11
Db 6 CFWKTCCT 12

RESULT 4
US-10-506-223-17
; Sequence 17, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa at position 3 is Nle
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 6,11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
US-10-506-223-17

Query Match      62.5%; Score 50; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTCCT 11
Db 6 CFWKTCCT 12

RESULT 5
US-10-506-223-39
; Sequence 39, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0

; OTHER INFORMATION: Xaa at position 3 is Nle
US-10-506-223-39

Query Match      62.5%; Score 50; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTCCT 11
Db 6 CFWKTCCT 12

RESULT 6
US-10-506-223-40
; Sequence 40, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa at position 3 is Nle
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 6,11
; OTHER INFORMATION: Cys at positions 6 and 11 are circularized
US-10-506-223-40

Query Match      62.5%; Score 50; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTCCT 11
Db 6 CFWKTCCT 12

RESULT 7
US-10-506-223-21
; Sequence 21, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
```

FILE REFERENCE: 07005/007002
CURRENT APPLICATION NUMBER: US/10/506,223
CURRENT FILING DATE: 2004-08-31
PRIOR APPLICATION NUMBER: PCT/03/06657
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,831
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: VARIANT
LOCATION: 4
OTHER INFORMATION: Xaa at position 4 is Nle
US-10-506-223-21

Query Match 62.5%; Score 50; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTKT 11
| | | | |
Db 7 CFWKTKT 13

RESULT 8
US-10-506-223-22
Sequence 22, Application US/10506223
Publication No. US20060009622A1
GENERAL INFORMATION:
APPLICANT: Fuselier, Joseph A.
TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
TITLE OF INVENTION: Agents and Biologically Active Peptides
FILE REFERENCE: 07005/007002
CURRENT APPLICATION NUMBER: US/10/506,223
CURRENT FILING DATE: 2004-08-31
PRIOR APPLICATION NUMBER: PCT/03/06657
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,831
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: VARIANT
LOCATION: 4
OTHER INFORMATION: Xaa at position 4 is Nle
US-10-506-223-22

Query Match 62.5%; Score 50; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTKT 11
| | | | |
Db 7 CFWKTKT 13

RESULT 9
US-10-506-223-23
Sequence 23, Application US/10506223
Publication No. US20060009622A1
GENERAL INFORMATION:
APPLICANT: Fuselier, Joseph A.
TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
TITLE OF INVENTION: Agents and Biologically Active Peptides
FILE REFERENCE: 07005/007002
CURRENT APPLICATION NUMBER: US/10/506,223
CURRENT FILING DATE: 2004-08-31
PRIOR APPLICATION NUMBER: PCT/03/06657
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,831
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: VARIANT
LOCATION: 5
OTHER INFORMATION: Xaa at position 5 is Nle
US-10-506-223-23

Query Match 62.5%; Score 50; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTKT 11
| | | | |
Db 8 CFWKTKT 14

RESULT 10
US-10-506-223-24
Sequence 24, Application US/10506223
Publication No. US20060009622A1
GENERAL INFORMATION:
APPLICANT: Fuselier, Joseph A.
TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
TITLE OF INVENTION: Agents and Biologically Active Peptides
FILE REFERENCE: 07005/007002
CURRENT APPLICATION NUMBER: US/10/506,223
CURRENT FILING DATE: 2004-08-31
PRIOR APPLICATION NUMBER: PCT/03/06657
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,831
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: VARIANT
LOCATION: 6
OTHER INFORMATION: Xaa at position 6 is Nle
US-10-506-223-24

Query Match 62.5%; Score 50; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CFWKTCCT 11
| | | | |
Db 9 CFWKTCCT 15

RESULT 11
US-10-506-223-25
; Sequence 25, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa at position 7 is Nle
US-10-506-223-25

Query Match 62.5%; Score 50; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CFWKTCCT 11
| | | | |
Db 10 CFWKTCCT 16

RESULT 12
US-10-506-223-26
; Sequence 26, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 8
; OTHER INFORMATION: Xaa at position 8 is Nle
US-10-506-223-26

Query Match 62.5%; Score 50; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CFWKTCCT 11
| | | | |
Db 11 CFWKTCCT 17

RESULT 13
US-10-506-223-27
; Sequence 27, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 9
; OTHER INFORMATION: Xaa at position 9 is Nle
US-10-506-223-27

Query Match 62.5%; Score 50; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CFWKTCCT 11
| | | | |
Db 12 CFWKTCCT 18

RESULT 14
US-10-506-223-28
; Sequence 28, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-506-223-28

```
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa at position 10 is Nle
US-10-506-223-28

Query Match      62.5%; Score 50; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CPWKTCCT 11
Db 13 CPWKTCCT 19

RESULT 15
US-10-506-223-29
; Sequence 29, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 11
; OTHER INFORMATION: Xaa at position 11 is Nle
US-10-506-223-29

Query Match      62.5%; Score 50; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CPWKTCCT 11
Db 14 CPWKTCCT 20

RESULT 16
US-10-506-223-30
; Sequence 30, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
```

```
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 12
; OTHER INFORMATION: Xaa at position 12 is Nle
US-10-506-223-30

Query Match      62.5%; Score 50; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CPWKTCCT 11
Db 15 CPWKTCCT 21

RESULT 17
US-10-506-223-31
; Sequence 31, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 13
; OTHER INFORMATION: Xaa at position 13 is Nle
US-10-506-223-31

Query Match      62.5%; Score 50; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CPWKTCCT 11
Db 16 CPWKTCCT 22

RESULT 18
US-10-506-223-32
; Sequence 32, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
```

; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 14
; OTHER INFORMATION: Xaa at position 14 is Nle
US-10-506-223-32

Query Match 62.5%; Score 50; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CPWKTCCT 11
Db 17 CPWKTCCT 23

RESULT 19
US-10-506-223-33
; Sequence 33, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 15
; OTHER INFORMATION: Xaa at position 15 is Nle
US-10-506-223-33

Query Match 62.5%; Score 50; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CPWKTCCT 11
Db 18 CPWKTCCT 24

RESULT 20
US-10-506-223-34
; Sequence 34, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides

; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 16
; OTHER INFORMATION: Xaa at position 16 is Nle
US-10-506-223-34

Query Match 62.5%; Score 50; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CPWKTCCT 11
Db 19 CPWKTCCT 25

RESULT 21
US-10-506-223-35
; Sequence 35, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 17
; OTHER INFORMATION: Xaa at position 17 is Nle
US-10-506-223-35

Query Match 62.5%; Score 50; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CPWKTCCT 11
Db 20 CPWKTCCT 26

RESULT 22
US-10-506-223-36
; Sequence 36, Application US/10506223
; Publication No. US20060009622A1

; GENERAL INFORMATION:
 ; APPLICANT: Fuselier, Joseph A.
 ; APPLICANT: Coy, David H.
 ; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
 ; TITLE OF INVENTION: Agents and Biologically Active Peptides
 ; FILE REFERENCE: 07005/007002
 ; CURRENT APPLICATION NUMBER: US/10/506,223
 ; CURRENT FILING DATE: 2004-08-31
 ; PRIOR APPLICATION NUMBER: PCT/03/06657
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/360,831
 ; PRIOR FILING DATE: 2002-03-01
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 36
 ; LENGTH: 27
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 18
 ; OTHER INFORMATION: Xaa at position 18 is Nle
 US-10-506-223-36

Query Match 62.5%; Score 50; DB 9; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.86;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 CFWKTCT 11
 Db 21 CFWKTCT 27

RESULT 23
 US-11-198-847-234
 ; Sequence 234, Application US/11198847
 ; Publication No. US20050271589A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Jones, Robert M.
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Olivera, Baldomero M.
 ; TITLE OF INVENTION: B-Superfamily Conotoxins
 ; FILE REFERENCE: 2314-296
 ; CURRENT APPLICATION NUMBER: US/11/198,847
 ; CURRENT FILING DATE: 2005-08-08
 ; PRIOR APPLICATION NUMBER: US 10/838,226
 ; PRIOR FILING DATE: 2004-05-05
 ; PRIOR APPLICATION NUMBER: US 10/058,053
 ; PRIOR FILING DATE: 2000-01-29
 ; PRIOR APPLICATION NUMBER: US 60/264323
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 340
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 234
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Conus geographus
 US-11-198-847-234

Query Match 61.3%; Score 49; DB 11; Length 21;
 Best Local Similarity 75.0%; Pred. No. 0.99;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YCFWKTCCT 11
 Db 2 CFWKSCT 9

RESULT 24
 US-11-198-847-231
 ; Sequence 231, Application US/11198847
 ; Publication No. US20050271589A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Jones, Robert M.
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Olivera, Baldomero M.
 ; TITLE OF INVENTION: B-Superfamily Conotoxins
 ; FILE REFERENCE: 2314-296
 ; CURRENT APPLICATION NUMBER: US/11/198,847
 ; CURRENT FILING DATE: 2005-08-08
 ; PRIOR APPLICATION NUMBER: US 10/838,226
 ; PRIOR FILING DATE: 2004-05-05
 ; PRIOR APPLICATION NUMBER: US 10/058,053
 ; PRIOR FILING DATE: 2000-01-29
 ; PRIOR APPLICATION NUMBER: US 60/264323
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 340
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 231
 ; LENGTH: 40
 ; TYPE: PRT
 ; ORGANISM: Conus geographus
 US-11-198-847-231

Query Match 61.3%; Score 49; DB 11; Length 40;
 Best Local Similarity 75.0%; Pred. No. 1.5;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YCFWKTCCT 11
 Db 21 CFWKSCT 28

RESULT 25
 US-11-198-847-116
 ; Sequence 116, Application US/11198847
 ; Publication No. US20050271589A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Jones, Robert M.
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Olivera, Baldomero M.
 ; TITLE OF INVENTION: B-Superfamily Conotoxins
 ; FILE REFERENCE: 2314-296
 ; CURRENT APPLICATION NUMBER: US/11/198,847
 ; CURRENT FILING DATE: 2005-08-08
 ; PRIOR APPLICATION NUMBER: US 10/838,226
 ; PRIOR FILING DATE: 2004-05-05
 ; PRIOR APPLICATION NUMBER: US 10/058,053
 ; PRIOR FILING DATE: 2000-01-29
 ; PRIOR APPLICATION NUMBER: US 60/264323
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 340
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 116
 ; LENGTH: 93
 ; TYPE: PRT
 ; ORGANISM: Conus geographus
 US-11-198-847-116

Query Match 61.3%; Score 49; DB 11; Length 93;
 Best Local Similarity 75.0%; Pred. No. 2.6;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YCFWKTCCT 11
 Db 21 CFWKSCT 9

Db 71 FCFWKSCT 78

RESULT 26

US-10-626-719-156
; Sequence 156, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARTSEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENGER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-626-719-156

Query Match 60.0%; Score 48; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YCFWKTKCT 11
:|||||
Db 1 FCFWKVCT 8

RESULT 27

US-11-198-847-280
; Sequence 280, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Conus cinereus
US-11-198-847-280

Query Match 57.5%; Score 46; DB 11; Length 45;
Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 CFWKTCT 11
:|||||
Db 12 CFWKSCT 18

RESULT 28

US-11-198-847-89
; Sequence 89, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Conus cinereus
US-11-198-847-89

Query Match 57.5%; Score 46; DB 11; Length 95;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 CFWKTCT 11
:|||||
Db 62 CFWKSCT 68

RESULT 29

US-10-506-223-37
; Sequence 37, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fueseller, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; TITLE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-506-223-37

Query Match 56.2%; Score 45; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
| | | | |
Db 1 CFWKTC 6

RESULT 30
US-10-506-223-38
; Sequence 38, Application US/10506223
; Publication No. US2006009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: COY, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MOD_RES
; LOCATION: 1, 6
; OTHER INFORMATION: Cys at positions 1 and 6 are circularized

US-10-506-223-38

Query Match 56.2%; Score 45; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CFWKTC 10
| | | | |
Db 1 CFWKTC 6

RESULT 31
US-10-626-719-157
; Sequence 157, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSENIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE OF INVENTION: FOR OPTICAL DIAGNOSIS
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 157
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-626-719-157

Query Match 56.2%; Score 45; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.9e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCFWKTC 11
: | : | : | : |
Db 1 FCFWKVCT 8

RESULT 32
US-11-198-847-322
; Sequence 322, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 322
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-322

Query Match 55.0%; Score 44; DB 11; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.9;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
: | : | : | : |
Db 1 FCFWKSC 7

RESULT 33
US-11-198-847-232
; Sequence 232, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05

; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 232
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Conus tulipa
US-11-198-847-232

Query Match 55.0%; Score 44; DB 11; Length 21;
Best Local Similarity 71.4%; Pred. No. 4.6;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:
Db 2 FCFWKSC 8

RESULT 34

US-11-198-847-233
; Sequence 233, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 233
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-233

Query Match 55.0%; Score 44; DB 11; Length 21;
Best Local Similarity 71.4%; Pred. No. 4.6;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:
Db 2 FCFWKSC 8

RESULT 35

US-11-198-847-229
; Sequence 229, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847

; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 229
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus tulipa
US-11-198-847-229

Query Match 55.0%; Score 44; DB 11; Length 40;
Best Local Similarity 71.4%; Pred. No. 7.1;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:
Db 21 FCFWKSC 27

RESULT 36

US-11-198-847-230
; Sequence 230, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 230
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus magus
US-11-198-847-230

Query Match 55.0%; Score 44; DB 11; Length 40;
Best Local Similarity 71.4%; Pred. No. 7.1;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
:||||:
Db 21 FCFWKSC 27

RESULT 37

US-11-198-847-32
; Sequence 32, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.

; TITLE OF INVENTION: B-Superfamily Conotoxins
 ; FILE REFERENCE: 2314-296
 ; CURRENT APPLICATION NUMBER: US/11/198,847
 ; CURRENT FILING DATE: 2005-08-08
 ; PRIOR APPLICATION NUMBER: US 10/838,226
 ; PRIOR FILING DATE: 2004-05-05
 ; PRIOR APPLICATION NUMBER: US 10/058,053
 ; PRIOR FILING DATE: 2000-01-29
 ; PRIOR APPLICATION NUMBER: US 60/264323
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 340
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 93
 ; TYPE: PRT
 ; ORGANISM: Conus tulipa
 US-11-198-847-32

Query Match 55.0%; Score 44; DB 11; Length 93;
 Best Local Similarity 71.4%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
 :|||||:
 Db 71 PCFWKSC 77

RESULT 38
 US-11-198-847-41
 ; Sequence 41, Application US/11/198847
 ; Publication No. US20050271589A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Jones, Robert M.
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Oliviera, Baldomero M.
 ; TITLE OF INVENTION: B-Superfamily Conotoxins
 ; FILE REFERENCE: 2314-296
 ; CURRENT APPLICATION NUMBER: US/11/198,847
 ; CURRENT FILING DATE: 2005-08-08
 ; PRIOR APPLICATION NUMBER: US 10/838,226
 ; PRIOR FILING DATE: 2004-05-05
 ; PRIOR APPLICATION NUMBER: US 10/058,053
 ; PRIOR FILING DATE: 2000-01-29
 ; PRIOR APPLICATION NUMBER: US 60/264323
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 340
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 41
 ; LENGTH: 93
 ; TYPE: PRT
 ; ORGANISM: Conus magus
 US-11-198-847-41

Query Match 55.0%; Score 44; DB 11; Length 93;
 Best Local Similarity 71.4%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCFWKTC 10
 :|||||:
 Db 71 PCFWKSC 77

RESULT 39
 US-11-045-004-1161
 ; Sequence 1161, Application US/11/045004
 ; Publication No. US20060078901A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BUCHRIESER, CARMEN
 ; APPLICANT: FRANGEUL, LIONEL
 ; APPLICANT: COUVE, ELISABETH

; APPLICANT: RUSNIOK, CHRISTOPHE
 ; APPLICANT: PSIH, HAFIDA
 ; APPLICANT: DEHOUX, PIERRE
 ; APPLICANT: DUSSURGET, OLIVIER
 ; APPLICANT: CHETOUANI, FARID
 ; APPLICANT: NEDJARI, HAFED
 ; APPLICANT: GLASER, PHILIPPE
 ; APPLICANT: KUNST, FRANCK
 ; APPLICANT: COSSART, PASCALE
 ; APPLICANT: DANIELS, JUSTIN
 ; APPLICANT: GOEBEL, WERNER
 ; APPLICANT: KREFT, JURGEN
 ; APPLICANT: KUHN, MICHAEL
 ; APPLICANT: NG, EVA
 ; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
 ; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
 ; APPLICANT: GARRIDO-GARCIA, PATRICIA
 ; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
 ; APPLICANT: AMEND, ALEXANDRA
 ; APPLICANT: CHAKRABORTY, TRINAD
 ; APPLICANT: DOMANN, EUGEN
 ; APPLICANT: HAIN, THORSTEN
 ; APPLICANT: BERCHE, PATRICK
 ; APPLICANT: CHARBIT, ALAIN
 ; APPLICANT: DURANT, LIONEL
 ; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
 ; APPLICANT: BAQUERO, FERNANDO
 ; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
 ; APPLICANT: GOMEZ-LOPEZ, NURIA
 ; APPLICANT: MADUENIO, ENCARNIA
 ; APPLICANT: PABLOS, BETRIZ DE
 ; APPLICANT: WESLAND, JURGEN
 ; APPLICANT: KARST, UWE
 ; APPLICANT: ENTIAN, KARL-DIETER
 ; APPLICANT: HAUF, JORG
 ; APPLICANT: ROSE, MATTHIAS
 ; APPLICANT: VOSS, HAMUT
 ; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
 ; FILE REFERENCE: 05394.0018-02
 ; CURRENT APPLICATION NUMBER: US/11/045,004
 ; CURRENT FILING DATE: 2005-01-28
 ; PRIOR APPLICATION NUMBER: 10/637,657
 ; PRIOR FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: 10/257,023
 ; PRIOR FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: PCT/FR01/01118
 ; PRIOR FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: FR 00/04,629
 ; PRIOR FILING DATE: 2000-04-11
 ; NUMBER OF SEQ ID NOS: 2854
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1161
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Listeria monocytogenes
 US-11-045-004-1161

Query Match 53.8%; Score 43; DB 11; Length 285;
 Best Local Similarity 65.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YYCYCPWKT 9
 :|||||:
 Db 61 YSIYCPWKS 69

RESULT 40
 US-11-096-568A-25706
 ; Sequence 25706, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nickolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

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; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25706
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(566)
; OTHER INFORMATION: Ceres Seq. ID no. 13493007
; US-11-096-568A-25706

Query Match      53.8%; Score 43; DB 11; Length 566;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YCYCFWK 8
      :|:|:|:
Db      218 FCFCFWR 224

RESULT 41
US-11-096-568A-25705
; Sequence 25705, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25705
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(593)
; OTHER INFORMATION: Ceres Seq. ID no. 13493006
; US-11-096-568A-25705

Query Match      53.8%; Score 43; DB 11; Length 593;
Best Local Similarity 57.1%; Pred. No. 57;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YCYCFWK 8
      :|:|:|:
Db      245 FCFCFWR 251

RESULT 42
US-11-096-568A-25704
; Sequence 25704, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25704
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)..(648)
; OTHER INFORMATION: Ceres Seq. ID no. 13493005
; US-11-096-568A-25704

Query Match      53.8%; Score 43; DB 11; Length 648;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YCYCFWK 8
      :|:|:|:
Db      300 FCFCFWR 306

RESULT 43
US-11-188-298-15828
; Sequence 15828, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 15828
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(131)
; OTHER INFORMATION: unsure at all Xaa locations
; US-11-188-298-15828

Query Match      52.5%; Score 42; DB 11; Length 131;
Best Local Similarity 55.6%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 YCYCFWK 9
      :|:|:|:
Db      19 YSCYCIWNS 27

RESULT 44
US-10-242-586-12
; Sequence 12, Application US/10242586
; Publication No. US20060073548A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C21
; CURRENT APPLICATION NUMBER: US/10/242,586
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
```

; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 12
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-586-12

Query Match 52.5%; Score 42; DB 9; Length 424;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YCYCFWK 8
:|:|:|:
Db 302 WCPCFWR 308

RESULT 45
US-10-242-902-12
; Sequence 12, Application US/10242902
; Publication No. US20060073549A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C54
; CURRENT APPLICATION NUMBER: US/10/242,902
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 12
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-902-12

Query Match 52.5%; Score 42; DB 9; Length 424;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YCYCFWK 8
:|:|:|:
Db 302 WCPCFWR 308

RESULT 46
US-10-243-116-12
; Sequence 12, Application US/10243116
; Publication No. US20060073550A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C58
; CURRENT APPLICATION NUMBER: US/10/243,116
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 12
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-116-12

Query Match 52.5%; Score 42; DB 9; Length 424;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YCYCFWK 8
:|:|:|:

Db 302 WCFW 308

RESULT 47

US-10-243-136-12
; Sequence 12, Application US/10243136
; Publication No. US20060074228A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C32

; CURRENT APPLICATION NUMBER: US/10/243,136

; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 12
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-243-136-12

Query Match 52.5%; Score 42; DB 9; Length 424;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YCYCFWK 8

:|:|:|:

Db 302 WCFW 308

RESULT 48

US-10-243-189-12
; Sequence 12, Application US/10243189
; Publication No. US20060074033A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C44

; CURRENT APPLICATION NUMBER: US/10/243,189

; PRIOR FILING DATE: 2002-09-12

; PRIOR APPLICATION NUMBER: 10/197942

; PRIOR FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/059114

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/063046

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/065027

; PRIOR FILING DATE: 1997-11-10

; PRIOR APPLICATION NUMBER: 60/079689

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/086478

; PRIOR FILING DATE: 1998-05-22

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/089801

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/090557

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: 60/090689

; PRIOR FILING DATE: 1998-06-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO 12

; LENGTH: 424

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-243-189-12

Query Match 52.5%; Score 42; DB 9; Length 424;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YCYCFWK 8

:|:|:|:

Db 302 WCFW 308

RESULT 49

US-10-243-215-12
; Sequence 12, Application US/10243215

; Publication No. US20060073551A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Baton, Dan

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Goddard, Audrey

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Phillippe

; APPLICANT: Watanabe, Colin

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; APPLICANT: Fong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3630R1C27

; CURRENT APPLICATION NUMBER: US/10/243,215

; PRIOR FILING DATE: 2002-09-12

; PRIOR APPLICATION NUMBER: 10/197942

; PRIOR FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/059114

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 12
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-215-12

Query Match      52.5%; Score 42; DB 9; Length 424;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YCYCFWK 8
Db      302 WCFCFWR 308

Search completed: May 9, 2006, 12:16:13
Job time : 17 secs
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 12
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-236-12

Query Match      52.5%; Score 42; DB 9; Length 424;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YCYCFWK 8
Db      302 WCFCFWR 308

Search completed: May 9, 2006, 12:16:13
Job time : 17 secs
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
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; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 12
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-215-12

Query Match      52.5%; Score 42; DB 9; Length 424;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YCYCFWK 8
Db      302 WCFCFWR 308

Search completed: May 9, 2006, 12:16:13
Job time : 17 secs
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RESULT 50
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; Sequence 12, Application US/10243236
; Publication No. US20060073552A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C35
; CURRENT APPLICATION NUMBER: US/10/243,236
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
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